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GenCore version 4.5
Copyright (c) 1993 · 2000 - Jumpugen 153.
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OM protein - protein search, using sw model

September 5, 2002, 15,22.15 . Scarch time 58.86 Seconds (without alignments) 3.735 Million cell updates/sec Run on.

US-09-744-804-35 53 Title: Perfect score:

1 KQGNENAWV 9 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Secting tuble:

231628 segs, 24425594 residues Searched:

Total number of bits satisfying chasen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Listing first 45 summaries Maximum Match 100% Post-processing: Minimum Match A%

Database :

Issued\_Patents\_AA:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

		æ			SUMMARIES	· .
Result No.	Score	Query Match	Query Match Length	DB	10	Description
1		1000		74	98-98-162-4028-12	Sequence 12, Appl
. 4	ری دی	100.0			-07 607 5	3, 4
m	53	190.0	717	14		٤,
4	53	100.0	218	٠.	4	c i
5	53	100 0	×	٠.	PS-BB-162-407R-2	۲ì
9	53	100.0	C 85	с.	RS-08-152-402H-6	ç,
۲.	53	100.0	46,0	c .	75-08 162 472R 9	æ
∞	39		359	~;	GS-68-454-554-5	Sequence 2, Appl:
σ	36	73.6	369	'n	PCT-US94 02891.69	63
10	۲. ۳.		3.21	-1	US-08-480-2290 21	-1
11	36	7	321	C a	13 -0583-659-86-86	Sequence 21, Appl
12	36	67.9	480	71	85-88-480-229C 10	10,
13	36	67	4 ∺ ○	٠.	115-08-654-2460-10	10,
14	35	67 9	513	CI	115-08-480-2290-14	_
15	36	6.29	۲. ۳	C 1	115 OR 659-2350 14	++
16	34	64 2	347	٠.	US-08-052 205 7	Sequence 7, April
17	34	64.2	347	_		7
18	34	64.2	36.9		11a-08-045 504 4	-;
19	34	64.2	369	-	118-08-595-974-4	4
0.21	23	62.3	t	-	ď	Sequence 4, Appli
; (-)	(3)	62.3		- 1	-08-121-	4,
C1 C1		62.3		رس	33 NR 448 478.2	c;
C1	C) M	€0.4	157	e a	US 08 162:4028:13	13,
ই	ing imi	60.4	320	٠,	480 LL9C.	707
C 1	(1) (1)	†. . ∩.,	200	٠.	118-08-618-53-C 50	Sequence 20, Appl
ä	3.5	<b>₹</b>	† 0 †	. 1	29 0267-282-80-80	51.0
	-1 (2)	- <del></del>	4	٠,	**************************************	Sequence 9, Appli

100.0%, Score 53, 58.5, Length 159, 100.0%; Pred. No. 0.034;

Query Match Best Local Similarity

STEANDEDNESS: unknown TOPOLOGY: unknown Malford E TYPF papt (de

US 08-162 1028-12

2. US 08 - 487 - 203 A 2 1. US 08 - 487 - 203 A 2 1. US 08 - 487 - 203 A 2 1. US 08 - 694 - 865 - 17 2. US - 08 - 597 - 837 A 3 3. US - 08 - 597 - 837 A 4 1. US - 08 - 597 - 1061 A 4 1. US - 08 - 296 - 791 - 5 1. US - 08 - 296 - 791 - 5 2. US - 08 - 296 - 791 - 5 3. US - 08 - 296 - 791 - 5 4. US - 08 - 296 - 791 - 5 5. US - 08 - 296 - 791 - 5 6. US - 08 - 296 - 791 - 5 6. US - 08 - 296 - 791 - 5 6. US - 08 - 296 - 791 - 5 7. US - 08 - 791 - 5 7. US		7 ·		,	. Kato 300 co 511		
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42					1 0000 000 80 80	G 30000000	, Ap
32 60.4 1334 6 5478657-1 32 60.4 1403 1 08-07-908-253-3 32 60.4 1403 2 08-08-694-865-17 32 60.4 1403 2 08-08-694-865-17 32 60.4 1403 3 08-08-694-865-17 32 60.4 1541 5 PCT-US95-10661A-3 34 60.4 1545 5 PCT-US95-0661A-4 35 60.4 1745 4 08-08-296-791-8 36 60.4 1702 4 08-08-296-791-5 37 58.5 107 2 08-08-49-609-4		£.0.4	1121	٠.	US 08-487-203A-2		Ας.
32 60.4 1403 1 0S-07-908-253-3 32 60.4 1403 2 0S-08-694 865-17 32 60.4 1403 3 0S-09-124 4917-3 32 60.4 1541 4 0S-09-124 4917-3 32 60.4 1545 5 PCT-0895-10661A-3 32 60.4 1545 5 PCT-0895-10661A-4 32 60.4 1545 5 PCT-0895-10661A-4 32 60.4 1702 4 0S-08-296-791-5 33 60.4 1702 5 PCT-0895-10661A-5 34 60.4 1702 5 PCT-0895-10661A-5 35 60.4 1702 5 PCT-0895-10661A-5 31 58.5 107 2 0S-08-449-609-4		70.0	1 6.0	(C)	5476657-1		5476657
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32 60.4 1463 2 05.98.537 827 3 32 60.4 1403 3 05.09.124 491-17 32 60.4 1541 5 PCT-0S95-10661A-3 32 60.4 1545 4 DCT-0S95-10661A-3 32 60.4 1545 5 PCT-0S95-10661A-4 32 60.4 1545 5 PCT-0S95-10641A-4 32 60.4 1702 4 05.98-251-0641A-5 33 58.5 1702 5 PCT-0S95-1061A-5 31 58.5 1702 5 PCT-0S95-1061A-5 31 58.5 1702 5 PCT-0S95-1061A-5 31 58.5 107 2 05.08-449-609-4		4.00	1403	10	US-08-694-865-17		17. Appl
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22 6.0 4 1541 4 18:08-596-791 3 3 60.4 1541 5 PCI-0859-1061A-3 3 60.4 1545 5 PCI-08595-1061A-4 3 60.4 1545 5 PCI-0895-1064A-4 3 60.4 1702 4 08-08-596-791-5 3 60.4 1702 5 PCI-0895-1064A-5 3 58.5 107 2 08-08-449-609-4 5 107 2 08-08-449-609-4		50.4	1403	(*)	US-09-124-491-17		17, Appl
32 60.4 1541 5 PCT-US95-10661A-3 32 60.4 1545 4 US-08-296-791-4 32 60.4 1762 4 US-08-296-791-5 32 60.4 1702 4 US-08-296-791-5 34 60.4 1702 5 PCT-US95-10604A-5 31 58-5 107 2 US-08-449-609-4 31 58-5 107 2 US-08-449-609-4		f, O ,	177	₹:	NS+08+296,741 3		3, Appli
32 60.4 1545 4 US-08-296-791-4 32 60.4 1545 5 PCT-US95-10661A-4 32 60.4 1702 4 US-08-296-791-5 32 60.4 1702 5 PCT-US95-10661A-5 31 58.5 107 2 US-08-449-609-4	3.2	50.4	1541	m	PCT-US95-10661A:3		
32 60.4 1545 5 PCT-US95-10661A-4 32 60.4 1702 4 US-08-296-791-5 32 60.4 1702 5 PCT-US95-10661A-5 31 58.5 107 1 US-08-049-4 31 58.5 107 2 US-08-449-609-4	2	50.4	1545	~	US-08-296-791-4	Sequence 4	~
32 60.4 1702 4 0S-08-296-791-5 32 60.4 1702 5 PCT-0895-1061A-5 31 58.5 170 103 08-036-210-4 31 58.5 107 2 0S-08-449-609-4	3.2	50.4	1545	ഗ	PCT-US95-10661A-4	Sequence 4	
32 60.4 1702 5 PCT-US95-10661A-5 31 58.5 107 1 US 08:036:210:4 31 58.5 107 2 US-08-449-609-4	3.2	£.03	1702	₽	US-08-296-791-5	Sequence 5	i, Appli
31 58.5 107 1 05 08·036·210·4 31 58.5 107 2 05·08·449·609·4	32	60.4	1702	'n	PCT-US95-10661A-5	Sequence 5	i, Appli
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	3.1	58.5	107	~	- 1	Sugarner 4	
31 58.5 159 2 US 08 162 402B 16	3.1	0.80	159	C4	US 08 162 402B 16	~-1	w)

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MARKAL TWFORMATION.
APPLICANT: CERIANI, ROBERTO L.
APPLICANT: PETERSON, JERRY A.
ALFLICANT: (AFGECA, FAVIS J.
ALTLE, A. HUVLET: N. 41, ELALICH HUMAN MILE FAT
TITLE, A. HUVLET: N. 41, ELALICH HUMAN MILE FAT
TITLE, A. HUVLETICN.
ATHER OF SPOUENCES. 29
                                                                                                                                                                                                                                                                                                                       COMPUTER. 1BM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASISED for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                 DEFENSION RUNNERS STREETS & Poplawski STREET: 444 South Flower St., 19th Floor
                                                                                                                                                                                                                                                                                                                                                                                                   ALTLOATION NUMBER, 05,04,102,402B
FILING LALE, 03-050 1333
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ERFERINGE/FOCKUT NUMBER: 1166 38215
TELECOMMUNICATION INFORMATION:
THIFFHOME: 214.602 7709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30,930
                                                                                                                                                                                                                                                                                                      3: Diskette
IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY AGENT INFORMATION:
NAME, Amach, Viviana
PECISTRATION HIMBER: 30,9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          i: 159 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOSEPH 213-489-4210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NOT SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                             STREET: 444 South
CITY: Los Angeles
                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE.
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                                                                                                                                                                                                                        CA
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APPLICANT: PETPRSON, JERRY A.
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                                                                                                                                                                                                                              Diskette
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Amzel, Viviana
PEGISTRATION NUMBER:
                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide
                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Walnut Creek
STAIE: California
                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                          Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
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                                                                                                                                                                           USA
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                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                            90071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE:
                                                                                                                                                                                                                                               COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
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US-07-607-538C-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX:
                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
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                                                                                                                                                                                                                                                 DAVIO J.

POLYPEPTIDE WITH 46

DIFFRENTIATION ANTIGEN RINGING SEPCIFITY AND CLEILING FACTORS V AND VIII LIGHT-CHAIN HOMOLOGIES,
FUSTON PROTEIN, POLYNICLEGIES AND PITYPIEGE WITH PROFIDE ENCODING THE POLYPERING ANTI-
O; Gaps
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O; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
O; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                    5455031th Broadway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PC-DUS/MS-DUS 5.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: CRFCC-004
TELECOMMENICATION INFORMATION:
                                                                                                                                                                                                         APPLICANT: Ceriani Dr., Roberto L. APPLICANT: Peterson Dr., Jerry A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 3, Application US, nels 24 mgg ; Patent No. 5972337
                                                                                                                                                       ; Sequence 3, Application US/07607538C
; Patent No. 5455031
                                                                                                                                                                                                                                                                                                                                                                    USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                       Amzel & Assoc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: CERIANI, ROBERTO L.
                                                                                                                                                                                                                                           Larocca, David J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (510) 943-1931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01 NCV 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (510) 545
met EFAX: (510) 943-1189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 217 amino acids
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9; Conservative
                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: POI
TITLE OF INVENTION: USI
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER PEADABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Viviana Amzel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Walnut Creek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Calitornia
                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                    2055 No.
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                                                                                                                                                                                                                                                            TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
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                                                                                                                                                                                          GENERAL INFORMATION:
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                                1 KOGNFNAWV 9
                                                                 43 KOGNFNAWV 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILLING DATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94596
                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                       US -07 -607 -538C-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-07-607-538C-3
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                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Matches
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                                                                                                                        RESULT
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APPLICANT: Ceriani Dr., Roberto L.
APPLICANT: Latocca, David J.
APFLICANT: Latocca, David J.
TITLE OF INVENTION: PREFERENTIATION ANTIGEN HINDING SPECIFITY AND CLOTTING TITLE OF INVENTION: FACTORS V AND VII LIGHT-CHAIN HOMOLOGIES, TITLE OF INVENTION: POSION PROFIEM.
TITLE OF INVENTION: PUSION PROFIEM.
POLYMOCLECTIDE AND POLYRIBO-
TITLE OF INVENTION: NUCLECTIDE ENCODING THE POLYPEPTIDE, ANTI-
APPLICANT: IARGCCA, DAVID J.
TITLE OF INVENTION: 46 KDALION HUMAN MILK FAF
TITLE OF INVENTION: GLOHULF (HMFS) ANTIGEN, FRAGMENTS & PUSION PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUSION PROTEIN, POLYMUCLEOTIDE AND POLYKING NUCLEOTIDE ENCODING THE POLYPEPTIDE, ANTI-POLYPEPTIDE ANTIFOLYPEPTIDE ANTIFOLYPEPTIDE ANTIFOLYPEPTIDE ANTIFOLYPEPTIDE ANTIFOLYPEPTIDE ANTIFOLYPEPTIDE ANTIFOLYPEPTIDE ANTIFOLYPE
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100.0%; Pred. No. 0.047;
Live 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: DOS
SÖFTWARE. FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                        ADDRESSEE: Pretty, Schroeder & Poplawski
STREET: 444 South Flower St., 19th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..... DATE: 03-DEC-1093
CLASSIFICATION: 435
APPLICATION: 435
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Patent No. 5455031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30,930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                              IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
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0

Gaps

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APPLICANT: CEKTANI, KOBERTO L.
APPLICANT: PETERSON, JERRY A.
APPLICANT: LAKOCCA, DAVID J.
TITLE OF INVENTION: 46 KDATICH HUMAN MILK FAT
TITLE OF INVENTION: GLORUE (HMPG) ANTIGEN, FRAGMENTS 6 FUSION PROTEIN
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100.0%; Prod No 0.084;
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Best Local Similarity 100.0%; Prod. No. 0.047;
Matches 9, Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: FastSEO for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/7162,402B
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STREET: 444 South Flower St., 19th Floor
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REPERENCE/DOCKET NUMBER: P66 38215
TELECOMMUNICATION INFORMATION:
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; Patent No. 5972337
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MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
                                                         INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-DEC-1993
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TELEPAX: 213-489-4210
TELEPHONE: 213-622-7700
TELEFAX: 213-489-4210
                                                                                               218 amino acids
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                                                                             SEQUENCE CHARACTERISTICS:
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                                                                                                                                                    TOPOLOGY: unknown
MOLECULE TYPE: peptide
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PRIOR APPLICATION DATA:
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                                                                                                                  TYPE: amino acid
STRANDEDNESS: unk
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es 9, Conserva
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                                                                                             LENGTH:
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APPLICANT: PETERSON, JERRY A.
APPLICANT: PAROCCA, DAVID J.
ATTILE OF INVENTION: 46 KDALITON HUMAN MILK FAT
TITLE OF INVENTION: GLOBULE (HMFG) ANTIGEN, FRAGMENTS & FUSION PROTEIN
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
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                                                                                           SOFTWAPF PatentIn Pelease #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/607,538c
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444 South Flower St., 19th Floor
                                                     COMPUTER: THM PC_COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
                                                                                                                        UMBER: US/07/607,538C
01-NOV-1990
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TELECOMMUNICATION INPORMATION:
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FILING DATE: 03-DEC-1993
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Patent No. 5972337
                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel
REGISTRATION NUMBER: 30,930
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MEDIUM TYPE: Diskette
COMPUTER: IRM Compatible
                                      MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                         (510) 943-193
(510) 943-1189
                                                                                                                                                                                                                                                                                                                                                                                         218 amino acids
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REGISTRATION NUMBER: 30
REFERENCE/TWINET NUMHER-
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MOLECULE TYPE: protein
FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                               single
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                COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: sin
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es 9: Conserv
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                                                                                                                                                    FILING DATE: 01
CLASSIFICATION:
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CLASSIFICATION:
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ZIP: 90071
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Gaps

us-09-744-804-35.rai

ADDRESSEE: MORGAN & FINNEGAN

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APPLICANT: CERTANI, ROBERTO I.,
APPLICANT: PETERSON, JERRY A.
APPLICANT: LAROCCA, DAVID J.
TITLE OF INVENTION: 46 KDALTON HUMAN MILK PAT
TITLE OF INVENTION: 41 PRICE (HMPG.) ANTIGEN, PPAGMPNIES & FUSION PROTEIN
NUMBER OF SEQUENCES: 29
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SOFTWARE: FASLSEQ for Windows Vorsion 2 0
CURRENT APPLICATION DATA:
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TITLE OF INVENTION: MURINE IL-2R CDNA AND
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                 E. Pretty, Schroeder & Poplawski
444 South Flower St., 19th Floor
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FILING DATE: 03-DEC-1993
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                                                                                                                               Sequence 8, Application US/08162402B
Patent No. 5972337
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Viviana
30,930
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TELEPHONE: 213-622-7700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY / AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 213-489-4210
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PKIOR APPLICATION DATA:
APPLICATION NUMBER:
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Best Local Similarity
                     271 KQGNFNAWV 279
                                                                                                                                                                  GENERAL INFORMATION:
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1 KUGNFNAWV 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Amzel
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                                                                                                                                                                                                                                                                                                                                                                       CA
                                                                                                                                                                                                                                                                                                                                                                                                               90671
                                                                                                           US 08 · 162 - 402B · 8
                                                                                                                                                                                                                                                                                                                   ADDRESSEE.
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                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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                                                                                                                                                                                                                                                                                                                                         STREET:
                                                                                                                                                                                                                                                                                                                                                                           STATE:
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                                                                                                                                                   Patient No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                         RESULT
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APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS APPLICANT. REPRESENTED BY THE SECRETARY, DEPARTMENT OF HEALTH AND HUMAN APPLICANT: SERVICES
APPLICANT: GFFLEE OF TECHNOLOGY TPANSFER, NATIONAL
APPLICANT: INSTITUTES OF HEALTH, BOX OTT, BETHESDA, MARYLAND 20892 USA TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND TREATMENT OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73.5%; Score 39; DB 2; Length 369; 85.7%; Fred. No. 26, tive 1, Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                      2026-4061US1
                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/424,224
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; GENERAL INFORMATION:
                                                                                                                                                              SYSTEM: PC-DOS/MS-DOS WORD PERFECT # 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WORD PERFECT # 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                           IBM FC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                              NAME: WILLIAM S. FEILER
PEGISTRATION NUMBER: 26,728
REPERENCE/POOTKET NUMBER: 202
                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
TELEX: 421792
                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
ARFLICATION NUMBER: 38/121
FILING DATE: 14-SEPT-1993
A.IOKNEY/AGENT INFORMATION:
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INDIVIDUAL ISOLATE: IL-2R
                                                                                                                      FLOPPY DISK
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Matches 6, Conservative
                                                                                                                                                                                                  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
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345 PARK AVE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DESCRIPTION: PROTEIN
                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: FLOPPY |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: FLOPPY I
                                                                                                                                                                                                                                                           CLASSIFICATION: 800
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                                                                                                                                                              OPERATING SYSTEM:
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                                          NEW YORK
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STATE: NEW YORK
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                       NEW YORK
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                                                             USA
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                                                                              10154
                                                                                                                                                                                                                                            FILING DATE
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                                                                                                                                           COMPUTER.
                                                                                                                                                                                   SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE:
                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY
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STREET:
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APPLICANT: Hogan, Brigid
APPLICANT: Snodgrass, H. Ralph
APPLICANT: Zupancie, Thomas J.
TITLE OF HAVENTION: DEVELOPMENTALLY-REGULATED ENDOTHERIAL
TITLE OF HAVENTION: CELL LOCUS-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67.9%; Score 36; 198-2; Length 321; 75.0%; Pred. No. 56;
                                                                                                                                                                                                                                                                                                                                                                             67.9%; Score 65; DB 2; Length 921; 75.0%; Pred. No. 56;
tire 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
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Patent No. 5877281
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TELEX: 66141 Pennie
INFOPMATION FOR SEQ ID NO: 21:
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IBM PC compatible
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                           TELEX: (514; wf.ewet.774
TELEX: 66141 Pennie
INFORMATION FOR SEQ. ID NO: 21:
SEQUENCE CHARACTERISTICS:
      (212) 790-9090
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JN: 435
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amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            United States
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Best Local Similarity 75.0
Matches 6; Conservative
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                                                                                                                                                                                                                                  TOPOLOGY: unknown
MOLECULE TYPE: protein
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
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MOLECULE TYPE: protein
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CORRESPONDENCE ADDRESS:
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FILING DATE: 05 JUN
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Hest Local Similarity 7
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OPERATING SYSTEM:
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                                                                                                                                                                                                       STRANDEDNESS:
         TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE
                                                                                                                                                                                                                                                                                            US-08-480-229C-21
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                                                                                                                                                    LENGIH:
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APPLICANT: Hogan, Brigda
APPLICANT: Hogan, Brigda
APPLICANT: Supancie, Thomas J.
TILLE OF INVENTION: DEVELOPMENTALLY *REGULATED ENDOTHELIAL
TITLE OF INVENTION: CELL LOCUS-1
NUMBER OF SEQUENCES: 29
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1155 Avenue of the Americas
                              por med 462893
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                                                                                                                                                                      FILING DATE: 12-MAR-1993
APPLICATION NUMBER: 08/121,435
                                                                                                                                                 08/031,143
                                                                                                                                                                                                                                                                                                                 REFERENCE, 100 NUMBER: 26,728
TESCOMMINTO A TAXALLE
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COMPUTER: IBM PC compatible
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REFERENCE/DOCKET NUMBER: 890
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                  FILING DATE: 14-SEPT-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: MURINE INDIVIDUAL ISOLATE: IL-2R
                                                                                                                                                                                                                                                                                                                                                                                                        212-758-4800
212-751-6849
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COUNTRY: United States
ZIP: 10036 2711
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INFOHMATION FOR SEQ ID NO:
SEQUENCE CHAPACTERISTICS:
CURPENT APPLICATION DATA:
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MEDIUM TYPE: Floppy of
                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DESCRIPTION: PROTEIN
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                              APPLICATION NUMBER.
                                                                                                                                                 APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UNKNOMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: AMINO ACID
TOPOLOGY: UNKNOWN
                                                                                                                                                                                                                                                                                            WILLIAM S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          304 QGNFSAW 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 QGNFNAW 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL:
                                                               FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDPESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCT-US94-02891-69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-480-229C-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE:
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CITY: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                              Patent No. 5874504

GENERAL INFORMATION:
APPLICANT: Quericemous, Thomas
APPLICANT: Bodgrass, H. Ralph
APPLICANT: Snodgrass, H. Ralph
APPLICANT: Snodgrass, H. Ralph
APPLICANT: Suparcic, Thomas J.
TITLE OF INVENTION: DEVELOPMENTALLY-REGULATED ENDOTHELIAL
TITLE OF INVENTION: Cal. LOCUS-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Quertermous, Thomas
APPLICANT: Hogan. Rrigid
APPLICANT: Bodarss, H. Ralph
APPLICANT: Snodyrass, H. Ralph
APPLICANT: Snodyrass, H. Ralph
TITLE OF INVENTION: DEVELOPMENTALLY-REGULATED ENDOTHELIAL
TITLE OF INVENTION: CELL LOCUS-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67.9%; Score 36; DB 2; Length 480; 75.0%; Pred. No. 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patentin Pelease #1 0, Version #1 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                              1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/480,229C
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC DOS/MS-DOS
                                                                                             US-08-480-229C-10
; Sequence 10, Application US/08480229C
; Patent No. 5874562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 10, Application US/UR6592350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (212) 869-8864/9741
TELEX: 66141 Pennie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 28,462
REFERENCE, THOMPRE: 890
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTOPNEY/AGENT INFOPMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Poissant, Brian M. REGISTRATION NUMBER: 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 480 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: United States ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Molecule TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
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360 KOGKVNAW 367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patient No. 5877281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-480-229C 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
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                                                                                                                                                                                                                                                                                                                                                                                               STATE:
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                                                                             RESULT
                9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67.9%; Score 36; DB 2; Length 480; 75.0%; Pred. No. 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Indels
                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/659,235C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATORS OF STEEM: PC-DOS/MS-DOS
SOFTWAPE: Patentin Pelease #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                     NAME: Poissant, Brian M.
Pristantion of Advantage Pristantion of Advantage Predection of Advantage of Advantage of TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Poissant, Brian M. ERGISTANTION WINDER: 28,462
PEFERENCE/POORET NUMBER: 8907-0026-999
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 МНЕК — PS,708,7480,229C
07-JUN-1995
                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC COMPATIBLE
OPERATING SYSTEM: PC:00S/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 14, Application US/U8480229C; Patent No. 5874562
; General inFORMATION;
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APPLICANT: Hodan, Brigid
APPLICANT: Snodgress, H. Kalph
APPLICANT: Zupancic, Thomas J.
                                                                                                                                                                                                                                                                                                                                                       (212) 790-9090
(212) 869-886479741
                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 66141 Pennie
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                       05-JUN-1996
                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                480 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA: APPLICATION NUMBER: US,
               United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: New York
COUNTRY: United States
ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER PEADARLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
New York
                                     10036-2711
                                                                                                                                                                                                         FILING DATE: 05 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       360 KOGKVNAW 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 KQGNFNAW 8
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                                                                                                                                                                                                                                                                                                                                                            TEL PPHONE
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; Sequence 14, App
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                             TELEFAX:
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(212) 790-9090

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Quertermous, Thomas
APPLICANT: Quertermous, Thomas
APPLICANT: Bogan, Brigid
APPLICANT: Snodarass, H. Ralph
APPLICANT: Lagarcic, Thomas J.
TITLE OF INVENTION: DEVELOPMENTALLY-REGULATED ENDOTHELIAI,
TITLE OF INVENTION: CELL LOCUS-1
NUMBER OF SEQUENCES: 29
COPRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                    Ouery Match 67.9%; Score 36; DB 2; Length 513; Best Local Similarity 75.0%; Pred. No. 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 67.9%; Score 36, DB 2, Length 513; Best Local Similarity 75.0%; Pred. No. 89; Astrhes 6; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 10036-2/11
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LHM PC compatible
COMERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 28,462
REFERENCE/LUGCKET NUMBER: 8907-0034-999
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 14, Application US/08659235C
; Patent No. 5877281
; GENERAL INFORMATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (212) 869-8864/9741
TELEX: 66141 Pennie
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
    (212) 869 8864/9741
TELEFAX: (212) 969 8864/978
TELEX: 66141 Pennie
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 05-JUN-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                        513 amino arids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Poissant, Brian M. REGISTRATION NUMBER: 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGIH: 513 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: New York COUNTRY: United States ZIP: 10036-2711
                                                                                                                                                                                                                                                                                            6; Conservative
                                                                                                                               unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unknown
                                                                                                                                             ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-480-229C-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: protein US-08-659-235C-14
                                                                                                       amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
                                                                                                                                                                                                                                                                                                                                                                             393 KQGKVNAW 400
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                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                        1 KOGNFNAW 8
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                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                              Matches
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1 KQCNFNAW 8

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Db 393 KOGKVNAW 400
Scarch completed: September 5, 2002, 15:27:33
Job time: 318 sec
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GenCore version 4.5
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OM protein - protein search, using sw model

(without alignments) 6.310 Million cell updates/sec Search time 158,43 Storals September 5, 2002, 15 20 20 , Kun on

US-09-744-804-35 53 1 KOCNFNAWV 9 Title: Perfect score Segmenton

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

747574 scqs, 111073796 residues Searched:

Total number of hits satistying chosen parameters

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Listing first 45 summaries Maximum Mat.ch 100% Post-processing: Minimum Match 0%

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[81158] Andara Alodd grossing decreasing septiments of the control of the cont

		Description	Lactadherin (BA-46	HMFG 46 kDa antige	HMRTS 46 NIVE GET LIGHT	HMFG 46 kDa antige	Human lactadherin	Bos taurus interle	Murine IL-2R gamma	Novel human diagno	Novel human diagno	Human brain expres	Human secreted pro
SUMMARIES		ID	AAY82840	AAR77253	AAF77254	AAR77252	AAY94454	AAB71682	AAP59044	APGLUSSES	ARG24996	AAMSSEES	AAB65971
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	or c	Σ K	10	10	10	10	10	Ĺ	7	7	7	Œ.	Ġ.
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AAB04058 AAB71691 AAB04607	AAR04066	AAB23543	AAR04073	AAY ?1810	AAn71581	AAW10364	AAW94683	AAW10365	AAW94685	AAM31946	AA002690	ABC05534	AAC19948	AAC43823	AAC44223	AAC40737	AAG13822	AAG44222	AAG52356	AAC52355	AAG49736	AAG43821	AAC44221	AAW00650	AAM78980	ABGCCCCC	AAM79964	AKM21 HIGH	AAV15-2-54	AN14 .7 **	ABRA7578
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0.07	15	16	13	18	S.F.	20	7.1	C1	53	7.4	ci in	97	7;	80	59	3.0	31	Ç	33	34	÷.	36	3.7	38	36	40	4.1	÷.,		••	4 ጉ

## ALIGNMENTS

AAY#2840 standard; peptide; 9 AA. AAYMZM40; AAY 8 2 8 4 0 RESULT

19-JUN-2000 (first entry)

Lariadherris (BA 45) peptido traggest (fumour associated astigen).

Leadurent, prevention, ours, and tumour varions metastases, busis bases, prestain garanas, eng. hyp.il, volon, stomach, carethona, MHC Class I; HLA-A2; human. Tunnut associated antigen peptide, IAA, cancer, carcinoMa; 

teratonarninoma derived growth factor, PSA, PSMA, PAP, CRIPT>-1. Major Histocompatibility Complex; uroplakin; prostate specific antigen; prostate specific membrane antiqen; prostate acid phosphatase, mucin, lactadherin;

Homo sapiens.

W0200006723-A1.

10 FEB-2000.

99W - 1100417. 16061-11... 160 9811.-0125608. 30-301-1998; (YEDA ) YEDA BES & DEV CO LID. (BLOT ) BIO-TECHNOLOGY GEN CORP.

Carmon L, Tirosh P, Bar haim D, Fan A, Fridkin M; Fitzer attus C, Elsenbach L.

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used in assays to determine the presence of a cancerous tumour of
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                                                                                                                                                                                                                                                         Tunnour associated antique peptides (TAA) may be used for the treatment, prevention and cure of educer or cancer metastasses. The cancer may be breast, bladder, prostate, parotess, ovary, thyroid, colon, stomach, head or neck cancer or a carcinoma. The tunnous associated antiques are presentable to the immune system by HtA-A2 molecules and are qenerally between 8 to 10 amino acids in length. The amino acids in length antiques are the anchor residues which participate in the binding to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MRC class I molecules, more specifically HLA-A2. More tunnour associated anniques are described in GNBESD records AAV828B6-Y82B82. Those tunnour associated autipens described in records AAV82B66-Y8ZB42 and AAV82RF5 YY8ZH69 are derived from Groplakin, such as Uroplakin II, Uroplakin il and Uroplakin, such as Uroplakin II records AAV8ZB55-Y8ZB29 are derived from prostate specific antigen (PSA). Those described in records AAV8ZB35 are derived from from the control of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 prostate specific membrane antigen (PSMA). Those described in records YY82836-AAY82839 are derived from prostate acid phosphotase (PAP). Those described in records AAY82840-Y82846 are derived from Lactadherin (BA-46). Those described in records AAY82847-Y82854 are derived from Much and those described in records AAY82871-Y82864 are derived from Teratocarcinoma derived growth factor (CRIPTO-1).
                                                                                        Tumor associated antigen peptides, especially derived from uroplakin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                    useful as vaccines to prevent or cure cancers including breast, bladder, prostate, parereas, ovary, thyroid, colon and stomach.
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                                                                                                                                                                                                       Claim 17; Page 99; 113pp; English.
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Best Local Similarity
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HMFG; haman milk fat globale, antiqen, jamunoqen, vaccine; viruelde;
epithelium; tumor; breast cancer, menoclenal antibody; MAb.
                                                           A partial cDNA clone BA46 i (AAQ91199) for the 46 kDa HMFG antiqen, a major component of the apical surface of the normal breast epithelial cell, was obtained by PVF of cDNA from a lactating breast cDNA library. The C-terminal region of the encoded protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A partial cDNA clone 6A46:1 (AAV)179) for the 46 kDa HMFG antiqen, a major component of the apical surface of the normal breast epithelial cell, was obtained by PCR of cDNA from a lactating
                                                                                                                breast cDNA library. The C-terminal region of the encoded profein showed 43% identify to corresp regions of human Factor-V and 38%
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                                                                                                                                                                                                                                                                  0;
epithelial origin, and in a vaccine against neoplastic tumours
                                                                                                                                                                                                                               199.9%, Serry 63; 198.16; tongth 217; 100.0%, pred No. 0.12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HMFG 46 kDa antigen partial sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 7; Page 38-40; 68pp; English.
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                            Claim 7; Page 41; 68pp; Enqlish.
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Fest foral Similarity Tuo
Fest foral 9; Conservative
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Homo sapiens
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 AAY94453;
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                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A complete cDNA sequence for the 46 kba HMFS antique, a Hajor component of the apical surface of the normal breast epithelial cell, was obtained by PCR and RACE methods. cDNA choise can be used to prepare MADS for use in immunotherapy, immunohistopathology, prognosis, diagnosis, imaging and therapy. Recombinant antigen can be extressed in probabilities of (11%-cs)lated) in cubalyctic cells.
                                                                                                                                                                                                                                                                                                                                                                                                                    46 KD apparent molecular weight human milk fat globule antigen used in assays to determine the presence of a cancerous Lumour of epithelial origin, and in a vaccine against neoplastic tumours
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                                          100.0%; Score 53; DB 16; Length 218; 100.0%; Pred. No. 0.12; ive 0; Mismatches 0; Indels
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100.0%; Pred No 0.20;
Live 0; Mismatches 0; Indels (
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ches 0; Indels
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                                                                                                                                                 AAR77252 standard; Protein; 387 AA.
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                                 Query Match
Best Local Similarity 100.vv..
9; Conservative
                                                                                                                                                                                                                                                                                                                                   93US-0162402,
                                                                                                                                                                                                                                                                                                                 04M0-11913967
                                                                                                                                                                                        (first entry)
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Best Loral Similarity 10g.,
9, Conservative
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breast cDNA library.
                                                                                                                                                                                                         HMFG 46 kDa antigen.
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                                                                                                   102 kggnfnawy 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              387 AA;
                  218 AA,
                                                                                 1 KOGNFNAWV 9
                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAQ91198.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 KQGNFNAWV 9
                                                                                                                                                                                                                                                                                                               05-DEC-1994;
                                                                                                                                                                                                                                                                                                                                  03-DEC-1993;
                                                                                                                                                                                       21-NOV-1995
                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                           WO9515171-A.
                                                                                                                                                                                                                                                                                                                                                                        Ceriani PL,
                  Sednence
                                                                                                                                                                   AAR77252;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                4
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                                                                                                                                       AAR77252
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Lactadherin protein was found in exceemes produced by dendritic cells. The protein is involved in the playertisis of particulate antiques by dendritic cells. Exceedes produced by dendritic cells capacity the common antiques increased in the mediation of an immune response. Lactadherin or variants of it may be used in the mediation of an immune response. Variants of lactadherin may be used for inhibition and/or simulation of the cross primity of antiques and stimulation of the playerytosis of antiques by dendritic cells, compositions derived from lactadherin can also be used to mention and immune, response, mere specifically a CTL (crucial Tipplayerte) response and also to produce CTLs specific for a selected antique. The present sequence is the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chimeric isolated (haman) lactadherin polypoptide that functions as an adaptor of cross-priming to eliminate pathogenic antiqens, e.g. in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                155.56, a.e.e.53, 56.51, Length 387;
100.0%; Pred. No. 0.22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                        Human; lactadherin; MGF-E8; anti-tumour; immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (INNM ) INSURM INST NAT SANTE & RECH MEDICALE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label- Integrin_binding_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                          /label= Secretion_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bos taurus interleukin-2 receptor gamma.
                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                          24..387
/label= Lactadherin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 3; Page 12; 20pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB71682 standard; protein; 363 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98EF-0402925.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98EP-0402925.
11 SEP 2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-MAY-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            west Match
Bost Local Similarity 100.0
Enc. 9, Conservative
                                                                    Human lactadherin protein.
                                                                                                                                                                            exosome; dendritic cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46..48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-352597/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lactadherin protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CURI-) INST CURIE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     271 kaganinawa 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            387 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 KOGNFNAWV 9
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                                                                                                                                                                                                                                                                     New nucleic acid molecule encoding a human cytokine receptor common qamma chain like polypeptide, useful for treating, preventing and/or diagnosing e.g. tumors, inflammatory diseases and immunodeficiency
                                                                                                                                                                                                                                                                                                                                                            The present invention relates to a human cytokine receptor common gamma chain like protein (CRCGCL). The invention is useful for treating, preventing and/or diagnosing conditions such
                                                                                                                                                                                                                                                                                                                                                                                                      as tumours, infections, inflammatory discasses, immune discreters, neurodesfererative disorder and cardiovascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Murine 11.2-R gamma; X-linked severe combined immunodeficiency; XSCID; interleukin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73.6%; score 39; DB 22; Length 363;
85.7%; Pred. No. 59;
          Cytokine receptor common gamma chain like, CRCCCL; human;
tumours; infections; inflammatory; immune disorder;
neurodegenerative; cardiovascular; disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note- "Coresponding codon CAG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glabel - M glycosylation_site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR59094 standard; Protein; 369 AA.
                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 2; 28gpp; English.
                                                                                                                                                                                                                      Moore PA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ä
                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                          17 - AUG-2000; 2000W0-US22493.
                                                                                                                                                                    9903-0376430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-MAY-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   258..284
                                                                                                                                                                                                                     Ruben SA, Rosen CA,
                                                                                                                                                                                                                                              WPI; 2001-147547/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Guery Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Murine IL-28 gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 363 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301 qqnfsaw 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mise-difference
                                                                                       W0200112672 A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 CCNFNAW 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                    18-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
                                                                                                                 22-FEB-2001.
                                                                                                                                                                                                                                                                                                                                                                                                       as tumours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR59094;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pept, i de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
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Human, chromosome mapping, gene mapping, gene therapy, forensic; food supplement, medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                             AA271977 is the DNA sequence of murine IL-2R gamma AAR54094, this was used in the development of a claimed method for the diagnosis of X linked severe combined immunodeficiency (XSCID), in female carriers and male sufferers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ं
                                                                                                                                                                                                                                                                                         Diagnosis of X-linked severe combined immunodeficiency (XSCID) comprises detecting mutated 11.2R gamma gene, also vectors and transgenic animals containing the mutated gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                         73.6%; Score 39; DH 15; Length 369;
85.7%; Pred. No. 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ċ,
        /label- N-glycosylation_site
96..98
/label- N-glycosylation_site
                                           159.161
/label N-glycosylation_site
255.257
/label N-glycosylation_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1, Mismatches
                                                                                                                                                                                                           (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel human diagnostic protein #29541.
                                                                                                                                                                                                                                  Leonard WJ, Mcbride WO, Noguchi M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABG29550 standard; Protein; 673 AA
                                                                                                                                                                                                                                                                                                                                        Example 1; Fig 7; 98pp; English.
                                                                                                                                                                        93US-0031143.
93US-0121435.
                                                                                                                                                 94WO-USU2891.
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23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6, Conservative
                                                                                                                                                                                                                                                       WPI; 1994-303046/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 369 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HYSE-) HYSEQ INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 QGNFNAW 8
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Modified-site
                      Modified-site
                                             Modified-site
                                                                  Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                        12-MAR-1993;
14-SEP-1993;
                                                                                                                                                  10-MAR-1994;
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                                                                                                     WC9420641-A.
                                                                                                                           15 SEF-1994.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               œ
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.. © Drmanac RT, Liu C, Tang YT;

WPI: 2001-6:9362/73.

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                                                                                                                                                                                                                                                                                                                                             polynorby did, sire also used in diamostics as expressed sequence tags for identifying expressed genes. (1) is useful in gene therapy techniques to restore memory activity ( (11) or to treat disease states in defini
                                                                                                                                                                                                                                                                                                                                                                                                                               quantifating a polypeptide in tissue, as molecular weight markers and as a food supplement. (I) and its binding pathers are aserui in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful in traditional expression of binding about the polymerical expression of binding activity. The polypeptide and polymerical sequences have applications in diagnostics, forensies, gene mapping, identification of metalicus responsible for genetic disorders or other traits to assess binding-its it.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diagnostic amino acid sequences of the invention.
Note: The sequence data for this patent did not appear in the printed
specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                      to restore [nerin_d] axivity ( (11) or to treat discuss states incolving (11) . (11) is useful for generating antibodies against it, detecting or
                                                                                                                                                                                                                                                             The invertion is lates to isolated polymacheotide (i) and polypeptide (ii) sequences. (I) is eastful as hybridisation probes, polymerase chain reaction (PCR) primers, olipomers, and for chromosome and gene mapping, and in recombinant production of (ii). The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6: Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and to produce other types of data and products dependent on DNA and amino acid sequences. ABG0010-ABG30377 represent novel human
                                                                                                                  New isolated polymorlantida and emoded polymphidus, useful in
diagnostics, forensics, gene mapping, identification of mutations
responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human: chromosome mapping; gene mapping, gene therapy, forensie, food supplement, medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 38; DB 22; Length 673;
Pred. No. 1.7e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
                                                                                                                                                                                                                          Claim 20; SEQ ID No 59909; 104pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABG24996 standard; Protein; 1087 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71.78;
85.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAP-2001; 2001W0-4508631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-MAR-2000; 20000S-0540217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Conservative
                   Drmanac RT, Liu C,
                                                        2001 639302,73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 673 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             432 gntsawv 438
                                                                             N-PSDB; AAS93737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 GNFNAWV 9
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                                                                                                                                                                                   biodiversity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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The invention relates to isolated polynucleotide (1) and polynectide (1) sequences. (1) is useful as hybridisation probes, polynectide (1) sequences. (1) is useful as hybridisation probes.

Delynectide thain reaction (EEE) primers, cliquents, and tear characteristic dark quantities are also used in diagnostics as expressed sequence tags. Or identifying expressed areases. (1) is useful in quentificates in the continuous to restore normal activity of (1) or to treat dark prepetide in tissue, as molecular weight marities involving quantitating a polypeptide in tissue, as molecular are useful in medical imaging of sites expression (11). (1) and (11) are useful in medical imaging of sites expressing (11). (1) and (11) are useful in medical imaging of sites expressing (11). (1) and (11) are useful in medical disorders involving aberrant protein expression or biological activity. The perpetride and polymerication identification of matations in disquestics and activity sequences have applications in disquestic animal trapers of data and products dependent on DNA and animal textures. Additional Actual and products dependent on DNA and animal actual asserts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human brain expressed single exon probe encoded protein SEG ID NO: 37670.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Note: the sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from NIPO at Itp.wipo.int/pub/pubished_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; brain expressed even, gene expression analysis; probe; microarray, Alzheimer's discase, multiple soletosis, schizophrenia;
                                                   New isolated polynucleotide and encoded polypeptides, useful in diaquestics, forensies, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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                                                                                                                                                                                                Claim 20; SEQ ID No 55355; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAM65565 standard; Protein; 51 AA.
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2000US-0608408.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-JAN-2001; 2001WO-5500667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04 FEB 2000; 2000US-0180312.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-0632366.
2000US-0234687.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1087 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post Local Similarity
Matches 6, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        epilepsy; cancer.
N PSDB; AAS89183.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      846 qnfsawv 852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 GNFNAWV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W0200157275 A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24 - MAY 2000,
30-JUN-2000,
03-AUG-2000,
21-SEP-2000;
                                                                                                                                            biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAM65565;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 10
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AAB04068
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                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                  The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may emable diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schlzophrenia, epilopsy and cancers. The present sequence is a protein encoded by one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cytostatic; immunosuppressive; nontropic; neuroprotective; antiviral; autialleraic; hepatotropic; antidiabetic; antiinflammatory; antiloter; vuluerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant, qene therapy, cancer; immuno disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The investion relates to the isolating of genes AAH45072-F45120 enoughing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence represents a
                                                                                                Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated nucleic acid molecule encoding a human secreted protein is used in preventing, treating or ameliorating a medical condition
                                                                                                                              Example 4, SEQ ID No. 37670; 650pp + Sequence Listing: English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human secreted protein BLAST search protein SEQ ID NC. 111.
                                                                                                                                                                                                                                                                            DB 22; Length 51;
                                                                                                                                                                                                                                                                                                  2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the human secreted proteins AAR65920-R65968
                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                            67,4%; Shore 36;
                                                     Chen W, Rank DR,
                                                                                                                                                                                                                                                                                      Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure, Page 514, 558pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Komatsoulis GA;
                                                                                                                                                                                                                                                                                                                                                                                                  AAB65971 standard; protein; 68 AA.
                               (MOLE-) MOLECULAR DYNAMICS INC
         2000dR-0024263.
27-SEP-2000; 2000HS 0236359.
                                                                                                                                                                                                                                                                                      75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2000; 2000WO-US14964.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                     the probes of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0138627
                                                                                                                                                                                                                                                                                                                                                                                                                                            03-APR-2001 (first entry)
                                                                                                                                                                                                                                                                                                  Conservative
                                                     Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Posen CA, Puben SM,
                                                                          WP1; 2001-483446/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-032308/04.
                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                    1 KOGNFNAW 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200077023-A1.
         04 - OCT - 2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-DEC-2000.
                                                                                                                                                                                                                                            Sednence
                                                                                                                                                                                                                                                                                                                                                                                                                        AAB65971;
                                                     Penn SG,
                                                                                                                                                                                                                                                                            المناصلة الاناءاتية
                                                                                                            brains
                                                                                                                                                                                                                                                                                                                                                                             RESULT 11
                                                                                                                                                                                                                                                                                                Matches
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(a) cancer, e.g. breast and ovarian cancer, and other cancers of the adrenal aland, bone marrow, breast, astrochisestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's discase, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis;
                              in the descriptor line. The sequence is a search result true a BLASTX homology search. The genes and proteins are useful for preventing, analytical conditions, e.g. by protein or gene therapy. The genes are isolated from a range of human fissues disclosed
                                                                                                                                                                             in the specification. The mucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of:
                                                                                                                                                                                                                                                                                                                                                                                                  diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardicvascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolating a nucleotide which encodes the zeytor 10 cytokine receptor enables the production of recombinant cells expressing the receptor. Those cells can then be used to detect the presence of modulater of asytorium by cultaring the cells in the presence of a test ligand and comparing levels of activity of mouse acytorium.
peptide fragment homologous to the protein encoded by the year given
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New cytokine receptor mouse zeytor 10, useful for detecting ligands
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        scytor 10 cytokine receptor; cytokine; receptor; amtibody; liqand; binding, detection; modulation; recombinant cell; lymph; haematopoletic cell; lymph; limmation; respector system, blood; bone; inflammatory response; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..
C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 22; Length 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rat zeytor 10 cytokine receptor peptide fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lok S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 33;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Secre 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Foster DC, Hammond AK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 3; Page 115; 134pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB04068 standard; Protein; 113 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0309861.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-MAY-2000; 2000W0-0S12924.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lymphoid and myeloid cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-APR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cucry Match
Best Local Similarity 55.5.
6. Conservative 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WP1; ZUU1-U16U96/U2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 eknnynawv 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 KQGNFNAWV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDR; AAA54463.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Presnell SR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              spleen; rat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-NOV-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                          Saks
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in the presence and absence of the test sumple. Similarly, detection of swaterly receptor lighted within a test shaste can be achieved
         The method comprising contacting a test sample can be indicated. The method comprising contacting a test sample containing an amino acid sequence for 78:5 1977 to Files of the Polypeptide to eytokine receptor and detecting the binding of the polypeptide to a ligand in the sample specified peptide transments of the zeroz in eytokine receptor and the methods described are used to identify
                                                                                                                      ligands that stimulate the proliferation and/or development of haematopoictic. Lymphoid and myeloid cells. Peptide transments of the cytokine teceptor are useful for treating lymphoid, immune, inflammatory, sphenes, klood or bone disoiders and for generating antibodies directed against the receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to a human cytokine receptor common quama chain like protein (GRGGL). The invention is useful for treating, perventing and/or disposing conditions such as tumours, inferions, inflammatory disposes, immune disorders, neutraboreative disposes.
                                                                                                                                                                                                                                                                                    67.9%; Score 36; DB 22; Length 113; 71.4%; Pred. No. 57; 1; Indels 1; Mismatches 1, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cytokine receptor common qamma chain like; CRCGCL; human;
tumours; infections; inflammatory; immune disorder;
neurodegenerative; cardiomascular; disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 18; 288pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB71691 standard; peptide; 181 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-AUG-2000; 2000W0-5822493.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06432-03366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CRCGCL related peptide #4.
                                                                                                                                                                                                                                                                                                                            5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Posen CA,
                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001 147547,715
                                                                                                                                                                                                                                  Sequence 113 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 AA;
                                                                                                                                                                                                                                                                                                                                                                                                41 gnfqawi 47
                                                                                                                                                                                                                                                                                                                                                            3 GNFNAWV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200112672-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     conditions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ruben SA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB71691;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seguence
                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB71691
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67 9%; Score 36; 38 22, Length 181;

Query Match

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The present sequence represents human milk fat globule protein MFG-EB, which has barriegy to the decelegratially regulated cadethelial cellicus; i (bel i). The feil protein has epidenmal growth factor (555) like domains and discoldin lifeator villilise domains. The bell proteins have an inhibitory effect on angiogenesis (blood vessel growth), this activity may be useful chindrally to prevent neovascularisation of tissues such as tumour nodules and prevention of metastases. The anti-angiogenesis activity of 50-1 may be used to treat absorbing conditions that result from angiogenesis, including cancer, diabetic retinopathy, then memoring after the angiogenesis in the post including cancer, diabetic retinopathy, angiogenesis in the post in the decides and result in the factor of the promotes. Since the promotes stroke, who as it can be asked to the decided its binds to alpha V beta 3 userual for promoteing bone formation. Del-1 binds to alpha V beta 3
                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Caps
                                                                                                                                                                                                                                                                                                                                Death, developmentally regarated endotherial cell bocus 1; cancer; discoidin 1; factor Vill-like domain; epidermal growth factor; EGF; diabetic retinopathy; rheumatoid arthritis; endometriosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tei 1 polypeptide acquences — nactul for treatment of canver, diabetic retinopathy, rheumatoid arthritis and endometriosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67.9%; Score (6; DB 20; Length 321;
75.0%; Pred. Mc, 1.76+02;
Live 0; Mismatches 2; Indels
                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shedgrass HE, Cupancic TJ;
                     e i
   Pred. No. 94;
1, Mismatches
Best Local Similarity 42.5%, Pred. No.
Matches 5, Conservative 1, Mismate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         integrin, and is an apoptosis inducer.
                                                                                                                                                                                                                                                                                                 Human milk fat globule protein MFG-E8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example, Column 63 64, 73pp, English.
                                                                                                                                                                                     AAW94697 standard, Frotein, 321 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9602-0659235.
9502-0480229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96US-0659235.
                                                                                                                                                                                                                                                              05-MAY-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hogan B, Questermons T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                      GNFNAWV 9
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                       Matches
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RESULT 15

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receptor enables the production of recombinant cells expressing the receptor. Those cells can then be used to detect the presence of a modulator of zeytor10 protein by culturing the cells in the presence of a test ligand and comparing levels of activity of mouse zeytor10 in the presence of the test sample. Similarly, detection of zeytor10 receptor ligand within a test sample can be achieved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The most hod comprising contacting a test sample containing an amino acid sequence from cys15 or 61/25. Its froats of the acytor 10 or cytokine receptor and detecting the binding of the polypeptide to a ligand in the sample. Specified peptide fragments of the acytor 10 acytokine receptor and the methods described are used to identify ligands that atimulate the proliferation and/or development of haematopoietic, Immphoid and myeloid cells. Peptide fragments of the cytokine receptor are useful to for treating lymphoid, immune, inflammatory, splenic, blood or hone disorders and for generating antibodies directed against the receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New cytokine receptor mouse zcytor 10, useful for detecting ligands
                                                                                                                                                                            scytor 19 cytokine receptor, cytokine, receptor, artibody, ligand, binding, detection; modulation recombinant cell; hymphication; lymphic cell; lymphic cell; lymphic cell; lymphic cell; lymphic limmune system; blood; bone, intlammatory response; inflammation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  that stimulate proliferation or development of haematopoietic, lymphoid and myeloid cells
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Presnell SR, Foster DC, Bammond AK, Lok S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 109-110; 134pp; English.
                      AABU4066 standard; Protein; 357 AA.
                                                                                                                                         Zeytor 10 eytokine receptor.
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                                                                                                  11-APR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ZYMO ) ZYMOGENETICS INC.
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                                                                                                                                                                                                                                                          spleen; human.
                                                                                                                                                                                                                                                                                                 Homo sapiens.
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                                                           AAB04066;
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AAB04066
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Ouery Match
67.9%; Score 36; DB 22; Length 357;
Best Local Similarity 71.4%; Pred. No. 1.9e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
by 3 GNFNAWV 9
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Search completed: September 5, 2002, 15:26:28 Job lime: 468 sec

280 gnfgawi 286

<u>a</u>

GenCore version 4.5 Copyright (c) 1993 - 2000 Compuger Ltd.

OM protein - profein search, using sw model

(without alignments) 12.393 Million cell updates/sec Search fire of 7x Seconds September 5, 2002, 18:22:56 Pur on:

US-09-744-804-35

1 KOGNFNAWV 9 Perfect score: Sequence:

RIOSHM62 Gapop 10.0 , Gapext 0.5 Scoring table

283138 seqs, 96089334 residues Searched:

Total number of hits satisfying chosen parameters:

Maximum DB seq length: 2000000000 Minimum DB seq length: 0

Post processing. Minimum Match OR

Listing first 45 summaries Maximum Match 100%

1: pirl:\* 2: pir2:\* 3: pir3:\* 4: pir4:\* .l∠ did Database .

Pred. No. is the number of results prodicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	Ë	QI.	Description
1						
٦	53	100.0	218	CN	A47285	milk tat globule p
C)	다 항	2.6%	7.54	- 1	S00704	photosystem 1 prot
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Œ	30		127	c.	AB0154	probable bacterion
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11	38	71.7	61	C1	C90821	
12	38	71.7	64	C4	D90832	
13	38	71.7	9	C4	F85689	2
14	38	Ξ.	74	C4	E30301	hypothetical prote
15	38	7 1 -	7.4	c	H8-743	- 20
16	38	71.7	401	7	565138	qlycoprotein antiq
17	38	71.7	409	~	T11743	
18	38	71.7	427	c	874211	
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21	æ	71.7	136	c:	11,000	Н
e e	37	63.8	373	۲4	AI344C	121
23	37		503	73	S64860	hypothetical prote
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(1)	7.	63 R	754	٠.	T67280	Participation I Page
97	37	69 B	735	C 1	541481	P700 chlorophyll a
27	3.7	69 B	736	C4	B28341	photosystem I P700
28	3.7	8.69	737	C4	T06839	probable photosyst
o.∂	27		741	- 1	820053	photosystem I prot

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human (fragment) milk fat globule protein

C.Species: Homo sapiens (man) C.Date: 31-fer 1992 #sequence\_remision 31-bon 1993 #foxt\_abunga 29 May 1999 C.Accession: A47285

Synacora, D.; Peterson, J.A.; Urrea, R.; Kuniyoshi, J.; Ristrain, A.M.; Ceriani, P. I. Cancer Res. 51, 4994-4998, 1991
Arithe: A.M. 4.; Con human milk for alchede protein that is highly expressed in human A; Reference number: A47285; MUID:91371351
A) Accession: A47285
A) Status: preliminary

A; Molecule type: mRNA

A)Residues: 1 218 (LAR)
A)Presidues: 1 218 (LAR)
A)Press references: (4.5%)[5]; NH: q.45,49; PIDN.AAR19771.1, PID:q238397
A)Presiduelly: wilk fat globule protein; discoldin 1 amino-terminal homology; PGF hom P:16,Domain: discoldin 1 amino terminal homology; (fragment) ADNL)
F:60-218/Domain: discoldin 1 amino terminal homology; (fragment) ADNL)

Gaps :**:** O 130.0%, Store 53: ER 2; Length 218; 100.0%; Pred. No. 0.019; Cive 0; Mismatches 0; Indels Query Match Best Local Similarity 180... Yes 9; Conservative

photosystem : protein A2 — aarden pea chloroplast.
C.Species. chloroplast Pisam sativum (garden pea)
C.Bactes. 28-Aug 1989 assequence\_remision 28 Aug 1980 #text\_charge 26-Aug-1909
C.Baccession. S00704; B30830
E.Lehnderk, J., Rashnassen, C.F., Bookjans, G.R.; Popsen, R.R.; Stummann, B.M.; Hennin Plant Mol. Biol. 7, 3-10, 1986
A.Tillus Sequence of two genes in pea chiar-plast GNA coling for F; and 82 kD pulppep A.Reference number: S00703

A Molecule type: DNA A.Residues. 1734 CLEH> A.C.C. residences. EMBINSTACS. BID.A.DISA. PICK.CAA29081.1, FID.A.DISA A.Nobe. the authors translated the codon AAT for residue 115 as 11e and ATT for resid

A,Genc. psaA2 A,Gence obtoropiast C.Sapertamit, plotus,stem 1 P755 uppritein C.Reywords, chloropiast, electrom transfer, membranerassoriatel complex, photosynthes

Query Match

DB 2, Length 734; 79.2%, Score 42, Gaps

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RiPerna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May
iller, E.; Gretbeck, E. I.; Davis, N.W.; Lim, A.; Dimalanta, F.; Potamousis, K.; Apoda
Nature 409, 529-533, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable bacteriophage protein (partial) YPO1259 [imported] · Yersinia postis (struin
C:Species: Yersinia pestis
C.Late. 02 Nov 2500] #sequence_revision 02 Nov 2500] #text_change 02 Nov 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P.Parkhill, T. Wran, R.W.; Thomson, N.P.; Tithall, P.W.; Holden, M.T.G.; Prentice. M. deno-Tarraga, A.M.; Chillindworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Doudan, G. Li, M., Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrel Nature 413, 523-527, 2001
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Proc. Natl. Acad. Sci. U.S. A. Go, 8444-8448, 1993
A.Tillia: Characterization of cDNAs encoding the marine interleukin. 2 receptor (11.28)
A.Reference number: A47514; MUID:93391374
                                                                                                                                                                                                                                                                                                 A. Recides. [1986 - 870].
A.P. sett-forcomes app Apostla, win gl2514762; pink-AAG55440 1- dSpDB;GN00145; UWID:
A.Pxporimental sourcom strain O157-H7, substrain PD1933
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Cydenetics:
      0]Barot 16 Pob 2001 #sequence_revision 16 Pob 2001 #fext_change 14-9op-2001
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C.Date. 27 Feb 1997 #Sequence_revisies 27 Feb 1997 #fext_ebangs 20 Pan 2000
C.Andessien (149280, A47514) NNF92; WA77F; SA7F82; 153398
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                                                                                                                                                  A,Title. Genome sequence of enterchemorrhagic Rscherichia coli 0157:H7.
A;Reference number. A85480, MGID.21074935, PMID:11206551
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Pred. No. 8.5;
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75.0%; Pred. No. 4.3;
1977 - 1; Mismatches 3; 10.30;
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A; Pesidues: 1-127 < KUF>
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P;Parkhill, T; Wren
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E. Wakasugi, T. Tsudruki, J. Ito, S. Nakashima, K., Tsudzuki, T., Sugiura, M.
E. Wakasugi, T. Tsudruki, J. Ito, S. Nakashima, K., Tsudzuki, T., Sugiura, M.
E. Martin, Arad. Sci. 1878, 91, 974-9798, 1994

A.Title: Loss of all adh qenes as defletimized by sequencing the entire chloroplast genome
A. Reversion: 707544

A. Acression: 707544

A. Stafus: preliminary; translated from GB/EMBL/DDBJ
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Cyspecies, Escherichia coll
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Azkeference numbor - A94629, MTD-21156231, PMID.11258796
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R:Hayashi, T: Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishili, K.; Yokoyama, K.; Han, C.G.
gasawara, N.: Yasunaga, T.; Kuñara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Pos 8, 11-22, 2401
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A:Experimental source: strain 0157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                   C;Species: chloroplas: Finus thadbergiata (Spanese black pine)
C;Date: 14-May-1999 #sequence_revision 14 May-1999 #fext_change 18-Aug-2000
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CiDate. 18-Jul.2003 #Sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
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C;Supertamily: photosystem I P700 apoprotein
C;Reywords: chloroplast, membrane associated complex: photosystem
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87 5%; Prod No 6 9;
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Pred No 5 9,
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                                  O. Mismatches
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H7 C4;
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Bost Local Similarity
Acas 7; Conserva
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      Best Local Similarity
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                                                                                                                                                     71 QGNFEAWV 78
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                                                                                          2 CONFINAWV 9
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Activity of Suyer, Fr. Herrmann, R.G.

Curr. Genet. 10, 843-855, 1986

A.Title. Nuclectide sequence of the clustered genes for two 8700 chlorophyll a apopro A.Reference number: 800444

A.Recession: 80444

A.Recession: S0444

A.Recession: S0445

A.Recession: S0446

A.Recession: B.H. Willer and B.H. 
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N.Alternate names: photosystem I P700 apoprotein A2: photosystem I reaction center pr
C.Species: chloroplast Antirrhinum majus (garden Snapdragon)
C.Date: 15 Feb 1996 #sequence_revision Ol:Mar 1996 #text_change 26-Ang-1999
C.Ancessin, S60184, S72395, S12394
R.Schafiner, C.; Lassch, H.; Hagemann, R.
Mol. Gen. Genet. 249, 533-644, 1995
A7fitle: Detection of point mutations in chloroplast genes of Antirrhinum majus L. I.
A.Reference number: S60184; MUID:96133694
                                                A.Residaca, 1734, (2000)
A.Experimental Society or, Bright Yellow 4
B.Schingerk E. Johnson M. Turnkly M. M. Matsagi, T., Hajaskida, N., Matsabajashi, T., Esfangashira, E. Johnson M., Turnkly M., M. Wasagi, T., Hajaskida, N., Matsabara, E.; Yamada, K.; Kusuda, J.; Laksiwa, F.; Kato, A.; Tohdoh, N., Enko, H.; Kamogashira, E.; Yamada, K.; Kusuda, J.; Laksiwa, F.; Kato, A.; Tohdoh, N.; Enko, J. S., 2042-2049; 1986
A.Tillia: The complete mucleutide sequence of the tobacco otherspiral genome. Its gene A; Reference number: A38013
                                                                                                                                                                                                                                                                                                                                                                                                                                             Alcontents: annotation; gene organization, sites, features C.Comment. This is one of the specific proteins associated with chiorophyll a of the s supplied by photosystem I: to Draubstance (an iron sulfar protein), which in turn r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Superfamily: photosystem 1-P700 apoprotein
Reywords: ellereglast, electros transfer, membrane prefein; photosynthosis; photosy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             photosystem I protein A2 · spinach chloropiast
C:Species: chloropiast Spinacia oleracea (spinach)
C:Enter O7-Inn-1999 #sequence_revision 97-Inn-1999 #text_change 20 Aug-1999
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75.9%, 0.od, B. 25;
ative l; Mismatches l; Indels
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Best Lord: Similarity 75.0%; Pred. No. 25;
Matches 6; Conservative 1; Mismatches 1; Indels
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hes 6, Conservative
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A; Molecule type: DNA
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Bust Local Si
Matches 6;
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            Alfocture agreement 20018, NID.9404067, PITN.AAA39286.1, FID.9404058
A) Residues: 1.369 CRE2.
A) Cross-references: GB.120018, NID.9404067, PITN.AAA39286.1, FID.9404068
E) Kumaki, S.; Kondo, M., Tabeshita, T., Asse, H.; Makamata, M., Sugamata, K.,
B) Colomber, Scondo, M., Tabeshita, T., Asse, H.; Makamata, M., Sugamata, K.,
B) Colomber Colomber and Colomb
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Bur. T. Timunol. 24, 324-321, 1994
Affitle: The murine interleukin 2 reveptor games chain gene: crganization, chromosomal 1
A;Reference number: 153398; MHP-95104285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CKeywords, Cytokine receptor, daplication, glycoprotein, transmembrane protein
F1-22/20main, signal sequence estatus predicted SIG,
F2-3-3-69/Product interlection to receptor gramma chain estatus predicted MAI.
F2-56-284/20main: transmembrane estatus predicted CMMX
F71,75,81,96,159,164,706/Finding site marbabydrate (ASE) (covalent) Estatus predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gross references, OR D19821, NTO 9436945, FIBM.BAA62974.1, PIE-9436345
R;Chiu, R.K.; Dougherty, G.J.
submitted to the BMBL Data Library, October 1993
A;Description: Regulation of CD44-mediated cellular adhesion by the IL-2 R gamma chain.
A;Peference number: S37582
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A;Pathway: Interleukin 2 stimulated grawth and lifferestiption of Toylls, Robells, NK
C;Superfamily: interleukin-2 receptor gamma chain
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C.Complex The bigh affinity receptor is a heterotimer of alpha (see FIR.UHMS2), beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gene 130, 303-504, 1993
Arittle: Cloning and sequencing of the CDNA encoding a mouse IL-2 receptor gamma.
Aketeronce number 100775; Millip-94466191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
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C.Species: chloroplast Nicotiana tabacum (common tobacco)
C.Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_cloude 17-Feb-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ascross references (OHTT) PSE, NHT 4365084, FiLN.BAR027651, Fib.gsUsed5
RiKobayashi, N.; Nakagawa, S.; Minami, Y.; Taniquchi, T.; Kono, T.
Gene 130, 303-304, 1993
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85.7%; Pred. No. 13;
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A;Status: prelimining, translated from SB;EMBL,SBBJ
A;Molecule type: DNA
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A;Reference number: A00149
A;Accession: A03466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <81,352-366,787,368-369 <CHI>
                                                                                                                                                                                                                                                                                                                                                                                A;Accession: JN0592
A;Status: nucleic acid sequence not shown
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A;Residues: 1-350,787,352-366,78
A;Cross-references: EMBL:X75337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Conservative
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Best Local Similarity
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A;Posidues: 1-369 <KOB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 369 < KUM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.369 <RES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type, mRNA
A;Residues: 1 369 <KUN
A;Cross references 14
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A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 QGNFNAW 8
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C;Function:
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85.7%;
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85.7%;
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Rest Local Similarity 85.77
Matches 6; Conservative
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Hest Local Similarity
6, Conserva
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Rest Local Similarity
       A; Residues: 1-64 <HAY>
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                                                                                                                                                                                                                                                                                                                             35 GNFSAWV 41
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                                                                                                                                                                                                                                                                            3 GNFNAWV 9
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A;Gene: ECs2181
                                                                                                  A;Gene: ECs1628
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A)Cross-reterences: EMBL:X84153
R:Schainter, C.; Lausch, H.; Biagemann, R.
submitted to the EMBL Data Library, Tanusry 1995
Submitted to the EMBL Data Library, Tanusry 1995
A:Description: Detection of point motations in chieroplast genes of Antirthinum majus L.
                                                                                                                                                                                                                                                                                                                                                                                                 C:Superfamily: photosystem I P700 apoprotein
C:Krywords: chloroplast, electron transfer; membrane-associated complex; photosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein ECs1539 (imported) · Bacherichia coli (atrain 0157.H7, substrain H1
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A/Title: Complete genome sequence of enterchemotrhagic Escherichia coll ols7-87 and geno A/Reterence number: A94629; Milh-21156231; PMIP-11268296
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C;Species: Escherichia coli
C;Date: 18-Jui-2001 #sequence_revision 18-Jui-2001 #text_change 18-Jui-2001
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qasawara, N.; Yasunaqa, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shibagawa, H.
DNA Res. 8, 11-22, 2001
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A:Experimental source: strain 0157:H7, substrain RIMD 0509952
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C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C;Aercession: C90821
                                                                                                                                                              A;Residues: [1566,717,568-734 <SCW>
A;Cross-references: EMBL,X84153, Nib.g669095, Pidn PAARR95R L, PID y669096
A;Acression: S52394
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C;Genetics:
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A;Aecession: D90832
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1; Mismatches
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Best Local Similarity 75.08
Matches 6; Conservative
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A; Accession: S52395
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Hest Local Similarity
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A; Residues: 1-61 < HAY>
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A;Molecule type: DNA
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Cispecies: Escherichia coli
Cibat. 18 Jan. 1901 #sequence_revistor 18 Jan. 1901 #text_change 18 Jal 2001
Cistat. 18 Jan. 190990
E.Hayashi, T.: Makino, K.: Ohnishi, M.: Kurokawa, K.: Ishii, K.: Vokeyama, K.: Han. C
qasawara, N.: Yasunqa, T.: Kuhara, S.: Shiba, T.: Hattori, M.: Shinaqawa, H.
PHA Rev. 8, 11:22, 2001
A;Tillo Camplete qenome sequence of enterohemorinatic Escherichia coli 0157:H7 and q
A;Reference number: A99629; MUID:21156231; PMID:11258796
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R,Perna, N.T., Flunkett III, G.; Burland, V.; Nau, B.; Glasner, J.D.; Kose, D.J.; May iller, L.; Grotleock, F. J.; Pavis, N.W.; Lim, A.; Dimalanta, F.; Potamousis, K.; Apoda Nature 409, 529-515, 2001
A,Tille: Genome sequence of enterohemorthagic Escherichia coli 0157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unknown protein encoded by prophage CP 933X (imported) - Escherichia voli (strain off
C/Species: Escherichia coli
C/Date | Escherichia sequence_revision 1/ Feb 2001 #fcxt_chasps 14 Sep 2001
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A,Gross references: GB.AE005174, NID.q12514809; PIDN:AAG58978.1; GSPDB:GN00145; UWGP:
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:
A;Cross-references: GB:BA000007; PIDN:BAB35051.1; PID:q1341092; GSPDR:GN00154
A;Experimental scarce: strain 0157:H7, substrain P!Wn 0509052
C;Genetics:
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A.Pross references: GM-KAOGOGO7; PIDM:BAB35604.1; PID:ql4361647: GSPDB:GNO0154
A.Experimental source: strain 0157:H7, substrain RIMD 0509952
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C,Genetics:
A,Gene: Z1881
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US-09-744-804-35 53 1 KQGNFNAWV 9 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

105224 seqs, 38719550 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 20nnnnnum

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SwissProt\_40:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the source of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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SOMMARIES	10		MFGM_HUMAN	FSAB_LOTUA	PSAB_OENHO	PSAB_PEA	PSAR_PINTH	PSAB_CYACA	CYRG_MOUSE	CYRG_BOVIN	PSAB_ANTMA	PSAB_SPIOI.	pgAa_TopAc	MFGM_P1G	MFGM_BOVIN	PSAB_ARATH	PSAB_MARPO	PSAB_ORYSA	PSAB_WHEAT	PSAB_MA12E	BGAL_STAXY	PSAR_ODOSI	PSAB_CHLVU	FSAB_GUITH	PSAB_MESVI	PSAR_CHIMO	PSAR_CHIRE	F-SAH_'YAFA	FSAB_SYNFW	PSAR_SYNFN	PSAH_PPOMA	EXOT_BOOK!	CPV1_MOUSE	CPV1_RAT	PSAB_SYNY3
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	ctadherin	(tormerly	BA46),	а тетрг	ane a	SSOCIAte	"Lactadherin (formerly BA45), a membrane associated glycoprotein	tein
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Lotus japonicus.
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                                                                                                                          This SWISS-PEOT entry is copyright. It is produced through a collaboration the SWISS institute of Bioinformatics and the EMH, outstation the European Bioinformatics Institute. There is no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for statement is not removed. Usage by and for compensation this is send an enable of iconsequence.
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O
                                                             MEDIA, OVEREXPRESSED IN SEVERAL CARCINOMAS.
-1- PTM- MEDIN HAS A PACCED N-TERMINIS WITH MINOP SPECIFS STARTING AT
       -i- FUNCTION: MAY BE INVOLVED IN PHOSPHOLIPID BINDING, BINDS SPECIFICALLY TO KOTAVIEUS AND INHIBITS ITS REPLICATION.
-i- FUNCTION: MEDIN IS THE MAIN CONSTITUENT OF ADETIC MEDIAL AMYLOTIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                       SURPETULIAN LOCATION: PERIPHENAL MEMBRANE PROTEIN
TISSUP SPECIFICITY: MAMMARY EPITHELLAL CELL SURFACES AND AGRILC
                                                                                                                                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY
N LINKED (GLCNAC. . ) (POTENTIAL).
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01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Photosystem I P700 chlorophyll A apoprotein A2 (PsaB) (PSI-B).
                                                                                                                                                                                                                                                                                                                                                                                                                     F5/8 TYPE C 1.
F5/8 TYPE C 2.
CELL ATTACHMENT SITE (POTENTIAL).
                                                                                                                                                                                                                                                                                         SMART: SM00181; EGF; 1.
SMART: SM00211; FA58C; 2.
PROSTITE: P850622; 1.
PROSTITE: P801186; EGF_2; 1.
PROSTITE: P801286; EGF_2; 1.
PROSTITE: P801286; FA58C_2; 2.
PROSTITE: P801286; FA58C_2; 2.
Signal; Glycoprotein; Milk: Repeat; EGF-like domain; Amyloid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100 0%; Srore 5%; DR 1; Length 387;
100 0%; Prod No 0 011;
.ive 0; Mismatches 0; Indels
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                                                                                           SIMILARITY: CONTAINS 1 E3F-1,1KE FOMAIN. SIMILARITY: CONTAINS 2 F5/8 TYPE C DOMAINS
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DNA Cell Biol, 16:861-869(1997).
                                                                                                                                                                                                                                                                                Pfam; PF00754; F5_F8_type_C; 2.
                                                                                                                                                                                                                                               InterPro; IPR000561; EGF-like.
InterPro; IPR000421; FAS<u>8_C.</u>
Ptam; PF00008; EGF; 1.
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EMBL, 856151; AAB19771.1; -.
MIM, 602281; ·.
                                                                                   AMING ACID 264 AND 273.
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(see http://www.ist.sib. Mjasmenne)
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                                                                                                                                                                                                                                                                                                                                                                                                    Jurian Feet 7:323-330(2000).

-i- FUNCTION: PsaA and psaB bind P700, the primary electron donor of photosystem I (PSI), as well as the electron acceptors A0, A1, and FX PSI functions as a plast-cyaning-proposed form-basin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pair and subsequent electron acceptors. The PSI reaction center of higher plants and algae is composed of one at least 11 subunits.
-!- SUHCELLUIAR LOCATION: Integral membrane protein. Chloroplast
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X (POTENTIAL).

X (POTENTIAL).

IRON SOLEUK FX (4FE-45) (BY SIMILARITY).

IRON-SOLEUK FX (4FE-45) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1- COFACTOR. P700 is a obtacophyll A dimor, A0 is chlorophyll A, Al is a phylloquinone and FX is a 4Fe-45 from sulfur center.
1- SUBUNIT: A psaA/B heterodimer binds the P700 chlorophyll special
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                            Eukaryota; Viridiplantae; Embryophyta; Trachochhyta; Spermatophyta;
Magneilophyta; eudicolyledons; core eudicots; Rosidae; eurosids I;
Eukales; Fahaceae; Papillionoldeae; Lotus.
                                                                                                                                                                                                                                      STRAIN-Accession MG-20; MEDLINE-21082749; PubMcG-11214967; MEDLINE-21082749; PubMcG-11214967; Makamura Y., Tabata S.; Canplert Structure of the chloroplast genome of a lequme, Lotus japonicus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PAGG SPECIAL PAIP CHIOROPHYLL AXIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Photosynthesis: Photosystem I, Electron transport, Chlorophast, Trylakoid, Transmembrane, Iron-sultur, 4Fe-4S, Chlorophyll. TRANSMEM 45 69 [ (POTENTIAL). TRANSMEM 175 199 III (POTENTIAL). TRANSMEM 175 199 III (POTENTIAL). TRANSMEM 273 291 IV (POTENTIAL). TRANSMEM 330 333 V (POPENTIAL). TRANSMEM 369 395 VI (POTENTIAL).
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A1 PHYLLOGUINONE (RY SIMILARITY).
F83F2357E9408DF6 CRC64;
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AQ CHLOROPHYLL (BY SIMILARITY).
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87.5%; Pred. No. 2.5;
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VIII (POTENTIAL).
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                                                                                                                                        NCBI_Tax ID=34305;
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Chloroplast
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                                                                                                                                                                                                                                                                                                                                                                                                            photosystem I (PSI), as well as the electron acceptors AO, AI, and EX, PSI fanctions as a plastoryoning by rections of ferrodoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             is a phyllogatrone and FX is a 4Fe 43 from saifur center.
-1- SURUNIT. A peak/R beterodimer binds the P700 chicapophyli special pair and subsequent electron acceptors. The PSI reaction center of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRON-SULFUR FX (4FE-4S) (BY SIMILARITY). IFON-SULFUR FX (4FE-4S) (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                  Eucomothera plastomes.";
Mol. Gen. Genet. 263:581 585(2006).
-!- FUNCTION: PsaA and psaR bind P200, the primary electron denor of
                                                                                                                                                                                                                                                                                                                                                                                                                                                             COFACTOR P700 is a chlorophyli A dimer, Au is chlorophyll A, Al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   higher plants and alwae is composed of one at least il submits. SUBCELLUIAR LOCATION: Integral membrane protein. Chicacoplast
                                                                                                                                         Fukaryola, Viridiplantae, Embryophyta, Tracheophyta, Spermatophyta,
Mannellophyta, endiestyledons, ente endicets, Eusidae, eurosids II,
Myttales: Onaqiaceae, benothera.
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                                                                                                                                                                                                                                                                                                Chin W -L., Sears B ; "Complete nucleotide sequence of the Cenethera elata plastid fixed array, representing plast-off the five distinguishable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001280; PsaA_psaB.
Ptam: PF00223; psaA_psaB. 1.
PRIME: PR00257; PH00EVSTSAAB. 1.
PR0SITE; PR00419: PH00EVSTEMA. 1.
PR0SITE; PR0419: PL010SYSTEMA. 1.
Ph010SYSTEMA. 1. Chloroplast. 1.
Ph010SYSTEMA. 1. Chloroplast. 1.
Ph010SYSTEMA. 1. Chloroplast. 1.
Ph010SYSTEMA. 1. Chloroplast. 1.
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AO CHICGEOPHYLL (BY SIMILARITY).
AT PHYLLOQUINONE (BY SIMILARITY).
AI PHYLLOQUINONE (BY SIMILARITY).
DBR713BBCC18AHDE CRC64;
09MTN7;
01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2007 (Pel. 41, Last annotation update)
Photosystem i P700 chlotophyll A apoptotein A2 (PsaB) (PSI-B).
                                                                                                                                                                                                                                                                                   Hupfer H., Swiatek M., Hornung S., Herrmann R.G., Maier R.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  I.IGAND (BY SIMILARITY).
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III (POTENTIAL).
IV (POTENTIAL).
V (POTENTIAL).
VI (POTENTIAL).
                                                                                                        Cenethera hookeri (Hooker's evening primrose).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         thylakeid membrane.
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                                                                                                                                                                                                                                   SEQUENCE FROM N A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              METAL
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                                                                                           PSAB.
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This SWISS PROT entry is supprinte. It is produced through a collaboration between the SWISS institute of Bioinformatics and the FMRL outstation the Buropean Rioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial outlies replaced and the statement (see NATH) of the commercial or send an exail to licensells sib.ch).
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C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pair and subsequent electron acceptors. The PSI reaction center of higher plants and algue is composed of one at least 11 subunits. SUBCELLUIAR FORMITON: Integral membrane protein. Chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  photosystem I (PSI), as well as the electron asseptors AO, AI, and FA, PSI functions as a plastocyanic/cytochrone of ferredoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stummann B.M., Honningson K.W.; "Sequence of two genes in pea chicarphast DWA coding for 84 and 82 kD polypetides of the photosystem 1 complex."; plant mol. Riol 7:4-10 (1986).
-!- FUNCION: EsaA and psaB bind P700. the primary electron donor of
                                                                                                                                                                                                                                                                                                                                            Eskaryčta; Viridiplantae, Streptipšyta, Embr<sub>io</sub>phyta, Liachesphyta;
Spermatophyta; Maunoliophyta; eudicotyledons, core eudicots, Rosidae;
eurosids I. Pabales; Pabaceae; Papilionoideae; Vicleae; Pisum.
NCRI_TaxTD-1888;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IRON-SULFUR FX (4FE-4S) (BY SIMILARITY).
TRON-SULFUR FX (4FE-4S) (RY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- COFACTOR: P700 is a chlorophyll A dimer, A0 is chlorophyll A, Al is a phyll-quinche and FX is a 4Fe-4S iron-sullur center.
-!- SURMINIT: A psaA/R heterodimer binds the P700 chlorophyll special
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PPGSTTF; PSGG419; PHOTOSYSTEM_I_PSAAB; 1.
Photosynthesis; Photosystem I; Flortrom transport; Chloroplast;
                                                                                                                                                                                                       P05311:
01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
01 MAR-2502 (Rel. 41, Last annetation update)
Photosystem [ F700 ohlbrophyll A apoprotein A2 (FsaH) (PSI-H).

    Isubsmembrane, Irob calfur, 4Fe 48, Chlorophyll.
46 69 T (POTENTIAL).

                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rasmussen O.F., Bookjans G.B., Jepsen B.R.,
                 -:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (\mathbb{D}_L) askerd scallage. Similarity: Belongs to the PSAA/PSAB FAMILY.
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                                                                                                                                                                                      7.54 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            II (POTENTIAL).
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87.5%; Pred. No. 2.5;
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  V (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PRU0257; PHOTSYSPSAAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X05423; CAA29004.1; -.
                                                                                                                                                                                                                                                                                                                      Pisum sativum (Garden pea).
                     Conservative
                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100
100
353
353
439
535
 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           oxidoreductase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SECTION FROM N.A. Lehmbeck L., Rasmu
                                                       2 OCNINAWV 9
                                                                                             71 OGNFEAWV 78
                                                                                                                                                                                                                                                                                                                                          Chloroplast.
                                                                                                                                                                                          F3AB_FEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSMEM
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                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  is a phylloganeare and FX is a 4Fe 4S iton-sailur center.

SUBUNIT: A psaA/B heterodimer binds the P700 chlorophyll special pair and subsequent electron acceptors. The PSI reaction center of higher plants and algae is composed of one at least 11 subunits.

-!- SUBCELLULAR LOCATION: Integral membrane protein. Chloroplast
                                                                                                                                                                                9. IPU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. COFACTOR: B760 is a chlorophyll A dimor. AG is oblorophyll A, Al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota: Viridiplantao: Streptophyta: Embryophyta: Tracheophyta:
 P700 SPECIAL PAIR CHLOROPHYLL AXIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro: ....
Plant PP0023; psaA_psab, ..
Plant PP0023; psaA_psab, ..
PROISTE: PROISTSYSPSAB.
PROISTE: PROINTS: PROISTSYSPSAB.
PROISTE: PROINTS: PROINTSYSPSAB.
PROISTE: PROINT S. PROINTSYSPEN I PROINTS I TARGET TRANSMEM 169 I (POTENTIAL).
TRANSMEM 145 154 II (POTENTIAL).
TRANSMEM 175 199 III (POTENTIAL).
TRANSMEM 175 199 III (POTENTIAL).
                                                                                                                                                                              ر.
                                                             A1 PHYLLOQUINONE (BY SIMILARITY)
A1 PHYLLOQUINONE (BY SIMILARITY)
2ACF1F77D46FA8E7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                        Photosystem I P700 chlorophyll A apoprotein A2 (PsaB) (PSI-B).
             LIGAND (BY SIMILARITY).
AO CHLOROPHYLL (BY SIMILARITY).
AO CHLOROPHYLL (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINF-95024047; PubMed-7937893;
Wakasuqi T., Tsudzuki J., Ito S., Nakashima K., Tsudzuki T.,
                                                                                                                                              Score 42; DB 1; Length 734; Pred. No. 2.5; Trub-1s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus
                                                                                                                                                                                                                                                                                                                                                                                                                                           Pinus thunbergii (Green pine) (Japanese black pine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -! SIMILARITY: BELONGS TO THE PSAA/PSAB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1995 (Rel. 32, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                             734 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001280; PsaA_psaB.
                                                                                                                                                                                                                                                                                                                                                          01-NoV-1995 (Rel. 32, Created)
                                                                                                82412 MW;
                                                                                                                                              79.2%:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; D17510; BAA04420.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FINth, psaB, 1.
                                                                                                                                                                              Pregretative
                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   thylakoid membrane,
                                          670
671
700
74 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     oxidoreductase.
                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCB1_TaxID= 3350;
                                                                                                                                                                                                                                            71 QGNFEAWV 78
                                                                                                                                                                                                             2 OGNENAWV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mendel: 9995,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sugiura M.;
                                                                                                                                                                                                                                                                                                                             PSAB_PINTH
                                                                             BINDING
SEQUENCE
                                            BINDING
                                                                                                                                              Query Match
                                BINDING
BINDING
                                                                                                                                                                                                                                                                                                            PSAB PINTH
                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                           PSAB.
 STITLES
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                                                                                                                                                                                                                                                                                                                                                                                 Ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1- COFATTOR: P700 is a chlorophyll A dimer, A0 is chlorophyll A, Al is a PHPU loquinous and PA is a 4PE-48 incursualizar center. I SubuNII. A psaA,B heterodimen binds the P700 chlorophyll special pair and subsequent electron acceptors. The P8I reaction center of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        photosystem I (PSI), as well as the electron acceptors AO, AD, and EX. PSI functions as a piasteryanin/eytechnome of terredoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Rhodophyta, Bangiophyceae, Porphyridiales, Porphyridiaceae,
                                                                                                                            IRON-SULFUR FX (4FE-4S) (BY SIMILARITY). IRON-SULFUR FX (4FE-4S).
                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         higher plants and algae is composed of one at least 11 subunits. SHRFELEHIAE LOPATION: Integral membrane protein. Chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: PsaA and psaB bind P700, the primary electron donor of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The structure and gene repertoire of an ancient red algal plastid
                                                                                                                                                                P700 SPECIAL PAIR CHLOROPHYLL AXIAL LIGAND (BY SIMILARITY).
AC CHL GEOFHYLL (BY SIMILARITY).
AI PHYLLOGGINONE (BY SIMILARITY).
AI PHYLLOGGINONE (BY SIMILARITY).
AI PHYLLOGGINONE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Last sequence update)
Ol-MAR-2002 (Rel. 41, Last annotation update)
Photosystem I P70S chloroph;ll A apoprotein A2 (PsaB) (PSI-B).
                                                                                                                                                                                                                                                                                                                                         79.2%; Score 42; DB 1; Longth 734; 87.5%; Pred. No. 2.5;
                                                                                                                                                                                                                                                                                                                                                                               l; Indels
                                                                                                                                                                                                                                                                                     OR3720PA7R19266F CPC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO THE PSAA/PSAB FAMILY.
                                  VII (POTENTIAL).
VIII (POTENTIAL).
                  VI (POTENTIAL).
                                                                        IX (POTENTIAL).
                                                                                                              XI (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      734 AA.
                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                            X (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MPDLINE-20446450; PurMcd-11040240;
Gloeckner G., Rosenthal A., Valentin K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09TL<u>0</u>6;
16-0CT-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mol. Evol. 51:382-390(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TPROOI280; PsaA_psaB.
                                                                                                                                                                                                                                                                                 82495 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF022186; AAF12881.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam, PF00223, psuA_psuB, 1
                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 thylakoid membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cyanidium caldarium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            oxidoreductase.
                                                                                                                                                                                                                                                                                   734 AA;
                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 7: Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SHOUTHOUT FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=2771;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          71 QGNFEAWV 78
                                                                      575
643
707
                                                                                                                                                                                                                                                                 700
                                                                                                                                                                                                                                                                                                                                                                                                                     2 QGNFNAWV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=RK-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PSAB_CYACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cyanidium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                             Query Match
FRANSMEM
                  PRANSMEM
                                    TRANSMEM
                                                        PANSMEM
                                                                        PANSMEM
                                                                                              LEANSMEM
                                                                                                              PRANSMEM
                                                                                                                                                                      RINDING
                                                                                                                                                                                                                                                                 BINDING
                                                                                                                                  METAL
                                                                                                                                                    METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PSAB_CYACA
                                                                                                                                                                                                                                                                                                                                                                               Matches
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MEDELINE 3371774, Fullwed 8378320, Cao X., Kozak C.A., Liu Y.J., Noquehi M., O'Conneil E., Leonard W.J., Cao X., Kozak C.A., Liu Y.J., Noquehi M., O'Conneil E., Leonard W.J., "Characterization of oppose unveiled the murine interleakin 2 receptor (IL-2P) gamma chains chosensemal mapping and tissue specificity of IL-2R gamma chain expression.", Proc. Nail Acad Sci. H.S.A. 90:8464-8468(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kumaki S., Kondo M., Takeshita T., Asao H., Nakamura M., Sugamura K., "Cloning of the mouse interleukin 2 receptor gamma chain-demonstration of functional differences between the mouse and human
                                                                                                                                                                                                                                                 TRON-SULEUR FX (4FE-4S) (BY SIMILARITY).
TRON-SULFUR FX (4FE-4S) (BY SIMILARITY).
P700 SPECIAL PAIR CHLOMOPHYLL AXIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kobayashi N., Nakayawa S., Minami Y., Taniquehi T., Kono I ;
"Cloning and sequencing of the cDNA encoding a mouse IL-2 receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota, Metazza; Cherdii, Creminta; Veriebratu; Eutoleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi, Muridae, Murinae, Mus.
PRINTS: PR00257; PHOTSYSPSAAB.
PPOSITE, PS00419; PHOTOSYSTEM I. PECTOR transport; Chloropiast; Photosynthesis; Photosystem I. Electron transport; Chloropiast; Thylaksid; Transmombrane; Iron Sallur, 4Fe 48; ChloroplyII.

[ POTENTIAL) .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-PEB-1994 (Pel. 28, last suquence update)
15-PEC-1998 (Pel. 37, Last annotation update)
Cytokine receptor common gamma chain presurser (Gamma-C)
(Interleukin-2 receptor gamma chain) (IL 28 gamma chain) (P64).
                                                                                                                                                                                                                                                                                                              AO CHIOPOPHYLL (BY SIMILARITY).
A) PHYLLOGUINONE (HY SIMILARITY).
A1 PHYLLOGUINONE (HY SIMILARITY).
A1 PHYLLOGUINONE (HY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                   Score 41: DB 1, Length 734;
Pred. No. 3.8;
1: Misma*ches 1: Indels
                                                                                                                                                                                                                                                                                                                                                                           4496AA2AE59CA9B9 CRC64;
                                                                                                                                                                                                                                                                                              LIGAND (BY SIMILARITY).
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                                                                                           II (POTENTIAL).
II (POTENTIAL).
IV (POTENTIAL).
V (POTENTIAL).
V (POTENTIAL).
VII (POTENTIAL).
VII (POTENTIAL).
VII (POTENTIAL).
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X (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=93366191; PubMed=8359699;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1994 (Rel. 28, Created)
                                                                                                                                                                                                                                                                                                                                                                         82359 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                      77.48,
75.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   enitakhijosuvu -9
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                                                                                 64
1158
1294
241
345
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                         734 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCB1_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71 UGNFEAWI 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C CONFINANT 9
                                                                                                                                          330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     receptors.";
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P34902;
                                                                                                              TPANSMEM
                                                                                                                             IRANSMEM
                                                                                                                                           FRANSMEM
                                                                                                                                                           TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                    METAI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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Gene 130:303-304(1993).

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the Buropean Holmformatics Institute. There are no restrictions on use by for profit instituting as long as its content is in no
                                                                                                                                                                                                                                                                                                                                                       "Molecular mechanisms regulating the Hyaluronan binding activity of the adhesion protein CD44.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SCHEMILL THE GAMMA CHAIN IS COMMON TO THE LL-2, IL-4, IL-7 AND PROBABLY ALSO THE IL-13 RECEPTORS.

- SUBCELLULAR LOCATION: Type I membrane protein.
-1- SIMILARITY: BELLONGS TO THE CYPOXINE FAMILY OF RECEPTORS.
-1- SIMILARITY: CONTAINS I FIBEONECTIN TYPE III-LIKE DOMAIN.
                                   MEDLINE-95104285; PubMed-7805729; Disanto J.F., Certain S., Wilson A., Macdonald H.R., Avner P., Fischor A., de Saint Basile G.; Everptor gamma chain gene: organization, chicassonal lovalization and expression in the adult thymus."; Eur. J. Immunol. 24:3014-3018(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transmembrane, Olympirotein: Signal.
22 BY SIMILARITY.
23 869 CYTCKINE EDULTCR COMMON GAMMA CHAIN.
23 263 EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-LINKED (GLCNAC. ..) (POTENTIAL).
N LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (FOTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                     J. Neurosneel. 26:23! 239(1995).
-i- FUNCTION: COMMON SUBUNIT FOR THE RECEPTORS FOR A VARIETY OF
                                                                                                                                                                                                                                                                                                   Chin R K , Droll A , Cooper D L , Dougherty S.T., Dirks J.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CB2D5AB459077AC7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYTOFLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIBEONETIN TYPE-III.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-1 INKED (GLONAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        interPro; IPR002996; CRIA.
InterPro; IPR003961; FW_III.
InterPro; IPR003531; Hematopo_receptor_S_F1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMARI; SMOUGO; FN3: 1.
PROSTIE; PSO1355; HEMATOPO_REC_S_F1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
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JOINED.
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EMBL; D13565, BAA02760.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            $75844; AAB32904.1;
$75845; AAB32904.1;
$75847; AAB32904.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S75851; AAB32904.1;
X75337; CAA53085.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB32904.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB32304.1,
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284
369
250
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72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MGD; MGI:96551; 112rg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR, JN0775; JN0775.
HSSP; P31785; JLLN.
                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           INTERLEUKINS.
                                                                                                                                                                                                                                                                                                                                 Dougherty G.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        875948;
875849;
875850;
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                                                                                                                                                                                                                                                      STRAIN-B6.S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
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CARROHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
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                                     .
O
                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- SUBUNIT: THE GAMMA CHAIN IS COMMON TO THE IL-2, IL-4, IL-7 AND PROBABLY ALSO THE IL-13 RECEPTORS.
-1- SUBCELLUIAR LOCATION: 17 yee I membrane protein.
-1- SIMILARITY: BELONGS TO THE CYTOKINE PAMITY OF PECEPTORS.
                                                                                                                                                                                                                                                                                                       Bos faurus (Bovino)
Eukaryota: Metazoa; Chordata; Craniala; Vertebrala; Putelenstemi;
Mammalia; Eutheria; Cetartiodaetyla; Puminantia; Pecera, Beveldea,
                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIJINE-96268473; PubMcd-8672241;
Yoo J., Stone R.T., Solinas-Toldo S., Fries R., Beattie C.W.;
"Closing and chromosomal mapping of bovine interleukin.2 receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYTOKINE RECEPTOR COMMON GAMMA CHAIN. EXTRACELLULAR (FOIENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-LINKED (GLCNAC ) (POTFNTTAL)
N-LINKED (GLCNAC ) (POTENTIAL)
N-LINKED (GLCNAC ) (POTENTIAL)
N-LINKED (GLCNAC ) (POTENTIAL)
                                     .;
                                                                                                                                                                                                                                                         Cytokine receptor common gamma chain precursor (Gamma-C) (Interleukin-2 receptor gamma chain) (IL 2R gamma chain) (P64).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: COMMON SUBUNIT FOR THE RECEPTORS FOR A VARIETY OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY CONTAINS I FIRPONECTIN TYPE III-LIKE DOMAIN.
Score 39; DR 1; Length 369;
Pred, No. 4.5;
                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33CFAD9C9B032178 CRC64:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FIBRONECTIN TYPE-III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Receptor, Transmembrane; Glycoprotein; Signal.
                                                                                                                                                                                                                           01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1998 (Rel. 36, Tast annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPM0039461; FN_III.
InterPro; IPM003531; Hematopo_receptor_S_F1.
                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam: PF00041; 1n3; 1.
SMART; SM00060; FN3; 1.
PROSITE; PS01355; HFMATOPO_BEC_S_F1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
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                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gamma gene.";
DNA Cell Biol. 15:453-459(1996).
                                                                                                                                                                                                          01-NOV-1997 (Rel. 35, Created)
 73.68;
85.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43037 MW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U33748; AAB07812.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4SSP; P31785; 11LN.
InterPro; 1PR002996; CR1A.
                                   6; Conservative
                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     379
                                                                                                                                                                                                                                                                                                                                                           Bovidae; Bovinae; Bos.
   Owery Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 166
171
379 AA,
                                                                                              304 QGNFSAW 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INTERLEUKINS
                                                                                                                                                                                                                                                                                                                                                                         NCBL_TaxID-9913;
                                                                 2 OGNENAW 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP; P31785;
                                                                                                                                                                            CYRG_BOVIN
Q95118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schaffner C., Laach H., Hagemann R.;
"Detection of point mutations in chloroplast genes of Antirrhinum majus. L. I. Identification of a point mutation in the psaB gene of a photosystem I plastone mutant.";
Mol. Gen. Genet. 249:533-544(1995).

'! FUNCTION. FsaA and psaB bind P700, the primary electron donor of photosystem I (PS1), as well as the electron acceptors A0, A1, and FX. PSI functions as a plastocyanin/cytochrome c6-terredoxin oxidoreductase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Copportion P000 is a chlorophyll A dimer, A0 is chlorophyll A, A1 is a phylloquinone and FX is a 4Fe-4S iron-sulfur center.
SUBUNIT: A psaA/B heterodimer binds the P700 chlorophyll special pail and subsequent electron acceptors. The FSI reaction center of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              beau Bioinformatics Institute. There are no restrictions on non-profit institutions as long as its content is in no
                                                                                            0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Franheophyta;
Epermatophyta, Maquoliophyta, Cudicotyledons, core endicots;
Asteridue, euasterids I; Lamiales; Veronicaceae; Antirrhinum.
NCBL_TaxID-4151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Primm; Provazor, F. PHOTSYSPSAAH, PRIMES PROMOSTS; PROMOSTS; PROFESSION PROMOSTS PROFESSION PROMOSTS PROFESSION PROFESSIO
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01-NoV-1997 (Rel. 35, Last sequence update)
01 MAR-2002 (Rel. 41, Last amostation update)
Photosystem I P700 chlorophyll A apoptotein A2 (PsaB) (PSI-B).
73.6%; Score 39; DB 1; Length 379; 85.7%; Pred. No. 4.6;
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VIII (POTENTIAL).
IX (POTENTIAL).
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VI (POTENTIAL).
                                                                                   1; Mismatches
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STRAIN-SO; TISSUR-Leaf;
MEDLINE=96133694; PubMed=8544819;
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InterPro; (PR6001280, PsaA_psaB.
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Mendel; 13513, ANTMA, psaB;2.
                                                                                        6; Conservative
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    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                  317 QGNFSAW 323
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the European Bloinformatics Institute. There are no restrictions on its use by no profit is it is not say buy as its perfect is in no way modified and this statement is not removed itsage by and for commografial entities requires a license alreaded (See http://www.lsh.sh.ch/ann.onery.cor.send.an.email to license@lsb.sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      is a phylloquinone and FX is a 4Fe-4S iron-sulfur center. SUBURIL A pspA (% hoter-10.50 Finds the P750 Finds the pth.) I special pair and subsequent electron acceptors. The PSI reaction center of higher plants and algae is composed of one at least II subunits.
IRON-SULFUR EX (4FE-4S) (BY SIMILARITY).
IRON-SULFUR EX (4FE-4S) (BY SIMILARITY).
PYOO SPECIAL PAIP CHLOPOPHYLL AXIAL
                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kirsch W., Seyer P., Herrmann R.G.; "Nucleotide sequence of the cluatered genes for two P700 chlorophyll a appropriate of the photosystem I reaction center and the ribosomal protein S14 of the spinach plastid chromosome."; curr. Genet. 10:843-855(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            oxidoreductase. COFACTOR- P700 is a chlorophyll A Al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukarysta, Viridiplantae, Etreptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, endicotyiedons, core endicots,
Caryophyllidae, Caryophyllales, Chenopodiaceae, Spinacia.
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                                                                                                Al PHYLLOQUINONE (BY SIMILARITY).
Al PHYLLOQUINONE (BY SIMILARITY).
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01-7AN 1988 (Pel 06, Lawi Sequence update)
01-MAP-2002 (Pel, 41, Lawi Sequence update)
Photosystem (P760 ellerophyil A approach A2 (Fsab) (FS: H).
                                                                 AO CHLOROPHYLL (BY SIMILARITY).
AO CHLOROPHYLL (BY SIMILARITY).
                                                                                                                                                                                   Score 39; DB 1; Length 734;
Pred. No. 9;
                                                                                                                                                                                                                     1; Indels
                                                                                                                                    LIGAND (BY SIMILARITY).
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                                                                                                                                                                     73.6%; Sco...
75.0%; Pred. No. 5,
... 1; Mismatches
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Schmitz-Linneweber 7, Mair
                                                                                                                                    82420
                                                                                                                                                                                                                     6; Conservative
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                                                                                                                              734 AA;
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Best Local Similarity
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EMBL; A.1400848; CARRET25.1.

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photosystem 1 (PSI), as well as the electron acceptors A0, A1, and FX - ESI fanctions as a plastony right problemme of ferredoxin
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                                                                                                                                                                                                                                                                                                                            IRON-SULFUR FX (4FE-4S) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                              (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Elicitaki E., Strom M., Chomwonder J., Bujashida N., Matsabayashi T., Zaita N., Chomwonder J., Obokata T., Yamaquchi-Shinozaki E., Ohto C., Torazawa K., Meng B.Y., Suqita M., Fetto H., Kamoqashira E., Yamada K., Kusuda J., Tukdiwa F., Kato A., Tohdoh N., Shimada H., Suqiura M., "The complete nucleotide sequence of the tobacco chloroplast genome:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        its gene organization and expression.";
EMBC J. 5.2042-2049(1986).
-!- FUNCTION: PsaA and psaB bind P700, the primary electron donor of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Edkarysta, Viridiplantae, Streptophyta, Embryophyta, Trachcophyta, Spermatophyta, Magnoliophyta, endicotyledons, core endicots, Asteridae, euasterids 1, Scianales, Solanaceae, Nicotiana.
                                                                                                                                                                                                                                                                                                                                                             P760 SPECIAL PAÍR CHLORÓPHYLL AXIAL
LIGAND (BY SIMILARITY).
                                                                                               Photosynthusis, Photosystem i, Electron transport, Chloroplast;
Inylakold, Transmembrane; Iron-sullur, 4Fe-48; Chlorophyll,
                                                                                                                                                                                                                                                                                                                                                                                                                 AU CHLOROPHYLL (BY SIMILAR(TY)).
A1 PHYLLOGUINGNE (BY SIMILARITY).
A1 PHYLLOGUINGNE (BY SIMILARITY).
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01.JAN-1948 [Pel. 06, Last Sequence apdate)
01.MAP-2002 [Pel. 41, Last annotation update)
Photosystem : PFGO Hierophyll A up-privin A2 (PsaB) (PSI-H).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73.6%; Score 39; DB 1; Length 734; 75.0%; Pred. No. 9;
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                                                                                                                                                                                                                                                                                                                                                IRON-SULFUR FX (4FE-4S)
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VIII (POTENTIAL).
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V (POTENTIAL).
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                                                                                   PROSITE, PS00419, PHOTOSYSTEM_I_PSAAB; 1.
Photosynthesis, Photosystem i, Electron L
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                Mendel; 2573; SPIOL;psaB;l.
InterPro; IPP001280; PsaA_psaB.
                                                                    FHOTSYSESAAB.
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                                           Pfam, PF00223; psaA_psaB;
PRINTS; PR06257; PHOTSYSP
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PIR; S00445; S00445.
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Matches 6, Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IRON-SULFUR FX (4FE-4S) (BY SIMILARITY).
IRON-SULFUR FX (4FE-4S) (BY SIMILARITY).
P700 SPECIAL PAIR CHLOROPHYLL AXIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saps
higher plants and algae is composed of one at least 11 subunits.
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30-MAY-2000 (Rel. 39, Last annotation update)
Lactadherin (Milk fat globule-EGF factor 8) (MFG-E8) (MFGM) (Sperm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cherdata, Craniata, Vertebrata, Euteleostomi,
Cetartiodactyla, Suina, Suidae, Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Photosynthesis: Photosystem 1; Electron transport; Chlorophyll.
Thylakoid; Transmembrane; Iron-sultur; 4Fe-4S; Chlorophyll.
TRANSMEM 45 69 I (POTENTIAL).
TRANSMEM 175 199 III (POTENTIAL).
TRANSMEM 277 291 IV (POTENTIAL).
TRANSMEM 330 373 291 IV (POTENTIAL).
TRANSMEM 369 395 VI (POTENTIAL).
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Al PHYLLOQUINONE (BY SIMILARITY)
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AO CHIOPOPHYLL (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OZ 41mABOP5414nBF /7P/54
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                                                                             -!- SIMILARITY: BELONGS TO THE PSAA/PSAB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VII (POTENTIAL).
VIII (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00419; PHOTOSYSTEM_I_PSAAB; 1.
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InterPro: IPR001280; PsaA_psaB.
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15-JUL-1998 (Rel. 36, Last sequ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PFINES, PR00223; PR04_PSAB, L. PRINTS, PR00257; PHOTSYSPSAAB.
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395
439
535
                                                      thylakoid membrane.
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Mammalia; Eutheria;
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700
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654
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Best Local S
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                                                                                                                                                                                                                                                                                                            modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb.sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND CAPROHYDRATE-LINKAGE SLIES.
STEAIN*HOLSTRIN, TISSUE Mammary gland;
MEDLINE=97008954; Pubmed=8850064;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F5/8 TYPE C 1.
F5/8 TYPE C 2.
CELL ATACHMENT SITE (POIENTIAL).
BY SIMILARHTY.
N. LINKED (GLCNAC. . ) (POTENTIAL).
N-LINKED (GLCNAC. . . )
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Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bevoidea,
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C
                     SUBCELLULAR LOCATION: PERIOHERAL MEMBRANE PROTEIN.
TISSUE SPECIFICITY: MAMMARY EPITHELIAL CELL SURFACES AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71.7%; Score 38; DB 1; Length 409; 85.7%; Pred. No. 7.7;
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                                                                                                           SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS. SIMILARITY: CONTAINS 2 PS/8 TYPE C DOMAINS.
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                                                                                                                                                                                                                                                                                                                                                                            or send an email to licensealsb sib ch).
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EGF-LIKE 2.
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Fiam: PF0775; F5_F8_Lype_C: 2.
SMART: SM00181; EGF: 2.
SMART; SM00231; FASBC: 2.
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InterPro, 1PR000421; FA58_C.
Pfam; PF00008; EGF; 2.
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PROSITE; PSO1186; PGF_2; 2.
PROSITE; PSO1285; PASSC_1; 2.
PROSITE; PSO1286; PASSC_2; 2.
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HSSP; P00740; 1EDM.
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BINDING PROTEIN.
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Best Local Similarity
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the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed "say. V_T and for connection entities requires a license afterment (See http://www.isb.sib.ch/announce/or send an email to license@18b-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS PPOT entry is engright It is produced through a collaboration between the Swiss Institute of Mioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biochem Mol. Biol Int 29-545-554(1993)
-1- FUNCTION: PROBABLY ASSOCIATES WITH PHOSPHOLIPIUS ON THE SURFACE OF MAMMARY EPITHELIAL CELLS AND MILK FAT GLOBULES. ZONA PELLUCIDABINDING PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SHORT FORM: ARE PRODUCTS: 2 ISCHOPMS; A LOWS FORM (SHOWN HERE) AND A SHORT FORM: ARE PRODUCED BY ALIERWATIVE SHICEING. THE SHOPT FOURM LACKS SY AMINO ACTOS WITHIN THE FS/A TYPE O I FOMAIN.

--- TISSUE SPECIFICITY: MILK AND SPERMATOZOAN.

--- PIM THE 2 OLITHED GLYCAMS CONSTIST OF GAL, SIGNAT AND FUS. WITH PROBLEABLY FUC AS REDUCING TERMINAL SUGAR.

--- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                               Mather I.H., Banghart L.R., Lane W.S.; "The major fat-globule membrane proteins, bovine components 15/16 and guinea-pig GP 55, are homologous to MGF-EB, a murine glycoprotein containing epideimal growth factor-like and factor v/VIII-like sequences."
                               "Characterization of glycoprotein PAS-6/7 from membranes of berine milk fat globules.";
                                                                                                                                                                                       "Molecular cheming of glycoprotein antiques MGF5755 recognized by monoclonal antibodies raised against bovine milk tat globule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CELL ATTACHMENT SITE (POTENTIAL).
Hyarrequard I., Andersen M.H., Berglund L., Rusmussen J.T.,
                                                                                                                                                    Aoki N., Kishi M., Taniguchi Y., Adachi T., Nakamura E.,
Matsuda T.,
                                                                                                                                                                                                                                                                                                                           Submitted (NOV-1997) to the EMRL/GenRank/PDRI databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Figure Profits Fried Lipe_C: 2.
SMART: SMO0181: BGF, 2.
SMART: SMO0181: BGF, 2.
SMART: SMO0181: FASRC: 2.
PROSITE: PS00A22: POF_1: 2.
PROSITE: PS01286: BASRC: 1: 2.
PROSITE: PS01286: FASRC: 1: 2.
PROSITE: PS01286: FASRC: 1: 2.
Signal: Glycoprotein: Milk, hepeat, E3F'like domain, Alternative splicing.
Signal: 1.
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EGF-LIKE 2.
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                                                                  Riochem, 240-628 636(1996)
                                                                                                                   TISSUE-Mammary gland;
MEDLINE=96125736; PubMed-8541316;
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                                                                                                 SECHENTE OF 18-427 FROM N.A.
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                Petersen T.E.;
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This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            oxidoreductase.

OCFACTOR. PTOC is a chlosophyll A dimor, A0 is chlorophyll A, A1 is a phylloquinone and FX is a 4Fe 4S from sulfur center.

SUBBUNIT. A psaA/B heterodimer binds the F700 chlorophyll special pair and saksoquent electrin acceptors. The PSI reaction center of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- FUNCTION PsaA and psaP bind P700, the primary electron donor of photosystem [ (PSI), as well as the electron acceptors A0, A1, and FM. FSI functions as a plastocyanin/cytochrome c6-lerrodoxin
                                                                                                                                                      . .) (HYBRID) (IN PAS -6
                                                                                                                                                                                     N-LINKED (GLCNAC. . .) (HIGH MANNOSE) (IN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota Viridiplantae, Streptophyta, Embryophyta, Trachcophyta, Special-phyta, Migh. Noffice, end outplot as, outpool discuss Ensidae; eurosids II; Brassicales, Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                 Caps
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30-MAY-2000 (Pel. 39, Last sequence update)
01-MAP-2002 (Pel. 41, Last annotation update)
thates;stem 1 F7(0 chieraphyll A apaptoteim AZ (Fsab) (FSI-B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sate S., Nakamura Y., Kaneko T., Asamizu E., Tabata S.; "Complete structure of the chloroplast genome of Arabidopsis thaliana.";
thaliana.";
PMA Bes. 6:283-298(1999).
                                                                                                                              O-LINKED (FUC. . .) (IN PAS-6).
O-LINKED (FUC. . .) (IN PAS-7).
                                                                                                                                                                                                                                                                                            71,78; Syrre 28; PR 1; Length 427; 85,78; Pred. No. 8;
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A > F (IN REF. 1).
L -> Q (IN REF. 1).
4 4CHBEE3AlDC4EB24 CRC64;
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                                                                                                                                                     N-LINKED (GLUNAC.
AND PAS-7).
                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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427 AA;
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Best Local Similarity
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TRON-SULFUE FX (4FE-4S) (RY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota: Viridiplantao, Stroptopbyta, Erligophyta, Marchulliophyta,
Marchanliales; Marchanliaceae; Marchanlia,
                                                                                                                                                                                                                                                                                                                                                                                                                                           O; Gaps
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Umesono K., Shiki Y., Takeuchi M., Chang Z., Aota S., Inokuchi H.,
                                                                                                                                                                                                                                                                                    P700 SPECIAL PAIR CHLOROPHYLL AXIAL
LIGAND (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Chloroplast gene organization deduced from complete sequence of
liverwort Marchantia polymorpha chloroplast DNA.";
Nature 322:572-574(1986).
                                                   PROSTE: PS00419; PHOTOSYSTEM_I PSAAB: 1.
Photosynthesis; Photosystem I, Electron transport; Chloroplast;
Thylukoid, Transmembrane, Iron sulfur, 4Fe 45; Chlorophyll
TRANSMEM 46 69 I (POTENTIAL).
                                                                                                                                                                                                                                                                                                              An CHIOPOPHYLI (BY SIMILABITY).
An CHIOPOPHYLI (BY SIMILABITY)
AN PHYLLOGUINONE (BY SIMILABITY)
Al PHYLLOGUINONE (BY SIMILABITY).
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01-JAN-1988 (Rel. 06, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Photosystem I P700 chlorophyll A apoprotein A2 (PsaB) (PSI-R)
                                                                                                                                                                                                                                                                                                                                                                                                            Score 38; DB 1; Length 734;
Pred. No. 14;
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VIII (POTENTIAL).
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MEDLINE=85087956; PubMcd-6393057;
             InterPro: IPR001280; PsaA_psaB.
                            Pfam, PF00223; psaA_psaB; 1.
PKINTS; PK00257; PHOTSYSPSAAB.
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75.0%;
EMBL; AP000423; BAA84384.1;
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or send an email to license@isb-sib.ch).
                          is a phylloquinone and FX is a 4Fe-4S iron-sulfur center. Surgunur. A psaAAR beterrodinor binds the P700 chlorophyll special pail and subsequent chectron accepture. The PSI traction center of higher plants and algae is composed of one at least 11 subunits. SUBCELLULAR LOCATION: Integral membrane protein. Chloroplast
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COFACTOR: P700 is a chlorophyll A dimer, A0 is chlorophyll A, Al
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AO CHLOKOPHYLL (BY SIMILAKITY).
AI PHYLLOGOTNONE (BY SIMILAKITY).
AI PHYLLOGUINONE (BY SIMILAKITY).
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Search completed: September 5, 2002, 15:41:39 Job time: 474 sec

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Gaps

0

1; Indels

Mismatches

Conservative

Matches

2 QGNFNAW 8 |||| || 1| 71 QGNFEAW 77

Query Match Best Local Similarity

71.7%; Score 38; DB 1; Length 734; 85.7%; Pred. No. 14;

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# Copyright (c) 1993 - 2000 compugen (rd

OM protein - protein search, using sw model

September 5, 2002, 15.23.15 , Starch time 122.86 Seconds
(without alignments)
12.673 Million cell updates/sec Pon Chi

US-09-744-804-35 Title: Perfect score:

1 KOGNFNAWV 9 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters: 562222 8645, 172994929 1881459 Searched:

562222

Maximum PR seq length: շոննդորոո Minimum DB seq length: 0

Listing first 45 summaries 100% Post-processing: Minimum Match 0% Maximum Match 100

fungi:\* gs Database

sp\_vertebrate:\*
sp\_unclassified.\*
sp\_rvirus:\*
sp\_bacteriup:\*
sp\_archeap:\* sp\_invertebrate:\* sp\_organelle:\* sp\_rodent:\* sp\_plant:\* sp\_virus:\* sp\_mammal:\* sp\_phage:\* sp\_human:\* sp\_mhc:\* 88... 10... 11... 11... 11... 11... 11...

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result boing printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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Result No.	Score	Query Match	Query Match Length DB	DB	ID	Description
7 7	53	100.0	335	. 4	09BTL9	O9bt19 bomo sapien
2	4 3	81 1	263	٠.	077718	
m	5.4	79.2	282	œ	Q9TNK3	Ogtoka anthogeros
4	4.2	19.5	591	a.	SINLEC	Obtail sphagnam ta
5	4.0	79.2	653	CI	Çapnar	Object Afraga Afraga
9	9.6	73.6	135	æ	033331	O33331 antirrhinum
7	38	71.7	04	7	P77085	
ထ	38	717	160	α	OGTN1.4	OOtz14 physicmitre
5	38	71.7	301	α	OGTNKG	Odtrika colonchapto
10	e e	7 1 7	5.8A	Œ	o I N I to C	Ontrio adjartum ca
11	38	71.7	604	œ	Q9TNJ4	O9tni4 haplomitriu
15	3.7	6.9	297	C	Q94RV6	2946v6 arabidepsis
13	3.7	8.59	345	10	Q9M3U4	O9m3u4 vitis vinif
14	3.7	69.8	379	C	094167	094107 arabidopsis
15	3.7	± 5€	502	٠,٠	<u>0.07</u> 474	Januar saccearano
16	3.7	8.69	817	16		P73619 synechogyst

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Gaps

091gp4 aichi virus	091464 aichi virus		99ep38 equine inte		oggelg equine inte	099dxl equine infe	gerbal alpha prote	Quuga3 dictyosteli	P94774 erwinia chr	Usjjb8 mus musculu	09jmd5 mus mascula	Q9jie7 mus musculu	Q9jiq7 mus musculu	U9hc73 homo sapien	043854 homo sapien	035474 mus musculu	29xy38 acanthamoeb	747dt8 bacillus ha	Q99n72 mus musculu	olf677 homo sapien	Q91v89 human immun	Q99e91 equine infe	ellamonución salmonella	Q57351 salmonella	Q54055 salmonella	y5404≯ salmon⊬ila	Q54045 salmonella	Q54047 salmonella
091004	091464	CHI MENTE	Q9EP38	Q99E51	D i Abaci	099DX1	C9EBU1	¿Velleč	5-3-1-4 P	Ф9ЛЛН8	Q9JMD5	Q9JIE7	091107	Q9HC73	043854	035474	99XY?8		Q99N72	015077	68AI6Ö	Q99E91	Üğül	057351	054055	054043	054045	054047
2	77		15	15	<u>د</u>	12		u ·		Ξ	-	<del></del>		4	٠,	,I	L7	;	Ξ	₹.	<u></u>	15	C a	7	~1	$\sim$ i	~	7
2432	2433	ζ.	135	135	4	135	655	L () -	1. 3	359	359	359	470	371	480	480	187	) (L	928	1564	8	135	14.7	147	147	147	147	147
8.69	69.8	7.		67.8	J.		67.5	6.72	6.19		67.6	67.9	£7 4	67.6	67.73	67.6	67.3	5 . LJ	67.4	67.9	0.99	0.99	0.00	0.99	949	0.99	0.99	0.99
1.7	3.7	τ. τ.	36	36	4°	36	3.6	36	; <b>3</b> ;	36	36	36	ţ	3.6	36	36	36	3.5	36	3.E	35	35	3 L	3.5	£.	10° 60°	35	35
17	18	<u> </u>	20	21	21	23	Ċ	25	36	27	28	29	30	31	C)	33	34	i.	36	3.7	38	36	÷	41	74	43	44	45

# ALIGNMENTS

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01-30W-2001 (TrEMBLrel. 17, Created)
01-30W-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
siMilas 10 Milk PAT GLOBULE NGF FACTOR 8 FNOTEIN.
Mono sapiens (Hunan).
Eukaryota: Metasuan).
Manmalia: Butheria: Primates: Catarrhin: Hominides: Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0\% Score 53; DB 4; Length 335; Best Loral Similarity 100.0%; Pred No 0.041; Matthes 4, Conservative 0; Mismatches 0; Indexes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stroughert P.)
Soberto d (FEE 2001) C. The EMBLYSHEROND TOLKS distances.
-1 SIMILARITY: CONTAINS 1 F5/8 TYPE C DOMAIN.
EMBL BC003610; AAH03610.1; -.
HSSP; P08709; 14F9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS, PRODUCT CEPBLOOD.
SMART; SMOOLD: BGF, 1.
SMART; SMOOLD: BGF, 1.
SMART; SMOOLD: BGF, 1.
SMART; SMOOLD: BGF, 1.
SMART; SMOOLD: BGF, 2.
PROSITE; PSOLOZD: BGF, 2.
PROSITE; PSOLOZD: BGF, 2.
PROSITE; PSOLOZB: BGF, 1.
PROSITE; PSOLOZB: FGF, 2.
PROSITE; PSOLOZB: FGF, 3.
PROSITE
                                                                           PRT; 335 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; iPR000561; EGF-like.
InterPro; iPR001438; EGF_II.
InterPro; iPR000421; FA58_C.
                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
TISSUE=MHLANOMA.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID:9606;
                                                                                                                        09BTL9;
                                                                                09BTL9
RESULT
                                                 O9HTL9
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PRINTS; PR00257; PHOTSYSPSAAB.
   Plam; PF00223; psaA_psaB; 1.
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"Molecular phylytenetic analysis amous bryophytes and Clachcophytes
based on combined data of plastid coded genes and the 18S IENA gene.";
Mol. Biol. Brol. 16:1027-1036(1999).
Biol. Brol. 16:1027-1036(1999).
BISSP: P25896; LIBO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryetu, Viridiplantae, Streptophyta, Embryophyta, Anthorerotephyta,
Anthorerotales, Anthorerotaceae, Anthoreros.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Galis
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Equus caballus (Horse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       c)
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97.5%; Pred. No. 6.5;
alive 0, Mismatches 1, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gentzel M., Toepfer-Petersen E.;
Submitted (AUG-1998) to the EMBL/GenBank/DDRJ databases
EMBL; AJ010121; CAA09010.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          363 AA: 40744 MW: TERBARGSAFR2338D CRC64;
                                                                                                                                                                                                                                                                                                                                                01-NvV-1998 (TrEMBLrel. 08, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SPERM-MEMBKANE ASSOCIATED PROTEIN P47 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2000 (TremBLrel. 13, Created)
01-MAY-2000 (TremBLrel. 13, Last sequence update)
01-DEC-2001 (TremBLrel. 19, Last annotation update)
PHOTOSYSTEM I P700 APOPROTEIN A2 (FRAGMENT).
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                                                                                                                                                                                                                                                . i.dd
                                                                                                                                                                                                                                                                                                                  01-NOV-1998 (TrEMBLirel, 08, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SMO0181; FGF; 1.
SMART; SMO0231; FA58C; 2.
PPRSTTE; PS0022; EGF_1: UNRNOWN_2.
PROSTTE: PS01186; EGF_2; 2.
PROSTTE; PS01285; FA58C_1; 1.
EGF like domain; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Interpro, IPR000561; EGF-1ike, Interpro, IPR000421; FA58_C. Ptam; PF00008; EGF; 1. Ptam; PF00754; F5_F8_type_C; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001280; PsaA_psaB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity Recessive
                                                                                                                                                                                                                                                PPPL LMINAPY;
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                                        271 KOGNENAWY 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SECUENCE FROM N.A.
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1 KOGNENAWV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCB1_Tax1D=9796;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FISSUE-TESTIS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chloroplast.
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NON_TER
SECTIFINGE
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"Molecular phylogenetic analysis among bryophytes and tracheophytes
based on combined data of plastid coded genes and the ISS TRNA gene.";
Mal. Riol. Erel. 16:1927-1936(1999).
                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gabs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptomyces coelicolor.
Battefia, Fimicates, Acticobactaria, Actinobacteridae;
Actinomycetaies, Streptomycineae; Streptomycetaeese: Streptomyces.
NGHLTax1D=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eckarysta, Viridiklantae, Strept-Abyta, Embryskhyta; Brysphyta;
Sphagnopsida: Sphagnales; Sphagnacede; Sphagnum,
NCBI_TaxID=53036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                         Query Match 79.2%; Sears 42; DB 8; Length 282; Best Local Similarity 87.5%; Pred. No. 7.5; Matches 7; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79.2%; Score 42; DB 8; Length 591; 87.5%; Pred. No. 17; Lize 0; Mismatches 1; Indels
Chloroplast.
NON_TER 282 282
SEQUENCE 282 AA; 31691 MW; D4036B585986044 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NON_1EA 221 221 SEQUENCE 591 AA: 65591 MW; 3715F744A52D1442 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-20nd (TrEMBLrel. 13, fast sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PHOTOSYSTEM I P700 APOPPOTEIN A2 (FRAGMENT).
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01-MAY-2000 (TrEMBLrel. 1%, Last sequence update)
01-UNN-2001 (TrEMBLrel. 17, Last annotation update)
PUTATIVE GLYCOSYL TRANSFERASE.
                                                                                                                                                                                                                                                                                                                                                                                                      591 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PKT; 653 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PEINIS; PE00257; PHOTSYSPSAAB.
PROSITE: PS00419; PHOTOSYSTEM_I_PSAAB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=10474899;
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Piam, PF09233, psaA_psaB, 1.
PRINIS, PR00257, PHOTSYSPSAAB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity 87.5%
3. Conservative
                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FRELIMINARY,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDILINE=99404147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sphagnum fallax.
                                                                                                                                                                                                                                                                          71 QGNFEAWV 78
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Chloroplast,
591
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                                                                                                                                                                                                                          2 QCNFNAWV 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP; P25896;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chloroplast.
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RESULT
RESULT
                              P77085
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                                                                                                                                                                                                                                                                                                                                          "A set of ordered cosmids and a detailed genetic and physical map for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=66133694; PubMed=8544819; Schaffner C., Laasch H., Haqemann P.; Schaffner C., Laasch H., Haqemann P.; Detection of point mudations in chloroglast genes of Autirhinum majus L. 1. Identification of a point mutation in the psab gene of a phonocurtam Tentartum mutant ".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Euraryota Viridiplantae, Streptophyta, Embryophyta; Tracheophyta;
Spermatephyta; Magnellophyta, endiestylsdens; Sere Sodists,
Asteridae; euasterids I; Lamiales; Veronicaceae; Antirthinum.
                                                                                                                                                                                                                                                                                       Redenbach M., Kieser H.M., Denapaite D., Pichner A., Cullum J.,
Kinashi H., Hopwood D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79.28; Score 42; DB 2; Length 653; 66.78; Pred; No. 19; 1; Indels dive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73.6%; Score 39; DB 8; Length 135; 75.0%; Pred. No. 12;
                                                                                                    STRAIN=A3(2);
Thomson N.R., Parkhill T., Harrell R.G., Pajandream M.A.;
Submitted (JAN 2000) to the EMBGANEGRADA (JAN 2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    l, indels
                      Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             653 AA; 73160 MW; 97#92D8A805B1A40 0P054;
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                                                                                                                                                                                                                                                                                                                                                                the 8 Mb Streptomyces coelicator A3(2) chromosome.";
Mol. Microbiol 21-77-96(1996).
EMBL; ALL36058; CAB65566 1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PHOTOSETEM I SUBBUNIT.
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Pfam; PF00535; Glycos_transf_2; l
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Mol. Gen. Genet 240-533-544(1995).
                                                                                                                                                                                                                                  STRAIN=A3(2);
MEDLINE-97000351; PubMed=8843436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, X84152; CAA58957.1;
HSSP; P25896; LUBO.
InterPro; IPPO01280, PsaA_psaB
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Seeger K.J., Harris D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
es 6; Conserv
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                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       239 KHGNYNAWL 247
                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=4151;
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SEQUENCE FROM N.A.
Chang E., Allen E., Arauje R., Aparlete A., Davis K., Dundan M.,
Federspiel N., Hyman R., Yalman S., Kemp C., Kurdi O., Lew H., Lin D.,
Namath A., Celner P., Poberts D., Schramm S., Pavis R.W.,
"Sequence of minutes 4.25 of Escherichia coli.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MIShiyama T., Kato M.; "Molecular Phylogenetic analysis among bryephylos and tracheophyles "Molecular phylogenetic analysis among bryephylos and tracheophyles based on combined data of plastid coded genes and the 185 rRNA gene."; MNI Riol From 16:1027-1046(1999).
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                                                                                                                                                                     Escherichia coli.
Bacteria; Proteobacteria, gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Entary day Viridiglandae, Firet' physa, Erby, physa, Roy dhydas
Bryopsida, Engarildae, Funariales, Funariaecae, Physocmitrella.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71.7%; Score 38; DB 2; Length 64; 85.7%; Prod No 9.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          submitted (ph)-1995; to the EMHL/Genhank/Finks databases.
BMHL, 08258; AAR40755.1; -.
Hyperhetical protein.
SEQUENCE 64 AA: 7520 MW; 7225B9EE5E680987 CRC64;
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291 AA: 32606 MW; 8PR9P7179F1E01DB CRC64;
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09TNLA
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PHOTOSYSTEM i P700 APOPROTEIN A2 (FRASMENT).
                                                                                 01-PEB-1997 (TrEMHIREL 02, Last sequence update)
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                                                       01-FEB-1997 (TrEMBLrel. 02, Created)
     PRT:
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PEINTS: PF00257; PHOTSYSPSAAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Physcomitrella patens (Moss).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
Bost Local Similarity 85.77
Matches 6, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
  PRELIMINARY;
                                                                                                                                           HYPOTHETICAL PROTEIN.
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                                                                                    01-PEB-1997
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SEQUENCE
                             P77085;
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P77085
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75.0%; Pred. No. 88;

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Best Local Similarity
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"Molecular phylogenetic analysis among bryophytes and trachcophytes based on combined data of plastid coded genes and the IRS FRNA gene.";
Mol. Biol. Evol. 16:1027-1034 (1999)
HENBL, AROLS6B: RAA83457.1;
HESSP: P25896; 1J80.
                                                                                                                                                                                                                     "Molecular phylogenetic analysis among bryophytes and trackcophytes based on combined data of plastid coded genes and the 18S rRNA gene."; Mol. Biol. Evol. 16:1027-1036(1999)
                                                                                                                            Bukuryota, Viridiplantae, Streptophyta, Coleochaetaceae, Coleochaete.
NORI_Taxib-78178;
                                                                                                                                                                                                                                                                                                                                                                                                           n; Gape
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Filicophyta, Filicopsida, Filicales, Adiantaceae, Adiantum.
                                                                                                                                                                                                                                                                                                                                                                                  71.7%; Score 38; DB 8; Length 301; 85.7%; Pred. No. 43;
                                                                                                                                                                                                                                                                                                                                                                                                            1; Indols
                                                                                                                                                                                                                                                                                                                                              301 AA; 33636 MW; 2572B2BA7B09247E CRC64,
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                                            0)-MAY-2000 (Trembirel 13, Created)
01-MAY-2000 (Trembirel 13, Last sequence update)
01-DEC-2001 (Trembirel 19, Last annotation update)
PHOTOSYSTEM I P700 APOPPOTEIN A2 (FPAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TFEMHITEL. 13, Created)
U-MAY-2000 (TFEMHITEL. 13, Last sequence update)
01-DEC-2001 (TFEMHITEL. 19, Last annotation update)
PHOTOSYSTEM I P700 APOPROTEIN A2 (FRAGMENT).
                      301 AA.
                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
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                      PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDITINES 99404147; PubMed 10474899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Adiantum capillus-veneris (Fern).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001280; PsaA_psaB.
                                                                                                                                                                                                                                                                               InterPro: IPR001280; PsaA_psaB.
                                                                                                                                                                                                                                                                                            Piam: PF00223; psaA_psaB; 1.
PRINTS; PR00257; PHOTSYSPSAAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ptam: PF00223; psaA_psaB; ].
PRINTS: PR00257; PHOTSYSPSAAB.
                                                                                                                                                                                                                                                         EMBL; AB013659; BAA83435.1; -
HSSP; P25896; 1JB0.
                                                                                                                                                                                                                                                                                                                                                                                                           6; Conservative
                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                         Coleochaete nitellarum.
                                                                                                                                                                                                                                                                                                                                   301
                                                                                                                                                                                                          Nishiyama T., Kato M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.R.6
                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN UTEX LB1261:
                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID-13818;
                                                                                                                                                                                                                                                                                                                                  301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               586
                                                                                                                                                                                                                                                                                                                                                                                                                                                  71 QGNFEAW 77
                                                                                                                                                                                                                                                                                                                                                                                                                                    2 QGNFNAW 8
                                                                                                                                                                                                                                                                                                                      Chloroplast.
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                                   COTINK9;
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                      C9TNKS
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                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                              PSAB.
          SANISO
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71.7%; Score 38; DB 8; Length 586

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                    Enkaryota, Viridiplantae, Streptophyta, Embryophyta; Marchantiophyta;
Calobryales, Haplomitriaceae; Haplomitrium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Viridiplantae, Stroptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudiootyledons: core oudioots, Rosidae, eurosids II, Biassicales, Biassicaceae; Atabidopsis.
    sdre)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cheak F., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J., Bowset L., Catuinel F., Dale J.M., Gibson H.A., Goldsmith A.D., Bowset L., Catuinel F., Dale J.M., Gibson H.A., Goldsmith A.D., Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M., Nuyaon M., Ondorra G.S., Palm C.J., Pham P. Y., Ceach H. I., Siferii T., Safeej M., Seylim C.J., Pang C.C., Torlumi M., Yamada K., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis and P. P. Feber J.R.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71.7%; Score 38; DB 8; Length 604; 85.7%; Pred. No. 91;
  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    604 AA: 66805 MW: 834AF409527B0078 CRC64;
                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              G1-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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                                                                                                                                                                                               604 AA.
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana (Mouse ear cress).
                                                                                                                                                                                             PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Interpret IPRGG1280; PsaA_psaB. Pfam; PF00223; psaA_psaB. 1. PPINTS; PPGG257; PHOTSYSPSAAB.
  6; Conservative
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                                                                                                                                                                                               PRELIMINARY;
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                                                                                     71 QGNFETWV 78
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                                             2 QCNFNAWV 9
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Spermatophyta, Magnellephyta, endleskyledens, care endiets, Vitacaca.
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01-DEC-2001 (TEMBLICEL 19, Last annotation update)
HYPOTHETICAL 42.7 KDA PROTEIN (FRAGMENT).
Exabidopsis thaliana (Mouse-car cress).
Evkaryota: Viridiplantae: Streptophyta: Embryophyta, Trachecphyta: Spermatophyta, Magnollophyta, eddicotytedons, core endicots, Rosidae; eurosids 11; Brassicales: Brassicaceae; Arabidopsis.
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                                                                                                                                                      69.8%; Score 37, DB 10, Length 297,
62.5%; Pred. No. 64;
Live 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
Submitted (HPN-2007) to the PMH, Penhark Discussion of the PMBL, AY039860; AAK63964.1; -- SEQUENCE 297 AA; 34133 MW; 2P29AA5P9A00E248 CPG64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=CV. PINOT NOIR;
Selbicke T., Buchholz G., Puegner A., Kassemeyer H.H.;
"Investigations of PP-gene expression in grape.",
Superity of (MAY-2000) to the BMEL/ConPack/FDB3 databases.
BMELLIFOR 79000 CARGISS4 1; -1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro: IPR000490; Glyco_hydro_17.
Pfum: PF00332; Glyco_hydro_17: 1.
PROSTE: PS00687: Glyco_hydro_17: 1.
SEQUENCE: 345 AA; 37456 MW; PP94y:1682131p985 CPC64;
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15, Last sequence update)
19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    345 AA.
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Hypothetical protein.
NON_IER 1
                                                                                                                                                   Query Match
Best Local Similarity 62.55
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vitis vinifera (Grape).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-0CT-2000 (TYFMRLTE)
01-0CT-2000 (TYFMRLTE)
01-DEC-2001 (TYFMRLTE)
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DR
S0
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Gaps
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Eukaryota: Fungi: Ascomycota: Saccharomycotina: Saccharomycetes:
Saccharomycetales: Saccharomycetaceae. Saccharomyces.
                                                                                                                   Ç,
                                                                   69.8%; Score 37; DB 10; Length 479; 100.0%; Pred. No. 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69.8%; Score 37; DP 3; Length 502; 62.5%; Pred: No. 1.16.02;
Live 2; Mismatches 1; Indels
                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Obermaier B., Piravandi E., Pinke M.;
Submitted (MAY-1990) to the EMBL/Genbank/DABJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schaffleyd (MAY 1945) to the FMBL/Confrant/CDFFF databases.
EMBL: 273205: QAA67557.1;
SCHOOLS SQOAD22: YILDSSW.
STGUENCE: 502 AA, 57794 MW, 8P8D01184DAELF6F CRC64;
  42237 MW, *44AAHDDDEtSBD410 CNCt4;
                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TrEMBLEEL 01, Last sequence update)
01-MAR-2001 (TrEMBLEEL 15, Last annotation update)
CHPCMOSLME XII PEAPING FPAMF OPF VIP033W.
                                                                                                                                                                                                                                                                                                                           502 AA
                                                                            100.0%; Pred. w...
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                                                                                                                                                                                                                                                                                                                           PPT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 52.5%
Post Local Sp. Conservative
                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                        PRELIMINAPY;
                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
AM HIS
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Concore porsion 4.5

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OM protein - protein scarch, using sw model

Pub ob: Scprombor E, 2002, 18-27:33 (Without alignments)

(without alignments)

11tle: US-09-744-804-36

Perfect score 1 NullePMWVT 9

Scoring table: BLOSUM62

Searched: 231628 seqs, 24425594 residues
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Total number of hits satisfying chosen parameters: 23162

Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : Issued Patents\_AA:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is delived by analysis of the total score distribution.

# SUMMARIES

		æ			COLUMNIA	
Result		Query				
NO.	Score	Match	Match Length	UB	ID	Description
П	49	100.0	160	C	US-08-162-402B-10	Sequence 10. Appl
€4	64	1000	7 H 7	c i	US 08-162-462B €	· .
3	49	100.0	465	C4	7	Sequence 8, Appli
4	35	65.3	с <u>а</u>	(3)	US:08 940 095:163	10
u)	32	65.3	(1) (1)	~;	US-08 940 093-163	
9	32	65.3	급	ر ب	US-08-940-096-163	163,
7	32	65.3	C4	٦,	US 09 465.719 163	163,
80	32	65.3	CI CI	<b>٠</b> ;	US-09 453-605-163	7
Ś	32	65.3	1147	_	US-08-131-365B-38	38, 7
10	32	65.3	1147	C1	9-80	38
11	31	63 3	342	~	HS OR 78 - 928 1	1
12	31	63.3	342	3	US-08-728-603-17	17,
13	30	61.2	5.50	❖	72-V5(6-074-80-80	Sequence 73, Appl
14	30		4		US-08-318-193-6	
15	30	61.2	4.0	W)	5200327 17	Patent No. 5205927
16	3.0	61.2	54		US-08-214-770 9	
17	30		54	ĽΩ	PCT US95-02885-9	0
18	30	сь (2)	្ម	٠.	0.5-04-070-060-3	~
19	3.0		852	m	US-09-357-746 3	m
20	30		854	<b>~1</b>	US-09-070-060-4	-4
27	30	61.2	854	~	US 09 357-746-4	4
C1	30	•	1091	_	07 - 695	~
23	35	(3) [3]	1041		3.5 - 1.5 -	₹.
24	57	59.5	5.0	4	US-09-177-249:262	35
25	6 <del>.</del>	59.5	182	C Į	US: 08:874 832:17	, ,1
52	62	59.5	185	(2)	08-09 097 233-17	-1
27	62	59.2	197	-	US+08 339 152A-21	21,

DB 2, Length 169;

Score 49, DB 2, Pred. No. 0.08;

100.0%, 100.0%,

Ower, Mutch Bost Loval Similarity

	Sequence 24, Appl
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US -08 - 699 - 1999 H - 12 US -08 - 689 - 276 A 12 US -08 - 689 - 276 A 12 US -099 - 293 - 8 US -099 - 293 - 8 US -099 - 291 -	US-08-111-939-24
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OPERATING SYSTEM: DOS
OPERATING SYSTEM: DOS
SOFTWARE: FASLSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
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          US-08-162-402B-10
; Sequence 10, Application US/U8162402B
; Patent No. 5972337
                                                                                                                                                                                                                                                                                                                                                                                                                                                     30,930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/GOCKET HOMBER, 760
TELECOMMUNICATION INFORMATION:
TELEPHONE: 213-622-7700
TELEFRAX: 213-489-4210
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                                                                                                                                                                                                                                                                  E: Diskette
IBM Compatible
                                                                                                                                                                                                                                                                                                                                     APELITATION NUMBER: US, OR
FILING DATE: 03-DEC-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   150 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                        Amzel, Viviana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: unknown
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
FRICE APPLICATION DATA:
APPLICATION NUMBEE:
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MEDIUM TYPE: Diskett
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                          USA
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                                                                                                                                                                                                                                      90071
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FITLE OF INVENTION: GLOBULE (HMFG) ANTIGEN, FRAGMENTS & FUSION PROTEIN
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STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                              REPERFINCE/DOCKET NUMBER: P66 38215
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; Patent No. 6004925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Dasseux, Jean-Louis
                                                                                                                                                                                                                                                                                                                                                                                                                                            30,930
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TELEPHONE: 213-622-7700
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APPLICANT: Buttner, Klaus
APPLICANT: Cornut, Isabelle
AFFLICANT: Met., Gutther
APPLICANT: Dutoureq, Jean
                                                                                                                                                                                                           IBM Compatible
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IBM Compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     465 amino acids
                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
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                                                                                                                                                                                           Diskette
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                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: peptide US-08-162-402B-8
                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE. Diskett
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CORRESPONDENCE ADDRESS:
                    NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                         APPLICATION NUMBER.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
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TITLE OF INVENTION:
                                                                                                                                                                                                               COMPUTER: IBM CONDERATING SYSTEM: SOFTWARE: FASTSE
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OPERATING SYSTEM:
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es 9; Conserv
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                                                                                                                                    COUNTRY:
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                                                                                                                STATE:
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                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: CERTANI, ROBERTO L.
APPLICANT: PETERSON, JERKY A.
APPLICANT: LAROCCA, DAVID J.
TITLE OF INVENTION: 4.6 FIGHTON HUMAN MILE FAT
TITLE OF INVENTION: GLOBULE (HMFG) ANTIGEN, FRAMENTS & FUSION PROTEIN
0; Gaps
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APPLICANT: PETERSON, JERRY A.
TITLE OF INVENTION: 46 KDALTON HUMAN MILK FAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SYSTEM: DOS
FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Pretty, Schroeder & Poplawski
STREET: 444 South Flower St., 19th Floor
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  0; Mismatches
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FILING DATE: 03-DEC-1993
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                                                                                                                                                                     Sequence 6, Application US/08162402B Patent No. 5972337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 8, Application US/08162402B
; Patent No. 5972337
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REGISTRATION NUMBER: 30,930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION TELEPHONE: 213-622-7700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IBM Compatible
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TELEPAX: 213-489-4210
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  9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: unknown
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MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Disketto
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                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Los Angeles
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
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                                                                        6.3 NLL.RRMWVT 7.1
                                    1 NLI.RKMWVT 9
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  Matches
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                                                                                                                                    RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 49; DB 2; Length 465; 150.0%; Pred. No. 9.22; tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                        SYSTEM: DOS
FastSEQ for Windows Version 2.0
ADDRESSEE: Pretty, Schroeder & Poplawski
STREET: 444 South Flower St., 19th Floor
CITY: Los Angeles
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Best Local Similarity 71.4%; Pred. No. 12;
Matches 5; Conservative 1; Mismatches 1; Indels
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                                                                                                                                                                                                                     QUAL 9 46 - 0004 - 999
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SOFTWARE: FastSEO Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: INS/OR/94/0.095 FILING DATE: 29-SEP-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: 115/08/940,
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APPLICANT: Sevul, Renate
APPLICANT: Buttner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
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                                                                                                                                                                                                  30,742
                                                                                                                                                                                                                     FEFFENCE/LOWKEF NUMBER OF TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                     TELEFAX: 650-444-5454
TELEX: 650-444-5454
INFORMATION FOR SEQ ID NO: 163: SEQUIFOR CHARACTERISTICS:
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US-08-940-095-163
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                                                                                                                                        FILING DATE: ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                             NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30
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TOPOLOGY: linear
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                                                                                                PRIOR APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      435
                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM:
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                                                                           CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE:
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                                                                                                                                                                                                                                                             TELEPHONE:
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Gaps
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TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
                                                                                                                                                                                                         Ouery Match
Best Local Similarity 71.4%; Pred. No. 12;
Matches 5; Conservative 1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Pennie & Edmonds LLP STREET: 1155 Avenue of the Americas
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                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 163, Application US/ORM40096
Patent No. 6046166
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FastSEQ Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Jass ax, Jean-Louis
APPLICANT: Schul, Renate
APPLICANT: Butther, Klaus
APPLICANT: Gorbut, Isabelle
APPLICANT: Merz, Gunther
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71.48;
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V: 530
                                                                                                                                      ) MOLECULE TYPE: NO. 6037323e
US-08-940-093-163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: COTUZZI, Laura A REGISTRATION NUMBER: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
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TELEX: 66141 PENNIE
INFOWMATION POP SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                      LENGIE: 22 amino acids
              TELEX: 66141 PENNIE
INFORMATION FOR SEG ID NO:
                                                  SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Diskette
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650-443-5556
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Best Local Similarity
                                                                                     amino acid
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                                                                                                    STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
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TELEFAX:
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REFERENCEZDOCKET NUMBER: 009196-0004-999
TELECOMMUNICATION INFORMATION:
                                                                                                                                                          STREET: 1155 Avenue of the Americas CITY: New York
                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:

APPLICATION NUMBER- 015/79/453,605
FILING DATE: 26:No. 6329341-1999
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE DESCRIPTION: SEQ ID NO: 163: 08-09-453-605-163
                                                                                                                                           ADDRESSEE: Pennie & Edmonds LLP
                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 08/940,095
                                                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEQ Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 40,742
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Patent No. 5527690
                                                                                                                                                                                                                                                                                 COMPUTER: 1BM Compatible OPERATING SYSTEM: DOS
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Buttner, Klaus
Cornut, Isabelle
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MOLECULE TYPE: No. 6329341e
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Coruzzi, Laura A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 22 amino acids
                                                                                                                                                                                                                                                                    MEDIUM TYPE: Diskette
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TELEX: 66141 PENNIE
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                                                       Dufourcq, Jean
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                                                                                                          258
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                                     Metz, Gunther
                                                                                                                                                                                                            COUNTRY: USA
ZIP: 10035 2811
COMPUTER READABLE FORM:
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Best Local Similarity 71.4%
Local 5, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
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                                                                                                          NUMBER OF SEQUENCES:
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STREET: P.v.
TV: Houston
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TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
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 1; Indels
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1; Mismatches
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                                                                                                                                                          Sequence 163, Application US/09465719
Patent No. 6265377
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Patent No. 6329341
GENERAL INFORMATION:
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FILING DATE: 29-SEP-1957
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                          APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Hartner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
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08-09-465-719-163
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TFLEPAX: 650-493-555
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INFORMATION FOR SEQ 1D NO:
SEQUENCE CHARACTERISTICS:
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5; Consorvativo
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                                                                                                                                                                                               GENERAL INFORMATION:
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08-09-453-605-163
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AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
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APPLICANT: Briggs Michael R.
APPLICANT: Wang, Xiaodong
APPLICANT: Goldstein, Joseph L.
TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING
TITLE OF INVENTION: TO STEROL REGULATORY ELEMENT BINDING
TITLE OF INVENTION: PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65.3%; Score 32; PB 4; Length 22; 71.4%; Pred. No. 12;
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TITLE OF INVENTION: APOLIFOPROTEIN A-1 AGONISTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  METHODS AND COMPOSITIONS RELATING
TO SIEKOL RECULATORY ELEMENT BINDING
PROTEINS
                              COMPUTER: IBM PC COMPACATION
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                              REFERENCE/IOSTRET NUMBER: UISU:372/PAR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
IELEFAX: (512) 474-757;
INFORMATION FOR SEQ ID NO: 38:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTPATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: UTSD:372/PAR
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 64
COPPESPONDENCE ADDRESS
ADDRESSEF Arnold, White & Durkee
STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US/08/668,12
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SYSTEM: PC-DOS/MS DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Brown, Michael S.
APPLICANT: Brigs, Michael R.
APPLICANT: Wang, Xidodouq
APPLICANT: Goldstein, Joseph L.
ITTLE OF INVENTION: METHODS AND C!
ITTLE OF INVENTION: TO SIEMOL REGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 38, Application US/OR668123; Patent No. 5891631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OR/141, 465
                  Eloppy disk
IBM PC compatible
                                                                                                                                                                ATTORNAL TOTAL TANDERS ATTORNAL NAME: Parker, David L. PEGISTPATION NAMEF: 32,165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (512) 418-3000
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ATTORNEY/AGENT INFOPMATION:
                                                                                                                               FILING DATE: 01-OCT-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                    LENGTH: 1147 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14 - TIIN - 1996
I: 435
                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA: APPLICATION NUMBER: US.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Parker, David L. REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
COMPUTER READARLE FORM: MEDIUM TYPE: Florey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                          amino acid
                                                                                                                                                                                                                                                                                                                                                                                             linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Houston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Texas
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                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-668-123-38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER:
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APPLICANT: Gershengorn, Marvin C.
APPLICANT: Arvanitakis, Leandros
APPLICANT: Geras-Raaka, Elizabeth
APPLICANT: Geras-Raaka, Elizabeth
APPLICANT: Cesarman, Ethel
TITLE OF INVENTION: RECEPTOR OF HAV 8 AND METHOD OF DENIED
TITLE OF INVENTION: ANTAGONISTS OF G PROTEIN COUPLED
TITLE OF INVENTION: ANTAGONISTS OF G PROTEIN COUPLED RECEPTORS
                                                                                                                                                                                                                                                                                  S, Galvs
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                                                                                                                                                                                                                                  Query Match 65.3%; Seore 32; DB 2; Londth 1147; Bost Local Similarity 62.5%; Prod. Ro. 5e:02; Matches 5; Conservative 3; Mismatches 9; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 05/08/785,928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Nikon, Hargrave, Eevans & Soyle LLP SIREET: Clinton Square, P.O. Box 1051
CITY: Rochester
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19603/1320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              // Sequence 1, Application 05/08785928
// Patent No. 6087115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Goldman, Michael L. REGISTRATION NUMBER: 30,727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/POCKET NUMBER: 196
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (716) 263-1304
TELEPAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 22-JAN-1997
CLASSIFICATION: 435
ATTOPHEY, ACTENT INFORMATION:
TELEPAX: (512) 474-7577
INPORMATION FOR SEQ ID NO: 38
SEQUENCE CHARACTERSICS:
LENUTH: 1147 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Floppy disk
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                                                                                                                                      MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: protein
US-08-785-928-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
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STRANDEDNESS:
                                                                                              amino acid
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                                                                                                                                                                                                                                                                                                                                                                           634 HLLQRLWV 641
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276 LLEREWI 282
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ZIP: 14603
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                                                                                                                TOPOLOGY:
                                                                                                                                                               118-04-458-123-38
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                                                      GENERAL INFORMATION:
APPLICANT: Cesarman, Ethel
APPLICANT: Knowles, Entiel M.
APPLICANT: Nowles, Entiel M.
TITLE OF INVENTION: PROTEINS OF KAPOSI'S SAPCOMA ASSOCIATED
TITLE OF INVENTION: HERPESVIKUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oucry Match 63.3%; Score 31; DB 3; Length 342; Hest Local Similarity 71.4%; Pred. No. 2.4e+02; Matches 5; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOUS/MS-DOUS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                         NUMBER OF SEQUENCES, 19
CORRESPONDENCE ALDRESS:
ADDRESSEE NIXON, HAPGRAVE, DEVANS & DOYLE ILP
STREET: Clinton Square, P.O. Box 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1155 Avenue of the Americas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/728,603
FILING DATE: 10-OCT-1996
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Patent No. 6309820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
AFFLICANT: HOFFMAN, No. 6309826h,
AFFLICANT: RAY, Brian K.
APPLICANT: FOWIKES, Dana M.
                 Sequence 17, Application US/U8728603
Patent No. 6093806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: McCONNELL, Stephen J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY AGENT INFORMATION:
NAME: BRAMAN, SUSAN J.
REGISTRATION NUMBER: 34,103
                                                                                                                                                                                                                                                                                                                                                                         IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE TO CKET NUMBER 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 716-263-1600
INFORMATION FOR SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                                                 Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 716-263-1636
716-263-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     342 amino acids
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US 08-728-603-17
                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
TITLE OF INVENTION
                                                                                                                                                                                                                                                                   New York
: USA
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US-08-728-604-17
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                                                                                                                                                                                                                                                                                       COUNTRY:
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APPLICANT: GARVIN, Robert T.

APPLICANT: MALEK, Lawrence T.

TITLE OF INVENTION: AN EXPRESSION SYSTEM FOR THE SECRETION

TITLE OF INVENTION: OF BLOADLIVE BUMAN GRANULOCTTE MACROPHAGE COLONY

TITLE OF INVENTION: STIMULATING FACTOR (GM CSF) AND OTHER HETEROLOGOUS

TITLE OF INVENTION: PROTEINS FROM STREPTOMYCES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61.2%, Score 30, DB 4, Length 39;
66.7%; Pred. No. 45;
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                                               CURRENT APPLICATION DAIN.

APPLICATION DAIN.
APPLICATION DAIN.
APPLICATION NUMBER: US/08/630,915*
FILING DATE: 03-APP-1008
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Foley & Latumer street 1800 biagonal Road, Suito 500
                                                                                                                                                                                                                        NAME. Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
PPPERBRUCE/DOCKET NUMBER: 1101-174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/07/935,314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IBM PC compatible
SYSIEM: PC-1008/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6, Application US/08318193
Patent No. 5641663
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                     NR: (212) 790-9090
(212) REG-REGA/9741
66141 PENNIE
                                    8: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54,768
                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PEPERENCE/TROCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                        39 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: BENT, Stephen A. REGISTRATION NUMBER: 20
                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               h; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: unknown
MOLECULE TYPE: peptide
                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: AN ITILE OF INVENTION: OF TITLE OF INVENTION: STITLE OF INVENTION: PINUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Virginia
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                                    MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILLING DATE:
                                                                                                                                                                                                                                                                                                       TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-630-915A-73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
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us-09-744-804-36.rai

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APPLICANT: GARVIN. ROBERT T.: MALEK, LAWRENCE T.
TILLE OF INVENTION: EXPRESSION SYSTEM FOR THE SECRETION OF SHOACTIVE HUMAN GRANDLOCYTE MACHORHAGE COLONY STIMULATING: FACTOR (GM-CSF) AND OTHER HETEROLOGOUS PROTEINS FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 61.2%, Score 30, DB 6, Length 40; Best Local Similarity 44.4%; Pred. No. 46; Matches 4; Conservative 3, Mismatches 2; Indels
                                                                                                                                                                                                                                                                                        Owery Match 61 2%; Score 30; DB 1; Length 40; Best Local Similarity 44.4%; Pred. No. 46; Matches 4; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scarch completed: September 5, 2002, 15:27:34
Job time: 319 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/37/224,568
FILING DATE: 26-JUL-1988
: TELECOMMUNICATION INFORMATION:
: TELEPAN: (703)836-9300
: TELEFAX: (703)683-4109
: TELEX: 899149
: INFORMATION FOR SEO ID NO: 6:
: SEQUENCE CHARACTERISTICS:
: LENGIH: 40 amino acids
: TYPE: amino acid
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
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5200327-17
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# GenCore version 4.5 copyright (c) 1993 2000 Compugen Ltd.

protein search, using sw model OM proteiu

September 5, 2002, 15-31-39; sourch time 23,39 seconds (without alignments) 10.252 Million cell updates/sec Ruti on:

US-09-744-804-36 49 1 NLL.RRMWVT 9 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters.

105224 seqs, 38719550 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post processing: Minimum Match 0%

Swissprot\_40.\* Database :

Listing first 45 summaries

Maximum Match 100%

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by unalysis of the total score distribution.

# SUMMARIES

	-	Description	Q08431 homo sapien	bos t	056892 yersinia cn		P41610 pinus thunb		P79385 Sus Scrola	P57388 buchnera ap			P46580 caenorhabdi	P55145 homo sapien		PSS442 rhizebium s	P50147 gallus gall	P44246 haemophilus			Q9asq4 populas tre	P56720 rattus norg		2604 (Controllars		Q93105 aedes aegyp	Q25490 manduca sex				m) sámm mer 361653			c ı	O66431 aquifex acc
SUMMARIES	į		MFGM_HUMAN	MPCM_BOVIN	FLCA_YEREN	RK20_MARPO	RK20_PINTH	P152_METTH	MFGM_PIG	ODO1_BUCA1	PK20_CHLPE	NU5C_DIGGR	YLR5_CAERI	ARGR_HUMAN	Y 195_CAREI	Y4FP_PHISN	GB12_CHICK	YE35_HAEIN	VIE4_FPG3V	EX7L_PASMU	FGMU_FOFTN	SPF1_PAT	MOH JO HOWAY	SKETTING	SRE1_HUMAN	INSR_AEDAE	AFLF_MANSE	RK20_POPPH	RK20_ARATH	FL20_SYNY3	PKCO_MAI?F	PK20_SPIOT	RK20_TOBAC	CPSR_STPAG	PI 3_AQUAE
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æ		Match	100.0	86.8	77.6	71.4	71.4	71.4	71.4	71.4	ъд Ф	69.4	٠.			и		ır,	ıc,	2	u)	u.	u .		ıo	ري		œ.		63.3	~	Ċ,	63.3	ر م	63.3
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### ALIGNMENTS

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		STANDARD;
		01:00T-1996 (Rel. 34, Created)
		01-NOV-1997 (Rel. 35, Last sequence update)
		16-56T-2001 (Rel. 40, Last annotation update)
	3	8) (MFG-H8)
	丑	Med
	Z	MFGE8.
	S	Homo sapiens (Human).
	ũ	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi:
	Š	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
	×	NCBI_TaxID=9606;
	Z.	
	æ.	SEQUENCE FROM N.A.
	S	TISSUE-Breast, and Breast careinoma;
	××	MEDLINE 96213908; Pubmed=8639264;
	٧×	Couto J.R., Taylor M.R., Godwin S.G., Ceriani R.L., Peterson J.A.;
	ţ	"Cloning and sequence analysis of human breast epithelial antigen
	Ç	BA46 receals an BGD oull adhesion sequence presented on an epiderma
	4.L	growth factor-like domain.";
	Ę	DNA Cell Biol. 15:281-286(1996).
	z.	(2)
	<u>.</u>	SHOUSENCE OF IVU-387 FROM N.A.
	Ų :	Tissur Mammary qiand;
	×	
	<b>≲</b> ;	D., Peterson J.A., Urrea R., Kumiyoshi J., Bistrain
	<b>5</b> 5	Certani K.L.;
	- 1	A Mr 46, 000 minan milk 1at atobute protein that is highly expresse
	₩;	in human breast tumors contains factor VIII-like domains.";
		Cancer Res. 51:1994-4998(1991).
	Z.	
	<u>د.</u>	PARTIAL SEGUDNOD, AND CHARACIERIZATION.
	Ç	TISSUE-Milk;
	×	MEDLINE-98194924; Pubmed-9535276;
	Υ.	Sintitida M.G., Caralette M., Cidnia C., Conta A.,
	<b>.</b> 5	Godovac Zimmermann J.:
	L	"Isolation and characterization of full and truncated forms of huma
	T.	breast cardinema protein BA46 from human milk tat globule membranes
	<del>-</del>	J. Protein Chem. 17:143-148(1998).
	ž	[4]
	5.5	SECUENCE OF 268 317, AND IDENTIFICATION OF MEDIN.
	×	MIDILINE 99342070, Pubmed 10411933;
	4	Harmanist B., Marshand H., Shetten H., Wistermark 5.11., Hucchiano
	<b>S</b>	Tiersberg 1.0., Nordstedt 0., Engstroem 0., Westermark P.,
	E	"Medin: an injectal tradment of acutic smooth muscle cell-produced
	- E	integral forms the most connected and only of all the
	1 5	1.5. SALINGTON OF THE CONTRACT
		These Maintenances between the constraints of the c
	z:	
	-	CHARACTER SATION.
	×	MEDLINE 97405885, Pubmed 026929;
	ζ.	Tajler M.E., Marr T.E., Stallan C.D., Ceriani K.L., Peterson J.A.,
	ŧ	"Lactadherin (turmerly BA46), a membrane associated glycoprotein
	E.	expressed in buman with and breast cardinamas, promotes Arg ${ m GLy} ext{-Asp}$

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SP47) (BP47) (Components 15/16).
                       MFGE8
 This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWIS institute of Bioinformatics and the EMBL outstafform the Buropean Richarders institute of Bioinformatics in the area are more restrictions on its use by non-profit institutions as long as its content is it no way modified and this statement is not removed. Usage by and for commercial entities requires a license alreaded the statement (See http://www.isb-sib.ch.) or send an email to license-isb-ch.
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                                              -!- FUNCTION: MEDIN IS THE MAIN CONSTITUENT OF ACHTEC MEDIAL, AMILEATOR -!- SUBCELLULAR LOCATION: PERIPHERAL MEMBRANP PROTEIN.
-!- TISSUE SPECIFICITY: MAMMARY RETTHELIAL OFLI. SUPFACES AND ACPTIC MEDIA. OVEREXPRESSED IN SEVERAL CARCINOMAS.
-!- PIM: MEDIN HAS A RAGED N-TERMINUS WITH MINOR SPECIES STARTING AT
             FUNCTION: MAY BE INVOLVED IN PHOSPHOLIPID BINDING. BINDS SPECIFICALLY TO POTAVIPIS AND INHIBITS ITS PEPLICATION. FUNCTION: MEDIN IS THE MAIN CONSTITUENT OF ACPTIC MEDIAL AMYLOID
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P5/8 TYPE C 2.
CELL ATTACHMENT SITE (POTENTIAL).
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SMARF: SM00181; EGF: 1.
PROSITE: PS00022: EGF: 1.
PROSITE: PS01285; EA58C_1: 2.
PROSITE: PS01285; EA58C_1: 2.
PROSITE: PS01285; EA58C_2: 2.
S40011; C1ycoprorecting Milk, Pepeat; EGF: 11ke demain: Amyloid, S100AL.
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100 0%; Pred No. 0.021;
tive 0, Mismatches 0, Indels
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N-LINKED (GIGNAC.
N-LINKED (GIGNAC.
                                                                                                                                                             SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN. SIMILARITY: CONTAINS 2 F5/8 TYPE C DOMAINS.
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DNA Cell Biol. 16:861-869(1997).
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InterPro; IPR000421; FA58_C.
Ptam; PF00008: EGF; 1.
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-!- FUNCTION: PROBALY ASSOCIALES WITH PROSHOLIFIUS ON THE SURFACE OF MAMARY EPITHELIAL CELLS AND MILK FAT GLOBULES. ZONA PELLUCIDABLINDING PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mather I.H., Banghart L.R., Lane W.S., "The major fat globale membrane profess. Estimated fat globale membrane profess. Estimated by S. are homologous to MGF-EB, a murine glycoprotein containing epidermal growth factor-like and factor V,VIII like sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -i- TISSUE SPECIFICITY: MILK AND SPERMATOZOAN.

FTM: THE 2 O LINKED GLYZANS CONSTIST OF GAL, GLCNAC AND FUC, WITH POPULARY FID: AS FEHICINY TERMINALS SUGAR.

FOCH LARRY FOR TOWN THE PROMAINS.

-I-SIMILARITY: CONTAINS 2 FSF-LIKE DOMAINS.
                                                                                                                                                                                                                                        SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND CARROHYDRATE-LINKAGE SITES.
STRAIN=HOLSTEIN, TISSUE-Mammary gland,
MEDLINE=97008954; Pubmed-8856064;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS, A LONG FORM (SHOWN HERE) AND A SHORT FORM, ARE PRODUCED BY ALTERNATIVE SPLICING. THE SHORT FORM LACKS 53 AMINO ACIDS WITHIN THE F5/8 TYPE C 1 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Melecular chesisa of appropriatein antites. MSFC2/S2 recognised by monoclosal antibodies raised against bovine milk fat globule membrana ".
Bos taurus (Bovine).
Fukaryota, Metazza, Chordata, Craniata, Vertebrata, Euteleosfomi;
Mammalia; Eutheria; Cetartiodactyla, Ruminantia, Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                              "Tharacterization of giycoprotein PAS-5/7 from membranes of boyine milk fat globules.",
                                                                                                                                                                                                                                                                                                                                                                  Hearregaard I , Andersen M.H., Berglund L., Pasmussen J.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Aoki N., Kishi M., Taniquchi Y., Adachi T., Nakamura R.,
Matsuda T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (SPV:1997) to the LMRC, Sentents, 2008 databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 140-146; 174-187; 233-246 AND 422-427.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Riochim, Biophys, Acta 1245:385-391(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J. Bicchem. 240:528-535(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Mammary qland;
MEDLINE=96125736; PubMed=8541316;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-93250576; PubMed-8485470;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PP00754; F5_F8_type_C; 2.
SMART; SM00181; EGF; 2.
SMART; SM00231; FA58C; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro: IPR000561; EGF-like.
InterPro: IPR000421; FA58_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 19-427 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SHUBENCE OF 18-427 FROM N.A.
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HSSP; P00740; 1EDM.
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PROSLIE; PROL186; EGE_2; 2.
                                                                                                                          Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00008; EGF; 2.
                                                                                                                                                                NCB1_TaxID=9913;
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                                                                                                                                                                                                                                                O-LINKED (FUC. . .) (IN PAS-5).
O-LINKED (FUC. . .) (IN PAS-7).
N-LINKED (GLONAC. . .) (HYPRID) (IN PAS-5).
                                                                                                                                                                                                                                                                                               H LINKED (CICNAC. . .) (HIGH MANNOSE) (IN PAS-6).
MISSING (IN SHORT ISOPORM).
                                                                                                                                                                                                                                                                                                                                                                                                                               Caps
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Faucennier A., Allacui A., Tan Misen A., Octholis G., Bollen A.,

Submitted (MAY-1995) to the EMBL/GenBank/DBbJ databases.

-!- FUNCTION: IN THE ASSEMBLY PROCESS OF THE P-RING
FORMATION. IT MAY ASSOCIATE WITH FIGE ON THE POD CONSTITUTING A
STRUCTINE FSSEMIAL FOR THE P-PING ASSEMBLY OF MAY ACT AS A
MODITATOR PROTEIN FOR THE P-PING ASSEMBLY (RY SIMILAPITY).

-!- SUBCELLULAR LOCATION, Periplasmic (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria, Enterbatteria, gamma subdivision, Enterobacteriaceae;
                                                                                                                        CELL ATTACHMENT SITE (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NoV-1997 (Rel. 35, Created)
01-NoV-1997 (Rel. 35, Last Sequence update)
30-MAY-2036 (Rel. 39, Last annotation update)
Flagella basal body P-ring formation protein flgA precursor
                                                                                                                                                                                                                                                                                                                                                                                                   89.8%; Score 44; DB 1; Length 427; 77:8%; Prod. No. 0.22; 19r 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                               4CBBEE3AlDC4EB24 CRC64;
                      Signal: Glycoprotein, Milk, Popent: FO: -like domain:
Alternative splicing.
                                                                                                                                                                                                                                                                                                                                      A -> F (IN REF. 1).
L -> Q (IN REF. 1).
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                                                           LACTADHERIN.
ESP-LIKE 1.
EGF-LIKE 2.
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PROSITE; PS01285; FA58C_1; 2.
PROSITE; PS01286; FA58C_2; 2.
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Best Local Similarity 77.89
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265
427
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35
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777
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105
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427 AA.
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Q56892:
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DOMAIN
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                                                                                                                                                                                    Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEGURECH FROM M.A.
MENLINE 8966867: PubMed=3199436;
Fukuzawa H., Kohchi T., Sano T., Shirai H., Umesono K., Inokuchi H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OZAKI H., Ohyama K.;
"Structure and organization of Marchantia polymorpha chloroplast
genome. III. Gene organization of the large single copy region from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chyama K., Fukudawa H., Kohchi I., Shirai H., Sano I., Sano S.,
Uncasus K., Shiki Y., Takeuchi M., Chang E., Acta S., inckuchi H.,
Ozeki H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Coding sequences for chloroplast ribosomal protein 312 from the "Coding sequences for chloropha, are separated far apart on the different DNA strands.";
PERS Letr. 198:11-15(1986).
! SIMILARITY. BELCHGS TO THE LEOP FAMILY OF KIBOSOMAL PROTEINS.
                                                               FLACELLA BASAL BODY P-RING FORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Chioroplast gene organization deduced from complete sequence of
liverwort Marchantia polymorpha chioroplast DNA.";
Nature 322:572-574(1986).
                                                                                                                                                                                    ö
                                                                                                                                              77.6%, Deare 39, DB 1, Longth 224 62.5%, Pred. No. 1.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fukuzawa H., Robchi I., Shirai B., Ohyama K., Umesono K.,
Inokuchi H., Ozeki H.;
                                                                                                                                                                                   0; Indels
                                                                                              B98B74FBC7862A49 CRC64:
                                                                                                                                                                                                                                                                                                                                                                      01-JAN-1988 (Rel. 06, Created)
01-BC-1992 (Rel. 24, Last sequence update)
16-GE - 2001 (Rel. 40, Last annotation update)
Chloroplast 50S ribosomal protein 120.
                                                                                                                                                                                                                                                                                                                                          PRT; 115 AA
                                                                                                                                                                                   2; Mismatches
                                                                               PROTEIN FLGA.
                                               POTENTIAL.
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Pram; PF00453; Ribosomat_L20; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Marchantia polymorpha (Liverwort).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mol. Biol. 203:333-351(1988).
                            Flagella, Periplasmic, Signal.
1 26 P
                                                                                               224 AA; 24351 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X04465; CAA28108.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mendel, 4704, MARpo, rp120;1.
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                                                                                                                                                                                 5; Concernative
              EMBL, 248169; CAA88191.1;
                                                                                                                                                                                                                                                                                                                                          STANDARD;
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Best Local Similarity
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                                                                                                                                                                                                                                                     159 NMLRRLWI 166
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                                                                                                                                                                                                                     1 NILLERMWV 8
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                                                                                               SECUENCE
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                                                                 CHAIN
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MFGM P1G
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                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eubaryota: Viridiplustae, stroptophyta, Pubcycphyta, Truchesphyta,
Spermotophyta: Conferopsida; Conferatos, Pinacége; Pinus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Loss of all ndb genes as determined by sequencing the entire chloroplast genome of the black pine Pinus thunbergih."; Proc. Natl. Acad. Sci. U.S.A. 91.9794-9798 (1994).
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                                                                                                                                                                                                                                                                                    Length 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71.4%; Score 35; DB 1; Length 118; 71.4%; Pred. No. 3.4;
                                                                                                                                                                                                                                                                                                                                                     0; Indels
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                                                                                                                                  0 0 BY SIMILARITY.
115 AA: 13475 MW: A91B680F1D777A39 CRC64;
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RGFF4020658B0673 0R064;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pinus thumbergii (Green pine) (Japanese black pine).
                                                                                                                                                                                                                                                                                71.4%; Score 35; DB 1;
71.4%; Fred. No. 3.3;
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PPOSITE; PS00937; RIBOSOMAL_L20; 1.
Ribosomal profein; rMNA-binding; Chloroplast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NoV-1995 (Rel. 32, Last sequence update)
16-ovr-2001 (Rel. 40, Last annotation update)
Chloroplast 50s ribosomal pretein L20.
                             Probom, Phon2289; Pibosomal_[20; 1
PROSITE; PS00937; R1BOSOMAL_L20; 1.
Ribosomal protein; FRNA-binding: Chioroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              186 AA.
                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mendel: 19014; FINth;rp120;1.
InterPro; IPR0010R1; Bibosomal_120.
Pfam; PP00453; Ribosomal_120; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIJINE-95024047; PubMed-7937893;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Rel. 32, Created)
(Rel. 32, Last sequ
PRINTS: PPOUCO62; RIROSOMALL20.
Probom, Phon2389; Pibosomal_L2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00062; RIBOSOMALL20
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                                                                                                                                                                                                                                                                                                             Best Local Similarity 71.49
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; D17510; BAA04342.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID-3350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56 LRRIMIT 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56 LRRLWIT 62
                                                                                                                                                                                                                                                                                                                                                                                                                       * L.K.KMWVT 9
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01-NoV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chloroplast
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sugiura M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P152_METTH
IO P152_METTH
                                                                                                                                  INIT_MET
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Smith D.R., Dougette Stamm L.A., Beloughery C., Lee H. M., Dudois J., Aldredge T., Bashirzadeh E., Blakely D., Cook R., Gilbort K., Harrison D., Hoang L., Keadle P., Lumm W., Pothier B., Oin D., Spadafora R., Vicare R., Waller P., Lumm W., Pothier B., Oin D., Fyadafora R., Vicare R., Wash D., Safer H., Patwell D., Prabhakar S., McFeugall S., Shimer G., Goyal A., Pietrovski S., Church G.M., Daniels C.J., Mao J.-1., Rice P., Noelling J., Revee J.N., Complete genome sequence of Methanobacterium thermonutotrophicum deltath functional analysis and comparative genomics.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Caps
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30-MAY-2000 (Rel. 39, Last annotation update)
Lactadherin (Milk fat globule BGF factor 8) (MFG E8) (MFGM) (Sperm MFGE8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         christendat D. Yee A. Dharamsi A. Kluqer Y. Savehonko A.,
Colt J.E., Booth V. Mickereth C.E., Sailfakis V., Eblel L.,
Forlev S., Maxwell K.L., Wu N., McIntesh L.P., Gehring K.,
Kennedy M.A., Davidson A.R., Pai E.F., Gerstein M., Edwards A.M.,
Arrowsmith C.H.;
                                                                                                                                                                                                              Archaea: Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71.4%, Score 35; DB 1; Length 186; 55.6%, Pred. No. 5.5;
1ive 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20323 MW; 6997E8C6D9234A89 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -! SIMILARITY: BELONGS TO THE FLAVOREDOXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Piam; PF01613; Flavin_Reduct; 1.
Flavopiolein; FMN; 3D-structure; Complete proteome
40, Created)
40, Last sequence update)
40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            409 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Structural proteomics of an archaeon."; Nat. Struct. Biol. 7:903-909(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to licensewisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
MEDLINE:20473232; PubMed-11017201;
                                                                                                                                                                           Methanobacterium thermoautotrophicum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PDB: 1EJE: 11-0CT-00.
InterPro: IPR002563; Flavin_Reduct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-98037514; PubMed-9371463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMMIL; AEGOOROR; AAR84658,1; -.
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Matches 5; Conservative
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                                                                                                                                                                                                                                              Methanothermobacter.
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                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                  NCB1_Tax1D-145z62;
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16-00T-2001 (Rel.
16-00T-2001 (Rel.
16-00T-2001 (Rel
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                                                                                                       Protein MTH152.
                                                                                                                                                                                                                                                                                                                                                                                      STRAIN DELTA H;
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                                                                                                          Submitted (NOV-1997) to the EMRL/Gerbank/EDRT databases.
-!- FUNCTION: MAY RE INVGLVED IN PROSPROLIPID BINDING. ZONA PELLUCIDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SdE
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N. 11 NKED (GLCNAC. . ) (POTENTIAL).
N. 11 NKED (GLCNAC. . ) (POTENTIAL).
         Bukaryota, Metažoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Cetarticdarfyla, Spina, Spidac, Sus.
NCBL_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BOCOTAPBOD29927A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-org-2051 (bel 45, created)
16-org-2051 (bel 40, last sequence update)
16-org-2051 (Rel 40, last annotation update)
2 oxoglutarate defydrogenase El component (EC 1.2.4.2) (Alpha-ketoglutarate dehydrogenase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CELL ATTACHMENT SITE (POTENTIAL).
                                                                                                                                                      -1- SUBCELLULAR LOCATION: PEPTPHEPAL MEMBPANF PPOTFIN.
-1- TISSUE SPECIFICITY: MAMMAPY EPITHELIAL CELL SUPFACES AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71.4%, Score 35; DB 1, Lkngth 409,
88.9%; Prod. Mo. 12;
Tyon 0; Mismatches 1; Indele
                                                                                                                                                                                                -1- SIMILARITY: CONTAINS 2 EGR-LIKE FOMAINS.
-1- SIMILARITY: CONTAINS 2 ES/8 IYVE G LOMAINS.
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PS/R TYPE C 2
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41 BGF-LIKE 1.
94 PMF-LIKE 2.
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                                                                                                                                                                                                                                                                                                                                                                                                            Pram; PP00008; EGF; 2.
Pram; PP00008; EGF; 2.
SWART; SMO118; FGF; 2.
SWAPT; SMO118; FGF; 2.
PROSITE; PS00022; EGF; 2.
PROSITE; PS01186; EGF; 2.
PROSITE; PS01185; EGF; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45725 MW;
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InterFig. IFR005561, FGF 178-
InterPro; IPR000421; FASE_C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE, FS01284, PAS80
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247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glycoprotein; Repeat;
                                                                                                                                        RINDING PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         152 NLLRPMPVT 160
                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                    SPERMATOZOAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 NLLERRMWVT 9
Sus serofa (Pig)
                                                                                   TISSUE-Testis;
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                                                                                                 Ensslin M.A.
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P57388:
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DOMAIN
POMAIN
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this SWISS-PPOL entry is empyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non profit institutions as Irng as its content is in no wa
                                                                                                                                                                                                                                                                                                                                                                                                           DATUTE 407: 81-26 (2000).

-!- FUNCTION: THE 2-6XOGLUTARATE DEHYDROGENASE COMPLEX CATALYZES THE COPERAL CONVERSION OF 2-6XOGLUTARATE TO SUCCITARI-COA & GO(2). IT CONVERSION OF 2-6XOGLUTARATE TO SUCCITARI-COA & GO(2). IT CONTAINS MULTILE COPIES OF 3 ENYMATIC COMPGNENTS: 2 GYGLUTARATE IGHTERMS: 2 AND IGHTERMS: 2 GYGLUTARATE IGHTERMS: 3 AND IGHTERMS: 2 GYGLUTARATE IGHTERMS: 3 GYGLUTARATE IG
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Burkhera aphidicola (subsp. Aryrthosiphon pisum) (Aryrthosiphon pisum
                                                                                                                                                                                                                                                                MEDLINE-20445173; PubMed-10993077;
Shiricnobu S., Vatanabe H., Ballori M., Sakaki Y., Ishikawa H.;
"Genese sequestive of the endocellalar bacterial symbiont of aphids
Buchnera sp. APS.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam, FP00676, EL_dehydrog; 1.
Olyvelysis, Paldoreductuse, Flavegrutein; Thiamine pyraphosphate;
Complete profesme.
SEQUENCE 555 AA, 105806 MW, AET39F80D9F90F8B 0R064:
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Chlamydomonadaceae; Chlamydomonas,

    SIMILARITY: BELONGS TO THE LOOP FAMILY OF RIBOSOMAL PROTEINS.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71.4%; Score 35; DB 1; Length 909; 55.6%; Pred. No. 29; 1; M. Smart here 2; Ind 3.
                                                                     Bacteria, Protechacteria, gamma subdivision, Buchmera.
NCBI_PaxID-118099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-AuG-1992 (Rel. 23, Created)
01-DEC-1992 (Rel. 24, Last Sequence update)
16-GT 2001 (Rel. 40, Last annotation update)
Chloroplast 50s fibosomal protein 220.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SURGNIT: HOMODOIMER (HY SIMILARIEY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : Läd
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AP001118; BAB13011.1; -. InterPro; IPR001017; El_dh.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro: IPR002088; PPTA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chlamydomonas reinhardtii.
Chloroplast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3. 1 to 138.3 C
                                            symbictic bacterium).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Bost Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  157 NLLEKQWIT 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SHOUENCE FROM N.A.
                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN FORYO 1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 NLLRRMWVT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCB1_TaxID=3055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-2137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHLRE
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P26565;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RK20_CHLRE
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the Buropean Riointormatics Institute. There are no restrictions on its use by construct institutions as Eura as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb.sib.ch/announce/or send an email to license@isb.sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      between the Swiss Institute of Bioinformatics and the EMBL outstation the Furopean Ricinformatics Institute. There are no restrictions on its most by non-profit institute, removed as its content is in 15 43 modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www isb sib objancement or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         olmstead k.G., Records P.A.; "Eveloperation of the polyphyly of the Scrophulariaceae based on chloroplast rbeb and ndhe sequences."; "Ann. Mo. Bot. Gard. R2-194-194(1945).
-!- CATALYLIC ACTIVITY: NADH + PLASFOONTHONE - NAD(+) + PLASFOONTHOL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
NADH plustoquinene exidereductase chain 5, chiotopiast (EC 1.6.5.3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryotu: Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; sore eudicots,
Asteridae; euasterids I; Lamiales; Veronicaceae; Digitalis.
                                                                                                                                                                                                                                                                                                                                                                              C
                                                                                                                                                                                                                                                                                                                                          69.4%; Score 34; DB 1; Length 111; 83 4%; Prod No 5.
                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                        BÝ SIMILARÍTY.
KORYPTOPHYTEPRPP OPOEK:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oxidoreductase; NAD; Plastoquinone, Chloroplast.
Non TER
                                                                                                                                                                                                                 ProDom; PD002389; Ribosomal L20; 1.
PROSITE; PS00937; RIBOSOMAL L20; 1.
Ribosomal protein; rRNA-binding; Chloroplast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 699 AA.
                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Digitalis grandiflora (Yellow foxglove).
                                                                                                                                                                  InterPro; IPROBIBAL; Ribosomal 120.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR002128; Oxidored_g1_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPRODISTA; CXIdored_gi_N.
                                                                                                                                                                               Pfam; PF00453; Ribosomal_L20; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ptam; PF01010; oxidored_q1_C; 1.
Ptam; PF00662; oxidored_q1_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mendel; 2414; DIGqr;ndhF;1.
Interpro; IPR001750; Oxidored_q1
                                                                                                                                                                                                                                                                        INIT_MET 0 0 B
SECTENCE 111 AA: 13417 MW:
                                                                                                                                                                                                    PRINTS; PR00062; RIBOSOMALL20
                                                                                                                                             Mendel; 4049; CHLre;rp120;1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ptam: PF00361; oxidored_q1;
                                                                                                           EMBL; X62566; CAA44439.1; -
                                                                                                                                                                                                                                                                                                                                                                                5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; 1.36399; AAA84203.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                PIR: S18026: P5KM20.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    57 KRMWIT 62
                                                                                                                                                                                                                                                                                                                                                                                                                    4 REMWVT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chloroplast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Fragment).
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Q32131;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Poblarycia, Metazea, Nemaicela, Chremaderea, Rhabditida, Phabditoidea,
Phabditidae, Pelederinae, Caenerhabditis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Capie
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                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16 orm-2091 (Rel. 40, Last innotation update)
Hypothetical 146.8 kDa protein C34E10.5 in chromosome III.
   28 l. Length 699;
                                                              1, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (JUN-1994) to the EMBL, Assidant/TOPRE databases.
-!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
-!- SIMILARITY: TO S.POMBE SKB1 AND YEAST YBK133C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; ladels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transmembrane; Zinc-finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                      1281 AA.
                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
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   Score 34,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
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                               Pred. No.
                                                                                                                                                                                                                                                                                                                                                                      PRT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL: U10402; AAA19067.1; -- WhinFig. C34E10.5; CE00185. InteCFC. IFE001841; ZnL_ring. Ffam: PF00097; Zf-C3HC4; L. PROSITE; PS00184; RING: L. PROSITE; PS00518; ZF_RING. I. PROSITE; PS00699; ZF_RING_2: I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1222 1267 RIN
1281 AA; 14677? MW;
69.48,
85.78;
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Best Local Similarity Soc...
5: Consurative
                                                                  6; Conservative
                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Caenorhabditis elegans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Query Mutch
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID: 6239;
                                                                                                                                                                                               26 NKLRRWW 32
                                                                                                                                1 NELRKMW 7
                                                                                                                                                                                                                                                                                                                                                           YLB5_CAEEL
P46580;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ARCE HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kirsten J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSMEM
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                                                                                                                                                                                                                                                                                                RESULT 11
                                                              Matches
                                                                                                                                                                                                                                                                                                                                       YLB5 CAREL
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NCB1\_Tax1D=6239;

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  0
  SEQUENCE PROM N A , AND VAPLANT CANCEP ARC-50 MEDIANE-96514400 Pubmod-8649454; SPLTIBLA E , BOSTLAN E , SALI S., Grignon D., Miller O.J., Smith D.I.; Mullius C., Bostlan E., Saki W., Grignon D., Miller O.J., Smith D.I.; A grignon D., Miller O.J., Smith D.I.; A sample of chromosomal band 3p21.1 encodes a bidhly conserved and Arrhine-rich protein and E samutated in renal cell carcinomas.", oncogene 12:1931-1939(1996).
   Shridhar V., Rivard S., Wang X., Shridhar R., Painley C., Mullins C., Reirnar I., Dugan M., Sarkar F., Miller C.T., Valtkevicius V.K., Santth D.T.;
  0; Caps
   Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Khabditoidea,
Phahalitidae, Pelederiane, Cuenorhabditis,
  Pictraskicwicz H., Ensicy J., Paulcy R., Grigson D., Saki W.,
Millor O.J., Smith D.L.;
"Mulations in the arginine-rich protein gene, in lung, breast, and
   prostate cancers, and in squamous cell cardinoma of the head and nexk.";
   "Mutations in the arginine-rich profess gene (ARP) in panereatie
Mammalia; Futheria; Primates; Catarrhini; Hominidae; Homo.
   Score 33, DB 1, Length 234;
Pred, No. 17;
  1; Indels
  01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
Hypothetical 52 8 kDa protein TOEE11 5 in chromosome IV.
   ZEGOE MW: HRARINEZERANOTAKA OBOSA,
   MENLINE-97126272; Furmed-8971156;
Stridhar B., Skridhar V., Blyand S., Singfrind I M.,
  /FIId-VAR_010245.
MISSING (IN CANCER).
  > K (IN CANCER).
  M -> R (IN CANCER).
   /FTIG=VAR_010246
   PRT; 468 AA
  1; Mismatches
  -! - SIMILARITY: BELONGS TO THE ARP FAMILY.
  /FTIG-VAR
   POLY-APC
  EMBL; M83751; AAB08753.1; ALT_INIT.
  MEDLINE=97316783; PubMed-9174057;
   Cancer Pes. 56:5576-5578(1996).
  VARIANTS IN PANCREATIC CANCERS.
   67.38.
  Uncogene 14:2213-2216(1997),
  Conservative
   STANDARD;
  Caenorhabditis elegans.
   Best Local Similarity
   234 AA;
   Disease mutation.
                   NCBI_TaxID-9606;
  20
   S
   æ
  2
  53 MRRMWAT 59
  VARIANT ARG-50.
   3 LRRMWVT 9
  MIM: 601916;
   YJ95_CAEEL
  5
   SEQUENCE
   Query Match
  VARIANT
   VARIANT
  VARIANT
   P49049
  YJ95_CAEEL
ID YJ95_C
  Matches
   ...
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  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBs outstalion the Furopean Ricinformatics Institute. There are no restrictions on its
   use by mon-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb.sib.ch/panhouner) or send an email to license@isb.sib.ch).
   Saps
  Prelborg C.A., Pellay R., Bairoch A., Proughton W.J., Posenthal A
  Plasmid sym pNGR234a.
Bacteria; Protacturia; alpha cabdirisica; Ehizobiaceae group;
   Nature 387:394-401(1997).
-!- SubsELULAE ESCATION. Istogral membrane protein (Potential).
   "Molecular basis of symbiosis between Phizobium and legumes.";
   67.3%; Score 33; DB 1; Lenath 468;
55.6%; Fred. No. 36;
   1; indels
   Salmattes (18% free) to the EMET, denkack, told databases.
1. SIMILARITY: TO YEAST YKL100C.
   WormPep; 105E11.5; CE06364.
Hypothetical protein.
SEQUENCE 468 AA; 52793 MW; GODFFACE679AA5F8 CRC64;
  50411A4A84557381 CRC64;
  01-NOV-1997 (Ref. 35, Created)
01-N-V-1497 (Pel 35, Last Sequence update)
01-NOV-1997 (Ref. 35, East annotation update)
  Hypothetical protein; Transmembrane; Plasmid.
  220 AA

 Mismatches

  POTENTIAL. POTENTIAL.
  Fred. No.
  POTENTIAL.
   Hypothetical 24.6 kDa protein Y4FD.
  PRT;
  MEDLINE-97305956, FubMed 9163424;
   Phisobium sp. (strain NCR334).
  EMBL; AE000072; AAB91661.1; -.
  24627 MW;
   -! - SIMILARITY: NONE OBVIOUS.
  55.68;
   DMBL, 268751, CAA92975.13
  Ouery Match
Best Local Similarity 55.68
Matches 5, Conservative
  ST ANDARD;
   Rhizoblaceae; Rhizobium.
   125
197
  177 1
220 AA;
  SEQUENCE FROM N.A.
  263 HILKRHWIT 271
                       SEQUENCE FROM N.A.
  STRAIN-PRISTOL NO;
   1 NITUREMMALL 6
  NCBI_TaxID-394;
  Y4FD_RHISN
  Kershaw J.;
   Perret X.;
  TRANSMEM
  TRANSMEM
   TPANSMEM
  P55442;
   Y4FD.
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65.0%, Seere 42, DB 1; Length 220;

Cuery Match

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              0
  -1- FUNCTION: GUANINE NUCLEGIUDE-BINDING PROTEINS (G PROTEINS) ARE INVOLVED AS MODULATORS OF TRANSDUCERS IN VARIOUS TRANSMEMBRANE SIGNALING SYSTEMS.
-1- FUNCTION: THE GGI, PROTEINS ARE INVOLVED IN HOPMONAL REGULATION OF ADENYLATE CYCLASE: THEY INHIBIT THE CYCLASE IN RESPONSE TO BETA-
   ADRENERGIC STIMULL.
SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, HETA & GAMMA).
THE ALPHA CHAIN CONTAINS THE GUANINE NUCLEOTIDE BINDING SITE.
SIMILARITY: BELONGS TO THE G-ALPHA FAMILY. SUBFAMILY 1
  Gallus gallus (Chicken).
Enkaryola: Metazoa: Chordata: Craniata; Vertebrata: Euteleostomi;
Archosauria; Aves: Neognathae, Galliformes; Phasianidae; Phasianinae;
   "Cloning of chans coding for the Galpha il and Galpha i2 G-proteins
                  Gaps
  01-0%IT-1996 (Rel. 34, Last sequence update)
h-0%IT-2000 (Rel. 40, Last annotation update)
Guanine nucleotide-binding protein G(i), alpha-2 subunit (Adenylate
cyclase-inhibiting G alpha protein).
              0;
  ADP-RIBOSYL[1] (BY ACTION OF CTX).
ADP-RIBOSYL[1] (BY ACTION OF IAP).
   GTP-binding; Transducer; ADP-ribosylation; Multigene family;
              0; indels
  MYRISTATE (BY SIMILARITY).
PALMITATE (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
  D9645493D9C5CC4F CRC64;
   354 AA.
              3, Mismatches
   BY SIMILARITY.
Best Local Similarity 57.1%; Pred. No. 25;
   or send an email to licensedisb-sib.ch).
  HSSP; P10824; IAS3.
InterPro; IPR001019; Gprotein_alpha.
InterPro; IPR001230; Prenyltn.
   FRT;
   Myristate; Palmitate; Lipoprotein.
INIT_MET 0 0 BY SI
   MEDLINE 95121926; PubMed-7821803;
  01-00T-1996 (Rel. 34, Created)
  40446 MW;
   Kilbourne E.J., Galper J.B.;
   EMBL: 1.24549; AAA65067.1; -
  PRINTS; PRO0318; GPROTEINA.
  SMART; SM00275; G-alpha; 1
              4; Conservative
   STANDARD;
  Ptam; PF00503; G-alpha; 1
   Gene 150:341-344(1994).
  178
151
354 AA;
   from chick brain.";
   SEQUENCE FROM N.A.
   (G(1/O/T/2)).
  NCB1_TaxID-9031;
   6 LRKLWIT 12
  1 L.R.R.MWVT 9
  GB12_CHICK
P50147:
  NP_BIND
NP_BIND
  MOD_RES
  ON IN IN
  LIPID
   1.11 P.11)
   GB12_CHTCK
   GNA12
              Matches
   <u>.</u>
  S
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0

Gaps

0

65.3%; Score 32; DB 1; Length 354; 57.1%; Pred. No. 42; ative 3; Mismatches 0; Indels

4; Conservative

Best Local Similarity

Matches

Query Match

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Db :25 NVIRELM 131
Search completed: September 5, 2002, 15:31:40
Job time: 475 sec
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1 NLLKRMW 7

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GenCore version 4.5
Copyright (c) 1992 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Suptember 5, 2002, 15 28 40 Run of

Scarch time 69 '8 sections (without alignments) 12.393 Million cell updates/sec

03-03-744-804-3E 1 NII PPMWVT 9 Title. Perfect score: Scoring table: Sequence

283138 seqs, 96089334 residues Gapop 10.0 , Gapext 0.5 Searched:

Total number of hits satisfying chosen parameters:

Maximum DB seq length: 200000000 Minimum DB seq length: 0

Listing first 45 summaries Post-processing: Minimum Match 0% Maximum Matab

1: pirt:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* PIP 71.\* Database .

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

|               |          | œ      |          |     | SOMMANTES      |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
|---------------|----------|--------|----------|-----|----------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Result<br>No. | Score    | Query  | Length   | DB  | ID             | Description                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
|               |          | 1      |          | . ! |                |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| 1             | 44       | 86.8   | 401      | C1  | 86138          | qlycoprotein antiq                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
| C1            | 44       | 83.8   | 427      | C1  | S74211         | 11.7                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
| C)            | 38       | 77.6   | 224      | ۲,  | S54218         | flaA protein - Fer                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
| 47            | 36       | 73.5   | C1<br>C1 | €4  | AC0219         | -                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| ď             | 36       | 7.5    | 390      | C1  | 151197         | tical c                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
| 9             | 36       | 73 5   | 40.0     | C   | A:3:40         | 1000 T 000 T |
| ۲,            | 36       | 73.5   | 425      | C1  | B98139         | tme3 rroteic (AF07                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
| œ             | œ,       | 7.5    | 1705     | C1  | T4 c c 8 4     | hypethetical prote                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
| 5             | 35       | 714    | 116      | ۲.  | PSIVIO         | ribesemal protein                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| 10            | 35       | 71.4   | 119      | ~   | T07464         | ribosomal protein                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| 11            | 35       | 71.4   | 186      | -   | 690069         | - 0                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
| 12            | u)<br>0) | 71.4   | 409      | C)  | T11743         |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| 13            | 35       | 71.4   |          | ~   | C84965         | ŏ                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| 14            | 34       | 69.4   |          |     | REKM20         | ribósomal protein                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| 15            | 34       | 69.4   | 338      | 7   | T24743         | hypothetical profe                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
| 16            | 34       | 69.4   | 645      | €4  | T12159         | NALEH dehydrogenase                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
| 17            | 34       | 69.4   | 099      | 2   | E95084         | cation-transportin                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
| 18            | 34       | ₽<br>0 | 707      | C1  | T12658         | NADH dehydrogenase                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
| 1,9           | 34       | 69.4   |          | C1  | T12664         | NADH debydregenase                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
| 20            | 34       | 69.4   | 707      | C4  | T12665         | NADH dehydrogenase                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
| Ę             | 34       |        | 100      | C : | Tll668         | NADE Johr drogenase                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
| 22            | 34       | ₽. ÷9  | 202      | C1  | T12671         | NADH dehydrogenase                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
| 23            | 34       | 69.4   | 707      | C ¥ | T12751         | NADH dehydrogenase                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
| ¥2            | 34       | 69.4   | 707      | < 1 | T12752         | NADH dehydrogenase                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
| C 3           | 3.1      | 69.4   |          | C Į | T12759         | NADH dehydrogenese                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
| ଡୁଅ           | 34       | 69.4   | 707      | - 1 | 12.38.4T       | MADE dehydrogenase                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
| C+            | 34       | † 6.9° | 707      | CI  | <b>サ</b> とひとし並 |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| 28            | 34       | 69.4   |          | CI  | 134444         |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| ಹೆಡ           | 24       | 4.69   |          | CI  | S76856         | hypothetica: prote                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
|               |          |        |          |     |                |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |

| H+/K+·exchanging A | hypothetical profe | hypothetical prote | arginine-rich prot | hypothetical prote | Egpothetical prote | hypothetical prote | ABOST LANGE | gramulowyte-marrop | probable methane m | hypothetical prote | Ejpothetical prote | hypothetical profe | hypothetical profe | hypothetical profe | Ci2 protein alpha- |
|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| A97952             | 115762             | G83792             | 827956             | C70813             | AR2527             | 724523             | , , , , ,   | FUMSOM             | A57266             | E70692             | T45662             | AD2179             | 084711             | T19834             | 150238             |
| a                  | C 1                | C1                 | ~                  | ~                  | c i                | C1                 | ٠.          | ,                  | C ¥                | C I                | C I                | ca                 | C 3                | ~                  | C1                 |
| 750                | 1281               | - 1                | 2 34               | 334                | 4 : 6              | 468                | :           | 153                | 5                  | 294                | 294                | 307                | * † ;              | 345                | នា<br>ទា<br>កា     |
| ₽.                 | 9.4                | 6.7.3              | 67.4               | 67.3               | 67.3               | 67.3               |             | e                  | 6.5.3              | 6.5.3              | 65.3               | 65.3               | 65.3               | 65.3               | 65.3               |
| 69                 | w.                 |                    |                    |                    |                    |                    |             |                    |                    |                    |                    |                    |                    |                    |                    |
| 34 69              | 34 6               | c)                 | 33                 | 33                 | (3.)<br>(3.)       | 33                 | ,           | 3.2                | C.                 | 32                 | 32                 | 32                 | 32                 | 3.2                | 32                 |

## ALIGNMENTS

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Accession: Solis; Janaguchi, Y.; Adachi, T.; Nakamura, R.; Matsuda, T. Biochim. Biophys. Acta 1245, 485-391, 1995

A.Title: Molecular clouds of 41y-341-04cia autitous MOPF7/53 recognized by monoclonal Artitle: Molecular clouds of 41y-341-04cia autitous MOPF7/53 recognized by monoclonal Artitle: Molecular clouds of 41y-341-04cia autitous MOPF7/53 recognized by monoclonal Artitle: Molecular clouds of 41y-341-04cia autitous MOPF7/53 recognized by monoclonal Artitle: Preliminary: not compared with conceptual translation Artitle: Perilminary: not compared with conceptual translation Artitle: The major fat globule membrane proteins, bovine components 15/16 and guinear Biochem. Mol. Biol. Int. 29, 545-554, 1993

A.Title: The major fat globule membrane proteins, bovine components 15/16 and guinear Artitle: The major fat globule membrane proteins.

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A.Accession: G4894

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C.Regacida shyoprotein
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144 NEMERKWAVT 152

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us-09-744-804-36.rpr

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demo-farrada, A.M.; Chillingworth, I.; Cronin, A.; Bayies, B.M.; Davis, P.; Douddh, G. H., M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitchead, S.; Hairel Nature 413, 523-527, 2001
  C.Species: Neurospora crassa
C.Date. 29 Jul-2010 #Sequence_feristen 28 Jul 2000 #text_thuse 04 Sep 1000
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R.Schulte, U.; Aign, V.; Boheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatu
submitted to the Protein Sequence Database, July 2000
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0,8pecies: Agrobacterium tumefaciens
0,8pecies: Agrobacterium tumefaciens
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Science 294, 2317-2323, 2001
  A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon Kam
   ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefacieus 058
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  Rjkim, D.H.; Kanno, C.; Mizokami, Y.
Biochim. Biophys. Acta 1122, 293-211, 1992
A.Fillier Purification and characterization of major glycoproteins, PAS-6 and PAS-7, from
A.Reference number: $23926, MUID:92353107
A.Reference sumber: $24181
   Askosiduras 38-394 KKIN-
Askosiduras 38-394 KKIN-
Cysuportamily milk far globule prototor dignoidin 1 amino-terminal homology; PoP homolo
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Py24-58/Domain: ECP homology <EG1>
   R/Fauconnier, A.; Allaoui, A.; van Elsen, A.; Cornelis, G.; Bollen, A. submitted to the iRMC. Data Library, Fib. any 1795. Alloseription. Clastering of Hageliat genes around invA, the Yersinia enterocolitica in A;Reference number: 854213.
  flagella basal budy P ring formation protein FigA [imported] · Yersinia pestis (strain d
   R.Parkhill, J., Wren, B.W., Thomson, N.R., Tittail, R.W., Holden, M.T.G., Prentice, M.R.
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   A:Cross-references, EMBL X91875, NIL.91632778, FIDN.GAAL2977.1, FID.91632775
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   P.59/227/Ninding Site: carbobydrate (Asn) (covalent) #status experimental P.109-265,252-256,276-427/Disulfide bonds. #status experimental
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A. Tille, Ellis List and councilation of Marchantia polymorphis chiorophast genome. 111. A. Keference number: Sul529; MulD:89ub8687.
A. Keference number: Sul529; MulD:89ub8687.
A. Molecule type: DNA A. Molecul
  F.Warenson, T. 1994-14; J. 11, S. Makish's F. Tsudowii, T., Suqiura, M. Proc. Nati. Acad. Sci. U.S.A. 91, 924-9798, 1994
A.Tithe Loss of all ndl genes as detechnised by sequencing the entire chloroplast gen A.Retorence number: 216930; MUID:95024047
A.Retorence number: 216930; MUID:95024047
A.Status Erri missay, Translated from day-Embi, 2008J
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A.Gross/references: EMBL, D17510; MII:9529643, FIBH.BAA04342.1, FID:31262635
  Library and John 1997 #sequence_received polymorphy, chicary case to consider particles and the consider of the consideration of the consideratio
   Aldross relevences: 38 X0440.5; 38 Youndo; Nibedli640; FibNetAAzMi08.1; Fibedli636
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  RiGoodner, R. Hinkle, G.; Gattung, S.; Milier, N.; Flanchard, M.; Gurollo, E.; Goidman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughry, D.; Srott, G.; Lappas, G.; Markelz, B.; Science 294, 2323-2329, 2001.
A/Title German Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A/Reference number: A97359; PMID:11743194
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  Ribargues, M., Collada, M.C., Ravarro, P., Totol, J., Porovialogas, M., Mowes, H.W. submitted to the Protein Sequence Database, December 1999
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O
A)Cross-references: GR-AE007870; PIDN-AAK88636 1; PID-915158357, GSPDB GN00170
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  R:Ensslin, M.; Vogel, T.; Calvete, J.J.; Thole, H.H.; Schmidtke, J., Matsuda, T., Toepfe
Biol. Reprod. 58, 1057-1064, 1998
   A,Title: Molecular cloning and characterization of F47, a novel boar sperm-associated ad
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C.Date: 02 Mar 2001 #Segenee_revision 02 Mar:2001 #1cxt_change 23 Mar 2001
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

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1 NLLRRMWVT 9 Scoring table:

562222 seqs, 172994929 residues Gapop 10.0 , Gapext 0.5 Searched:

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Listing first 45 summaries Maximum Match 100% Post-processing: Minimum Match 08

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sp\_unclassified.\* sp\_invertebrate:\* sp\_vitus.\* sp\_vertebrate:\* sp\_rvirus:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the tend of section in

SUMMARIES

|          | Description                   | 0995tl9 homo sapien | 094736 houng sapion | 095001 homo sapien | 092616 home sapien | 09p3c0 neurospora | Ogsado arabidoesis | 091450 cruz 0341iv | O25913 plasmodium | 096158 homo sapien | 002310 cacnorhabdi | Q93cu8 shiqella bo | O46945 heliotropin | 097rr4 streptococc | Ogtita tournaforti | 09t148 rhamnus day | OSSOSA ASSOCIATION |
|----------|-------------------------------|---------------------|---------------------|--------------------|--------------------|-------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| COLUMNIA | ID                            | Q\$BTL9             | 98.2560             | 095001             | 092616             |                   |                    |                    | ( •               | 0961.58            | 002310             | งัยงกับห           | 046945             | Q97RR4             | 61116Ŭ             | Q9T1.48            | 02303A             |
|          | DB                            | 4                   | 4                   | 4                  | 4                  | ۲.                | 10                 |                    | Ľ                 | 4                  | Ľ,                 | 2                  | œ                  | 16                 | α                  | œ.                 | Ľ                  |
|          | °<br>Ouery<br>Match Length DB | 335                 | 1928                | 2392               | 2412               | 340               | 3071               | 1292               | C: C              | 329                | 338                | 404                | 645                | 099                | 700                | 706                | 707                |
| of       | ouery<br>Match                | 100.0               | 83.7                | 83.7               | 83.7               | 73.5              | 73 5               | 71.4               | ₹ ७५              | 4.69               | 69.4               | 69 4               | 69.4               | 69.4               | <b>9</b> 69        | 69.4               | V 0 9              |
|          | Score                         | 4.9                 | 4.                  | 41                 | 4 1                | 36                | 36                 | 35                 | 34                | 34                 | 34                 | 34                 | 34                 | 34                 | 34                 | 34                 | 7.4                |
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| Ω9v)c6 drosophila  | ŏ∂A:1Ċĕ  | ď          | 4010         | 67.3              | 3.3      | 4.5        |
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|                    | 09NNG2   | S)         | 955          | 67.3              | er<br>er | 4 ع        |
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|                    | 09TLG0   | œ          | 700          | 67.3              | * *      | 500        |
|                    | 0.9UHD3  | -1         | 233          | 67.3              | **       | 38         |
| C91jyl arabidopsis | 0.00mm;  | ÷.         | u?<br>₽÷     |                   | ~ ;      | E-1        |
|                    | Q9MS91   | œ          | 431          | 67.3              | **       | 36         |
| C53855 mycobacteri |          | - 1        | 33.1         | 67.3              | ~;       | 35         |
| Q92rcJ rhizobium m |          | 16         | 237          | 67.3              | **       | 3.4        |
| Q96is4 homo sapien |          | ₹          | 182          | 67.3              | er<br>gr | eri<br>eri |
| 29khl4 streptomyre | Q'AKHE4  | c į        | 100          | 67.3              | -        | C1<br>21   |
| n                  |          | <u>-</u> - | L-1          | 67.4              | *;       | 3.1        |
|                    |          | 2          | අ:<br>ප<br>ව | 69.4              | **       | O¥         |
| C94jil organ satir | 0 094511 | Ξ          | \$88<br>8    | 69.4              | ř.,      | 53         |
|                    | Q9TLB7   | œ          | 746          | 1                 | 34       | 28         |
| synechury          | . 574652 | <u>ت</u>   | 733          | 69.4              | *#<br>** | r.<br>Ci   |
| P92273 ceanothus p | _        | a:         | 707          | ٠٠<br>وي          | 7.       | 35         |
| P92272 ceasethus p | F90070   | 3)         | 707          | 63                | 7.7      | 63<br>64   |
| P92262 deamothus c | #3:5:1   | a.         | 207          | · .               |          | ť.         |
| P92284 ceanothus v | P92284   | သ          | 20Z          | 4.69              | 5.5      | £3         |
| P92281 ceanothus t | P92281   | ဏ          | 707          | ÷ : 69            | 5        | CI<br>CI   |
| P92279 ceanothus s | P92279   | a:         | 707          | 69.4              | ~        | 5          |
| P92268 ceanothus i | P92269   | σ.;        | F.O.F.       | 69.4              | **<br>** | 62         |
| PG2265 ceanothus f | 197565   | æ          | TO L         | جه.<br>دون<br>دون | 7        | - 1        |
| P92201 reanothus c | 195564   | ತ್ರ        | r -          | <br>              | ¥.       | g)         |
| P92256 ceanothus a | P92256   | œ          | 707          | 69.4              | 14       | 1.7        |
|                    |          |            |              |                   |          |            |

#### ALIGNMENTS

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Homo sapiens (Human).
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;
   | T. SERIEMPROMENTATION | T. SERIEMPE | T. S
   100.0%; Score 49; DB 4; Length 335; 100.0%; pred; No 0.11; atlive 0; Mismatches 0; Indels
  Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
   01-JUN-2001 (TFEMBLEEL. 17, Created)
01-JUN-2001 (TFEMBLEEL. 17, Last sequence update)
01-DEC-2001 (TEMBLEEL. 19, Last annotation update)
SIMHIAM TO MILK HAT GLORUIF-PRE FARTOR 8 PROTEIN.
  335 AA.
  PRT;
   Query Match
Rost Local Similarity 100.0
Enc. the 9, Conservative
  PRELIMINARY;
  SEQUENCE FROM N.A.
  TISSUE-MELANOMA.;
   NCBI_TaxID-9606;
   09BTL9;
  99BTL9
RESULT
  99BTL9
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Gaps

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SEQUENCE FROM N.A.
TISSUE-BONE MARROW:
   Rest Local Similarity
  846 NLLRRLWV 853
  866 NILERELWV 873
  NCB1_TaxID=9606;
   1 NLLKRMWV 8
   1 NLI.RRMWV 8
   NON_TER
SEQUENCE
  InterPro;
  KIAA0219.
   Query Match
  B7N4.40.
   Q9P3C0;
   092616;
   005460
   092616
   4
   KESULT 5
   Matches
   RESULT
  09P3C0
   092616
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   Gaps
  "Evidence that GCNI and GCN20, franslational regulators of GCN4, function on elongating ribosomes in activation of elf2alpha kinase
   Enkaryota, Motazoa, Chordata, Graniata, Vertebrata, Euteleostomi,
Mammalia: Eutheria: Primates, Catarrhini, Hominidae; Homo.
   Homo sapiens (Human).
Eukaryota, Motazoa, Chordata, Graniata, Vertebrata, Enteleostomi,
Mammalia; Eutheria; Primates, Catarrhini; Hominidae; Homo.
   Ö
   MEDLINE-97378024; Pubmed 9234705;
Marton M.J., Varquez de Aldana C.E., gis H., Chakraburtty K.,
Hinnebusch A.G.;
  83.7%; Score 41; DB 4; Length 1928; 87.5%; Prof No. 22;
   0; Indels
   Submitted (54C 1998) to the EMBLyCh chark,752BJ databases.
EMBL: AC004812; AAC83183.1; -.
InterPro; IPR000357; HEAT_repeat.
InterPro; IPR000847; HTH_TysP
  SEQUENCE 1928 AA; 211510 MW; 8R82070007A8FE08 0P064;
  Robling T., Clarke K., Bauer C., Morris M.,
"The sequence of Homo sapiens PAC clone 267D11,";
Submitted (THN-1998) to the EMRE/WHAT databases
   Last sequence update)
Last annotation update)
   01-MAY-1999 (TrEMBLrel. 10, Created)
U-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
WIGSC-H_267D11.3 PROTEIN (FPAGMENT).
  PLAM: PF02985, HEAT; 7
PROSITE; PS50077; HEAT_REPEAT; 3.
PROSITE; PS00044; HTH_LYSR_FAMILY; UNKNOWN_1.
  PRT; 1928 AA
   PRT: 2397 AA
   Prod No. 22;
1; Mismatches
  (Leasted)
   Mol. Cell. Biol. 17:4474-4489(1947)
EMHI. UJ7700. AACSIG48.1.
InterPro. 1PR000357; HAAT_repeat.
InterPro. 1PR000847; HTH_Lysk.
   InterPro; IPR000663; Natr_peptide
  01-JAN-1998 (TrEMBLE) 95,
01-DEC-2001 (TrEMBLE), 19,
  01-MAY-1997 (TEFMBLEGT 03,
  Best Local Similarity - 87 59
Matches - 7, Conservative
   PRELIMINARY;
   PRELIMINARY;
   SEQUENCE FROM N.A.
TISSUE-SKELETAL MUSCLE;
  Homo sapiens (Human)
   131 NLLRRMWVT 139
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  SECUENCE FROM N.A.
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  WOGSC:H_267D11.3.
I NI.I.RRMWVT 9
   NCB1_Tax1D=9606;
  NCB1_TaxID:9606;
   I NULLERMWV 8
  Waterston R.
  Query Match
  099736
099736;
   NON TER
  HSGCN1.
   0.95001
   Matches
   RESULT
   KESEL 1
   099736
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  Nagase T., Seki N., Ishikawa K., Ohira M., Kawarabayasi Y., Ohara O., Tanska A., Kotani H., Miyajima N., Nomura N.; Profestion of the coding sequences of unidentified human genes. VI. the coding sequences of 80 new genes (KIAA0201 KIAA0280) deduced by analysis of cDNA clones from cell line KG-1 and brain."; DNA Res. 3:321 229(1996).

EMBL: D86973; DAA13209-1; --
InterPro; IPR000847; HTH_LysR.
   Caps
   Gaps
   Homo sapiens (Human).
Eukaryota: Metazoa: Chordata: Craniata; Vertobrata: Eutoleostomi:
Mammalia: Eutheria: Primates; Catarrhini; Hominidae; Homo.
   ÷
   :
O
   Neurospora crassa.
Eukaryota, Pungi, Ascomyceta, Peninomysotina, Serdariomycetes,
   Score 41; DB 4; Length 2492; Pred. No. 27;
  h 83.7%; Score 41; DB 4; Length 2412; Similarity 87.5%; Pred. No. 27; 7; Conservative 1; Mismatches 0; Indels
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   NON_TER 1 1 SEQUENCE 2392 AA; 1915A227CCA33BA9 CRC64;
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  01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TIEMBLRel. 02, Last sequence update)
01-PEB-2001 (TEMBLRel. 19, Last annotation update)
KIAA0219 PROTFIN (FFAGMENT).
   01.0CF 2000 (TrEMELREL. 15, Created)
01.0CF-2000 (TrEMELREL. 15, Last sequence update)
01.PEC-2001 (TrEMELREL. 14, Last annotation update)
SCANSERVED HYFOTHETICAL PROTEIN.
PTAM: PF02985; HEAL: 7.
PRINTS: PRO5710; WATPEFTIDES.
PROSITE: PS50071; HEAT REPEAT: 3.
PROSITE; PS00044; HTH_LYSR_FAMILY; UNKNOWN_1.
  PRINTS: PROOTIO: NATPEPTIDES.
PROSITE: PS50077; HEAT_REPEAT; 3.
PROSITE; PS00044; HTH_LYSR_FAMILY; UNKNOWN_1.
   PRT; 2412 AA
  350 AA.
   1, Mismatches
   Sordariales, Sordariaceae, Neurospora.
  PRT;
  Pro; IPR000663; Natr_peptide. PF02985; HEAT; 7.
   MEDLINE 97191544; PubMed 9039502;
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7, Conservative
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  PRELIMINARY:
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01-NOV-1996 (TrEMBLrel, 01, Created)
   144595 MW;
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  PRINTS; PR00364; DISEASERSIST.
SMART: SM00370; LRR; 5.
  InterPro; IPR003592; LRR_out.
InterPro; IFR062182; NB-ARC.
Pfam; PP00560; LRR; 14.
  MALARIA ANTIGEN (FRAGMENT).
   PF00931; NB-ARC; 1.
  Conservative
   FRELIMINARY;
   LELIMINAEN,
   Plasmodium falciparum.
   1292 AA;
   Best Local Similarity
   :||||:|:
1158 SLLRREWI 1165
  Ehrhartoidoue, 71
NGBI_TaxID=4530;
   Eukaryota; Alves.
   124 NLLKKMW 130
  1 NLLRRMWV 8
   Clone: Pussybil.
   I NI.I.RRMW 7
   SEQUENCE
  Query Match
  025913;
  096158;
  025313
  996158
  æ
  Matches
  025913
  RESULT
   096158
  ò
  0
   Arabidopsis thaliana (Mouse-ear cress).

Fikaryota, Viridiplantue, Streptophyta, Edepophyta, Trachesphyta, Spermatophyta, Magnolicphyta; eudioctyledons, sore eudiocts, Rosidae, eurosids III, Brassicales, Brassicaceae, Arabidopsis.
  Gaps
   Gaps
   Holland E.
  Rarques M., Collade M.C., Navarro P., Terel J., Perez-Alonso M.,
Mewes H.W., Endd S., Lemeke K., Mayer K.P.X., Quetler F.,
Salanoubat M.;
   0
  ć
   73.5%; Score 36; DB 10; Length 3071; 75.0%; Pred. No. 3.2c+02; 1; e. 1; Mismatches 1, Indels (i.e. 1)
  Schulte U., Aign V., Hoheisel J., Brandt F., Faithmann B.,
Nyakatura G., Mewes H.W., Mannhaupt G.,
Submitted (JUL-2000) to the EMBL/GonBank/DDRI databases
  73.5%; Score 36; DB 3; Length 390;
85.7%; Pred. No. 42;
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   Hypothetical protein. = - - SEQUENCE 3071 AA; 343688 MW; 4A3F7C9F71C92A25 CRC64;
  German Neurospora genear projects
Submitted (JUL-2020) 1. the FMFL/Grebonk/Gift databases
EMBL: AL390218; CAB9235.1; 1. Hypotherical protein.
SEQUENCE: 390 AA; 44439 MW; EIBES13D57672BD9 CRC64;
   Submitted (NOV-1999) to the EMRE//SenBank/TUREJ databases
  the EMK, Washingh, here difficience
  01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 343.7 KDA PROTEIN.
  Last sequence update)
   PROSITE: PS00041; HTH_APAC_PAMI:Y_1; GNKNOWN_1.
   PRT; 1292 AA.
   PRT; 3071 AA
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01-007-2000 (TrEMBLrel. 15, Last sequ
01-077-2001 (TrEMBLrel 19, Last anno
ESIS AUD78742(P1888).
07yza sativa (Rice).
   EU Arabidopsis sequencing project;
   S.Louittel (AFB.2000) + 'hê F
EMBL: AL132976; CAB62317.1; -
   InterPro; IPR000005; HTHAraC.
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Best Local Similarity 75.0%
Matches 6: Conservative
  Best Local Similarity 85.7
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   SEQUENCE FROM N.A.
  SEQUENCE FROM N.A.
   601 NLIREMWIL 608
   272 NFLRRMW 278
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   NCBL_TaxID=3702;
  1 NLLPPMWV 9
   I NI L'RRMW 7
  Query Match
  Q9LG50;
   :00NS50
   0GNS60
  085/160
   7
  Matches
   RESULI
   OGNS50
  09160
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Gaps
Bukaryota, Viridiplantac, Stieptophyta, Embryophyta, Trachosphyta;
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
   ..
O
   SEQUENCE FROM N.A.

STRAIN-MALAYAN CAMP:

Milling N. Johnson C. Saul A.;

Cheng Q. Johnson G. Liu E.X., Kidson C., Saul A.;

Cheng Q. Johnson G. Liu E.X., Kidson C., Saul A.;

"identification of a common phasmodium faleiparumepitope (CPE)

recognized by a pan specific inhibitorymencelonal antibody.";

ROJ. Biochem. Farasitol. 49.73 82(1991).

BMIL, MS3277: AAA29642.1; -..

NON_TER
   "crysa sativa nipposbare(GA3) qenomic DNA, chromosome 1, PAC
  71.4%; Score 35; DB 10; Length 1292; 62.5%; Pred. Mo. 2.20.02;
tive 3; Mismatches 0; Indels (
   Alveelata: Apicemplexa: Haemesporida: Plasmodium.
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Best Local Similarity 71.4%; Pred. No. 62;
Matches 5; Conservative 2; Mismatches 9; Indels
   Sabmitted (301.2003) to the EMBL/GenBank/7078J databases.
EMBL, APRO2817, PAB03441.1: -.
InterPro: IPR000767; Disease_resist.
InterPro: IPR001611; LRK.
   3DBAB30DE947F767 CRC64;
   SPOUPNOY 232 AA; 27535 MW; 7239P691PC6867A8 CRC64;
   0.1627-2001 (TrEMBLrel. 19, Greated)
01-04C-2001 (TrEMBLrel. 19, Last sequence update)
01-04C-2001 (TrIMBLrel. 19, Last annotation update)
   01-NOV-1996 (TrEMBLref. 01, Last sequence update)
01-DEC-2001 (TrEMBLref. 19, Last annotation update)
   FRT; 329 AA.
   SPRAIN-CV. NIPPONBARE;
Sasaki I., Matsumoto I., Yamamoto K.;
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O-ANTIGEN FLIPPASE.
  Heliotropium.
  Chloroplast.
  Shiqella.
   SHOUENCE
  046945;
   046945
  RESULT 12
   046945
 QQ
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  Hai X., Zhan D., Brown J.K., Hennet T., Eski J.D.,
"Blosynthesis of the linkure region of glycosaminoglycans: Cloning and
"Blosynthesis of the linkure region of glycosaminoglycans: Cloning and
stivity of galactosyltransferase lamily (briadcalfe).";
Submitted (AUG-2001) to the EMH/Geordankyluki databases.
EMBL: AVE05070. AALIHA42.1: "
ITRACTOR ALIHA42.1: "
SKQUENCE 329 AA, 37123 MW; 3753F61B000DEA313 CRC64;
   Gaps
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   Bukaryota, Metassa, Nematuda, Chromadorea, Fhabditida, Bhabditsidea;
Rhabditidae, Peloderinae, Casnorhabditis
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Eukaryota: Motazou, Chordata: Craniata; Vertebrata; Euteleostemi,
Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.
  .:
   ċ
  Score 44, D8 4, Length 329,
Pred. No. 87;
   "Genome sequence of the nematode C.elegans: A platform for
   Scare 34; DB 5, Length 338,
Pred. No. 90,
  1; Indels
   l: Indole
   Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases
   247056804024362D CRC64,
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01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
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01-DEC-2001 (TFEMBLEEL 19, Last annotation update)
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InterPro; IPR002659; Galactosyl_T.
  MEDLINE 99069613; PubMed=9851916;
BETA-1, 3-GALACTOSYLTRANSFERASE-6
   Plam: PF01762; Galactosyl_f; I
SEQUENCE 338 AA; 38916 MW,
  69.48
85.78
  Science 282:2012-2018(1998).
EMBL, 281147, CAB03537.1,
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55.68,
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  PRELIMINARY;
  investigating biology.";
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96 NVL.RKTWMT 104
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   SEQUENCE FROM N.A.
  TOSELL 10 PROTEIN.
  1 NILLERMWVT 9
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  I NIJ.KKMW 7
  Z NIJERAM 8
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  0930118;
  002310
  093008
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002310
   Matches
  RESULT 11
   Matches
   93008
5
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   5
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C
   Wang L., Qu W., Reeves P.R.;
"Sequence Analysis of Four Shigella Loydii D Antigen Loci: Implication for Escherichia coli and Shigella Relationships.";
Inter. Immun. 69:6923-6930(2001).
ENLIST ARADZAIS.
SHOUGHCE 409 AA; 47677 MW, 9759920EAGSCBIA CRC64;
   "Phylogenetic analysis and circumscription of Hydrophyllaceae based on
  Schranz E., Olmstead R.G.;
submitted (JUL 1997) to the EMBLyGenhamk/DDBJ databases.
-!- CATALYTIC ACTIVITY: NADH + PLASTOQUINONE - NAD(*) + PLASTOQUINOL.
  Gaps
   Gaps
   Eskaryota, Viridiplantae, Streptephyta, Emity-phyta, Trachcophyta,
Spermatophyta, Magnoliophyta, eudlootyledons, core eudicots;
Asteridae, euasterids I, euasterids i incertae sedis; Boraginaceae;
Shigella boydii.
Barteria, Proteobacteria: gamma subdivision; Enterobacteriaees
  ..
   :
   Query Match 69.48; Score 34; DB 2; Length 409; Best Local Stailarity 62.52, Fred. No. 1.1e-02; Matches 5; Conservative 2; Mismatches 1; Indels
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01.DEC-2001 (TrEMBLrel. 19, Last annotation update)
   Chloroplast; NAD; Oxidoreductase; Plastoquinone.
  NADH DEHYDROGENASE SUBUNII F (FRAGMENT).
  Interpro; 1PR002128; Oxidored_gl_C.
Interpro; 1PR001516; Oxidored_gl_N.
   MEDITINE-21481970, PubMed-11598067;
  EMBL: AF014000; AAB94517.2; -.
InterFro, IPR001750; Gxidored_q1.
  Pfam, PP00361; exidered_q1; 1.
Pfam; PP01010; exidered_q1_C; 1.
Ptam; PP00962; exidered_q1_N; 1.
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  SEQUENCE FROM N.A.
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   645
   NCBI_TaxID=621;
  28 LRRMWV 33
   3 LRRMWV 8
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Search completed: September 5, 2002, 15:31:01
  Ouery Match
Best Local Similarity
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  700 AA:
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  Rhamnus dayurica.
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  28 LPRMWV 33
  27 LEREWW 32
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  LPPMWV 8
   Chioroplast
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  SEQUENCE
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   Q9TL48
Q9TL48;
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   Q9TL48
  ź
   Tettelin H., Nolson, K.F., Paulson (T., Fison J.A., Bead T.D., Peterson S., Heldelberg (L., DeRoy P.T., Haft D.H., Dodson R.J., Durkin A.S., Gwinn M., Kolonay T.F., Nolson W.C., Peterson J.D., Umayam L.A., While O., Salzberg S.L., Lewis M.R., Radune D., Holtzupple E., Khouri H., Welf A.M., Hitterback T.P., Hansen C.I., McDonald L.A., Peldblyum T.V., Angiuoli S., Dickinson T., Hickey E.K., Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M., Complete genome sequence of a virulent isolate of Streptococcus
   Bacteria: Firmicutes, Bacillus/Clostridium group; Streptogogogoges
   Bukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta; Spermatophyta, Magnellophyta, eudicotyledons; core eudicots; Astoridae: eusterids I; Selnales; Hydrophyllaeele, Testrefortia.
  69.4%; Score 34; DB 16; Length 660; 55 6%; Prod No 1 704.02; tive 3; Mismatches 1, todals
  660 AA: 70670 MW: 0A992661A9P470AF OP064;
  01-OCT-2001 (TrEMRITE). 18. Created) (U-CXT-2001 (TrEMRITE). 88 Last apprending the U-DEC-2001 (TrEMRITE). 19. Last annotation update) CAIION-TRANSPORTING ATPASE, E1-E2 FAMILY.
  01-MAY-2000 (TrEMBLED. 13, Created)
01-MAY-2000 (TrEMBLED. 13, Last sequence update)
01-DEC-2001 (TrEMBLED. 19, Last annotation update)
  700 AA.
   PROSITE; PSO0154: ATPASE_EL_E2; UNKNOWN_1.
PROSITE: PS01229; COF_2; UNKNOWN_1.
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                                PRT;
  MEDIINE-21357209; PubMed-11463914;
  Interpro; IPR001756; Cu_ATPase.
Interpro; IPR001757; E1-E2 ATPase.
Interpro; IPR001454; Hydrolase.
Interpro; IPR00150; Hydrolase.
Pfam: PP00122; E1-E2-ATPase; I.
Pfam; PP00702; Hydrolase; I.
   Science 293:498-506(2001).
EMBL, AE007381- AAK74870 1; -
  NADH DEHYDROGENASE (FPAGMENT)
  PRINTS; PROOTIG: CATATPASE PRINTS; PROOG43; CUATPASE.
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Best Local Similarity 55 mm
Best Local Similarity 55 mm
   Streptococcus pneumoniae.
                               PRELIMINARY;
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  Complete proteome.
   SEQUENCE FROM N.A.
  19 SLLQRFWIT 27
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  1 NLI.RRMWVT 9
  Streptococcus.
NCBI_TaxID=1313;
  SP0729; -
   Ferguson D.M.;
   pneumoniae.";
   Chloroplast.
  STRAIN-TIGE4
  SECUFINGE
   Q9T1T9;
   097RR4;
   Q11179
                             Q97PR4
RESULT 13
   RESULT 14
  NDHF.
   09TIT9
                Q97RR4
```

```
"Phylogenetic analysis and circumscription of Hydrophyllaceae based on ndhF sequence data.";
  Eukaryota, Viridiplantac, Streptophyta, Embryophyta, Trachcophyta, Spermatophyta, Magnoliophyta; eudiectyledons, core eudicots, Rosidae, eurosids I; Rosales, Rhamnaceae, Rhamnus.
  Syst. Bot. 0:0-0(1998).

Syst. Bot. 0:0-0(1998).

CATALYTIC ACTIVITY: NADH + PLASTOQUINONE NAD(+) + FLASTOQUINOL.

FMBL. AF047813, AAF22420.1; -.

InterPro. IPR001228; Oxidored_q1.

InterPro. IFR051516, Oxidored_q1.

Piam: PF00581 Oxidored_q1.2; 1.

Piam: PF00501 Oxidored_q1.2; 1.

Chloroplast: NAD: Oxidored_q1.N; 1.

Chloroplast: NAD: Oxidored_q1.N; 1.
  qene sequences.";
Mol. Phylogenet. Evol. 16:96 112(2000).
Mol. Phylogenet. Evol. 16:96 112(2000).
EMBL: AF130225; AAF08181.1;
InterPro. 178001728; Oxidored_q1.
InterPro. 178001728; Oxidored_q1.
InterPro. 178001516; Oxidored_q1_N.
   Caps
   MEDLINE 20349987; FubMod-10877943;
Olmstead R.G., Kim K.J., Jansen R.K., Waqstaff S.J.;
"The phylogeny of the asteridae sensu lato based on chloroplast ndhF
  Sdbb
   ..
   ċ
  Length 700;
   69.4%; Score 34; DB 9; Length 706;
  69.4%; Score 34; DB 9; Length 700
Harity 108.0%; Pred. No. 1.8e-52;
Conservative 9; Mismatches 0; Indels
  o Indels
   796U8 MW; B96A/EA644BEC555 CRC64;
  78889 BW; 968A728EAEA7570G CRC64;
   01-MAY-2009 (TrEMBLrel. 18, Created)
01 MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
NOJH DEHYDRUGENASE SUBUNIT F (FRAGMENT).
   Chloroplast, NAD: Oxidoreductase, Plastoquinone.
NON_IER 1
NON_IER 706
SEQUENCE / UP AA; //YOUR MW; BYDA/EAÖ448EGDE.
  1.9e+02;
   100.0%; Pred. No. .
Twe O; Mismatches
  PRT;
   Pfam; PF00361; oxidored_q1; 1.
Pfam; PF01010; oxidored_q1_C; 1.
Pfam; PF00662; oxidored_q1_N; 1.
   6; Conservative
   PRELIMINARY;
   700
```

.; 0

Job time: 466 sec

.

```
GenCore version 4.5
Copyright (c) 1993 - 2000 Gempugen 11d.
```

OM protein - protein seatch, using sw model

| Spare: Fime 158 43 Species (Without alignments) | 6.310 Million cell updates/sec September 5, 2002, 15:26:78 Pun on:

US-09-744-804-36 49 1 NLLRPMWVT 9 Perfect score. sednence:

Gapop 10.0 , Capext 0.5 RI OSTIM62 Scoring table:

747574 segs, 111073796 residues Searched:

lotal pumber of hite satisfying choson parameters:

7-մարդանում 2012 Minimum DB seq length: 0 Maximum DB seq iength:

Listing first 45 summaries 1001 Post-processing: Minimum Match 0% Maximum Match

A\_Ceneseq\_032802.\* Database

/SIBSL/gegdata/hold-geneseg/genesegp-embl/AAN(9) 1 nar \* /SIBSL/gegdata/a/hold-geneseg/genesegp. entt, AA1993.0A...
-ontl, AA1993.0A... /SIBSL/gogdata/hold-goneseq/geneseqp-embl/AA1997\_nAt+.\* /SIBSL/gogdata/hold-geneseq/geneseqp-embl/AA1997\_nAt+.\* /SIDS1/gegdata/held-geneseg/genesegp embl/AAzenie tATe+ /SlDS1/gegdata/hold-geneseg/geneseqp-embl/AAlจิติ กลีก.\* /SIDS1/gcgdata/hold-geneseg/genesegp\_embl/AA1998.DAT:\* /31081/30gdata/hold-genesel/geneselp-entityAAlaas nai \* ombl/AA1992.DAT:\* . S. USSTAGO (attazlada) garasan, gararan, attata, AAL982 DAT.\* /SIDST/geyddalazhold-gemeseqzgenesenp-embizAAL988 DAT.\* 78.1787Zyrydatazhend opensenyden senji emit zadi aktii (An. • 78.1081Zgrydatazhend genesenyg in senji emid Zadi 381.1041. • /SlbSi/gcgdata/hold-geneseq/qeneseqp-embi/AA1984.DAT:\* /SIDS1/gegdata/hold-geneseq/genesedp-embl/AAlqus /SIDSI/graphata/heid-geneseq/qeneseqprounti/AA1983. /SIDSI,/gradata/hr!d-grnrary/qrnrarqp-rmbl/AA1982 , is list, grydata, b. d. gransky, bransky fra 17. 781DS1/gogdata, hold gepreny frankrythe († 17. m Willer Gradult had been proposed. /STDS1/goadata/hold-goneseg/genesedp 100 1125 1127 1138 1138 1139 1139 1139 1139

Pred. No. is the number of results predicted by charce to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

73.10.517/3013data/h.dd-grazeset//grazesetp.com/d/AAz3001.1461

# SUMMARIES

| nescription                      | Tactadherin (BA-46 | HMFS 46 kDa artige | Human lactadherin | Human EST encoded | Human protein SEQ | Human protein SEO | Novel hands carries | Novel human diagno | Human 3GnT protein | Streptococcus pneu | Novel human diagno |
|----------------------------------|--------------------|--------------------|-------------------|-------------------|-------------------|-------------------|---------------------|--------------------|--------------------|--------------------|--------------------|
| 010                              | AAYR2841           | AAR77252           | AAY44453          | AAM23507          | AAM78911          | AAM79895          | AAU23593            | ABG28776           | AAY51901           | AAU37812           | ABC] 4088          |
| # <u>1</u>                       | 21                 | ď.                 | 7                 | C 3               | C1                | 2.5               | C 1                 | ei<br>ei           | C4                 | 51                 | C•                 |
| %<br>Query<br>Match Length DB ID | σ                  | 387                | 1×7               | 1763              | 2473              | 2668              | 112                 | 999                | 329                | 750                | 997                |
| %<br>Query<br>Match              | 100 0              | 100 0              | 100 0             | 83.7              | 83.7              | 83.7              | 73.5                | 71.4               | 69.4               | 69.4               | 4 94               |
| Score                            | 49                 | 49                 | 49                | 41                | 41                | 41                | 36                  | 35                 | 34                 | 34                 | 34                 |
| Result<br>No.                    | 1                  | C1                 | 3                 | 4                 | Ŋ                 | 9                 | 7                   | œ                  | 6                  | 10                 | 11                 |

Fridkin M;

Pac A,

Bar haim E,

Carmon L, Tircsh B,

Eiserbach L, Co Fitner-attas C,

(BIOT.) BIC-TECHNOLOGY GEN CORP.

| Amino acid sequenc | Arabidopsis thalia |          | Arabidopsis thalia | d glutamicum prote | C. qlutamicum SRT | Arabidopsis thalia | Prosophila melanog | Droscphila melanog | Lecithin:cholester | Lecithin: cholester | Legithin chelester | Lecithin: rholester | Novel human diagno | Arabidopsis thalia | Arabidopsis thalla | Propionibacterium | Propion:bacterium | Propionibacterium | Corynebacterium gl                      | Human nomel extrac | Arabidopsis thalia | Nevel human diagno | C glutamicum prote | Drosophila melanog | Promise. |           | Arabidopsis thalia | Arabidopsis thalia                                           | Protein which is s | Mouse pheromone re | Mouse pheromone re | Mouse pheromone re | Human cytopequiovi |
|--------------------|--------------------|----------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|---------------------|--------------------|---------------------|--------------------|--------------------|--------------------|-------------------|-------------------|-------------------|-----------------------------------------|--------------------|--------------------|--------------------|--------------------|--------------------|----------|-----------|--------------------|--------------------------------------------------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| AAG65919           | AAC28778           | AAR90765 | AAG28777           | AAG91417           | AAB78933          | AAG28776           | Approach1          | ABB61520           | AAY19350           | AAY19096            | AAY18842           | AAY18579            | AEG29861           | AAG52749           | AAG52747           | AAU66974          | AAU40249          | AAU65412          | AAB79239                                | AAU19724           | AAG46935           | ABC13349           | AAC91558           | ABB63737           | ABG05013 | AEG13423  | AAG46934           | AAG46933                                                     | AAY34979           | AAW94905           | AAW54314           | AAW94904           | AAW27085           |
| 급<br>라             | <br>ci             | C)       | er<br>Ci           | 2.2                | (4<br>(4          | 2                  | ç.                 | CI                 | 00                 | 0                   | ()<br>()           | ()<br>()            | CI<br>CI           | ci                 | ā                  | C1<br>C1          | 급                 | C1                | er<br>er                                | <u>:1</u>          | 2.1                | 즵                  | <u> </u>           | 22                 | CI       | <u>:1</u> | 2.                 | 2.1                                                          | 0.7                | ÷,                 | ु                  | 07                 | x:                 |
| 187                | 204                | 234      | 258                | 293                | 5.50<br>(3.00)    | 304                | 100.               | 4010               | CI<br>CI           | CI                  | 검                  | C1                  | er<br>Ci           | 57                 | CI<br>CI           | 94                | 117               | 160               | C - C - C - C - C - C - C - C - C - C - | 308                | 321                | 999                | 371                | 376                | 300      | 424       | 440                | 456                                                          | 003                | r<br>Fo            | 854                | æ:<br>€1           | 946                |
| 67.3               | 67.3               | 67.3     | 67.3               | 67.3               | 6.7.3             | 67.3               |                    | 67.3               | 65.3               | 65.3                | 5 25               | 55.3                | 65.3               | 65.3               | E. 20              | 65.3              | 65.3              | e : 5             | 62.3                                    | (5.3               | 65.3               | γ.<br>101<br>140   |                    |                    | 65.3     |           | 65.3               | 5.55<br>5.55<br>5.50<br>5.50<br>5.50<br>5.50<br>5.50<br>5.50 | 6.00               | *                  | 65.3               | ~<br>              | *1<br>121<br>20    |
| 33                 | en<br>en           | 33       | 33                 | 33                 | ·*)               | 3.3                | 33                 | 33                 | <u></u>            | 33                  | (1)<br>(2)         | C1                  | C.≱<br>~:          | 32                 | C1                 | 32                | 32                | 35                | 32                                      | 25                 | 3.2                | ല                  | 24<br>25           | 32                 | 32       | 25        | 3.5                | 3.2                                                          | 32                 | •                  | 120                | e.                 | 7.5                |
| 12                 | 13                 | 14       | 15                 | 16                 | 17                | 18                 | e :-               | 20                 | 21                 | 01<br>04            | č                  | ŧ                   | 61<br>61           | 97                 | 2.7                | 87                | 29                | €°;               | 3.1                                     | 즻                  | 33                 | 34                 | Ş                  | 36                 | 3.7      | 38        | 58                 | 40                                                           | , , <del>, ,</del> |                    | . <del></del>      | 1.4                | 45                 |

#### ALIGNMENTS

```
(1actadherin (BA-46) peptide fragment (tumour associated antigen).
  Major Histocompatibility Complex, aroplakin, prostate specific antigen; prostate specific membrane antigen; prostate acid phosphatase; mucin; lactadherin; terate acid phosphatase; mucin; lactadherin; teratocancinoma derived growth factor; PSA; PSMA; PAP; CRIPT:-1.
   immour associated antique populate, IAA, cancer; carcinoma; incomments of prevention; enco, anti-inmour vaccino; metastases; prevention; practices, eval;, throid; colon; stomach; carcinoma; MHC Class I; HLA-A2; human;
                         AAYW1911 of a band, peptides 9 AA
   (YEDA ) YEDA RES & DEV CO LTD
   9811-0125608.
  AAMO-IITOU417
   (tirst entry)
   WU200006723-A1.
  Homo sapiens.
  29-JUL-1999;
   10 - JUL- 1498;
   ∂∂∂r?-Nıπ-nI
  10-PER-2000
   AA1:22841;
            AAY82841
RESULT
```

```
46 kD apparent molecular weight human milk fat globule antigen
  Peptide
  Protein
   Matches
   AAY94453
       ò
  0
   Those tumour associated antiqens described in records AAY82806-Y82824 and AAY82855-YY82806 are derived from Uroplakin, such as Uroplakin II, Uroplakin Ta, Uroplakin III and Uroplakin Ib. Those described in records AAY82825-Y82829 are derived from prostate specific antigen (PSA). Those described in records AAY8283 are derived from prostate specific membrane antigen (PSAA). Those described in
   from Lactadherin (BA-46)— Those described in records AAY82847-Y82854 are derived from Mucin and those described in records AAY$2871-Y82882 are derived from Teratocarcinoma derived growth factor (CRIPTO-1).
   Tumor associated antiqen peptides, especially derived from uroplakin, useful as vaccines to prevent or cure cancers including breast, bladder, prostate, pancreas, ovary, thyroid, colon and stomach -
   The amino acids located at positions 2 and 9 of the tumour associated antiques are the anchor residues which participate in the binding to MHC class I molecules, more specifically HLA-A2. More tumour associated antiques are described in GENESEQ records AAY82805 Y82882.
   Gaps
   HMFG; human milk fat globule; antigen; immunogen; vaceine; virucide;
  YY82836 AAY82839 are derived from prostate acid phosphotase
Those described in records AAYM2M40-YM2M46 are derived
  treatment, prevention and cure of cancer or cancer metastases. The cancer may be breast, bladder, prostate, parecreas, ovary, thyroid, colon, stomach, head or neck cancer or a careinoma. The tumour associated antigens are presentable to the famine system by BLA As molecules and are generally between 8 to 10 amino acids in length.
   0;
   fumour associated antiqen peptides (TAA) may be used for the
  100.0%; Score 49; DB 21; Length 9; 100.0%; Pred No. 6.40+05;
   opitholium; tumor; bréast cancer; monochonal antibody; MAb.
   Indels
  0
  0; Mismatches
  Ceriani RL, Larocca DJ, Peterson JA;
  records YY82836 AAY82839 are derived
   (CANC-) CANCER PES FUND CONTRA COSTA
   AAR77252 standard, Protein, 387 AA
  Claim 17; Page 99; 113pp; English.
  94WO-US13967.
   93US-0162402.
  21-NOV-1995 (first entry)
   Conservative
   HMFG 46 kDa antiqen.
                                    WP1; 2000-205463/18.
   WPI: 1995-215151/28.
   Best Local Similarity
Matches 9, Conserv
   1 NLLI-REMWVT 9
   N-PSCB; AAQ91198.
  9 AA;
   05-DEC-1994;
  03-DEC-1993;
  Homo sapiens
  W09515171-A.
   08-JUN-1995,
  AAR77252;
  Sequence
  Query Match
   (PAP)
  Matches
  RESULT
  AAR772
  <u>a</u>
        \begin{array}{l} x \times y + y + y \times y \\ x \times y + y + y \times y \\ x \times y + y + y \times y \\ x \times y + y \times y \\ x \times y 
  Š
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Lactadherin protein was found in exosomes produced by dendritic cells. The protein is involved in the phagocyrosis of particulate antiqens by dendritic cells. Exosomes produced by dendritic cells exposed to tumour antiques induce potent immune responses, lactadherin or variants of it may be used in the mediation of an immune response. Variants of
   Chimeric isolated (human) lactadherin polypeptide that functions as an adaptor of cross-priming to eliminate pathogenic antiqens, e.q. in
  Gaps
   used to prepare MABs for use in immunotherapy, immunohistopathology, prognosis, diagnosis, imaging and therapy. Recombinant antiqen can be expressed in prokaryotic or (glycosylated) in cukaryotic cells.
used in assays to determine the presence of a cancerous tumour of
  A complete cuNA sequence for the 46 kDa HMPG antigen, a major component of the apical surface of the normal breast epithelial cell, was obtained by PCR and RACE methods. CDNA clones can be
  ..
C
                                  epithelial origin, and in a vaccine against neoplastic tumours
  100.0%, Secretary, DB-16; Length 387; 100.0%, Pred. No. 0.42; e.ve. 0. Mismatches 0: Indels (
  Human; lactadherin; MGF-ER; anti-tumour; immune response; exosome; dendritic cell.
  (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
  Integrin_binding_site
  Secretion_signal
   24..387
/label- Lactadherin
   Location/Qualitiers
  Claim 6; Page 46-47; 68pp; English.
   AAY94453 standard; Protein; 387 AA
   Example 3; Page 12; 20pp; English.
  98EP-0402925.
   98EP-0402925
  (first entry)
  Human lactadherin protein.
  9, Conservative
   /label-
   1..23
/label
   48
   WP1: 2000-352597/31.
  Covery Match
Best Local Similarity
   (CURI-) INST CURIE.
  131 nllrrmwvt 139
  387 AA;
  1 NLLRRMWVT 9
   N-PSDB; AAA27140.
   Homo sapiens.
  24-NCV-1998;
   24-NOV-1998;
   11-SEP-2000
   Rinding-site
  EP1004664-A1
   31-MAY-2000.
  AAY94453;
   Seguence
```

5555555**x**3

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0

Gaps

Ö

0, 164-18

Mismatches

Score 41; DB 22; Length 1763; Pred. No. 53;

83.7%;

Ower, Match Best Local Similarity

Mateches

1 NILLRRMWV 8

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ó
   The present invention provides the protein and coding sequences of movel proteins from a rariety of cradisms, including homen, but, horse, cow, pig, hamster, monkey, macaque, yeast, backeria, full (I), sea urchin and tomato. These were durined from expressed sequence tags (ESIs) from the organism of interest. They can be used in diagnostics, toronsics, gene mapping, identification of muchtons, to ussess biodiversity and for nutritional purposes. The present sequence is a protein of the invention.
lactadherin may be used for inhibition and/or stimulation of the cross-priming of antigens and stimulation of the phagocytosis of antigens by dendrific cells. Compositions derived from factadherin can also be used on monitor an immune response, more specifically a CTL (cytotoxic T lymphocyte) response and also to produce CTLs specific for a selected antigen. The present sequence is the human
   Gaps
  Isolated polypeptide for treatment of Hisonary, Hagnastics, raising antibodies and research use
  Human, sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
   Chen E. Asandi V.
   0;
  tomato; monkey, doq. sea urchin, expressed sequence tag; EST; diaquostics; forensic test; gene mapping; genetic disorder; biodiversity; gene therapy; nutrition.
  100 0%; Score 49; PR 21; Longth 387;
100.0%; Prod. Ho. 6.42;
ive 0; Mismatches 0; Indels
  , blu C, blow F, Qion NR, Wary E, Drmanac RA, Zhang J, Werhman T;
   Human EST encoded protein SEG ID NO: 1032.
   Claim 20; Page 788 792, 1275pp; English.
   AAM23507 standard, Protein, 1763 AA
   100.0%,
  25-JAN-2000; 2000US-0491404.
17-JUL-2000; 2000US 0617744.
   25-JAN 2001; 2001WO-US02687.
   15-SEP-2000; 2000US-0663870
  03-AUG-2000; 2000US-0631451
  12-00T-2041 (first cnfry)
   9; Conservative
   lactadherin protein.
  WPI; 2001-476164,751
   Quory Match
Best Local Similarity
  131 nllrrmwvt 139
  Sequence 387 AA;
  (HYSE-) HYSEQ INC
   1 NILLERMWVT 9
   N-PSDB; AAH98166.
   W0200154477 - A2.
   Homo sapiems
   02-AUG-2001
   Tang YT,
   Cao Y,
   Matches
  RESULT
AAM2350
```

```
The invention relates to pelynometerides (AAPS1456-AAPS3435) and the encoded pelynomials (AAMS8325) that eather activity clating to eytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The
   polytachadas and polypeptides are useful in gene therapy, the incer peptide therapy. The polypeptides have various cytokine like activities, e.g. stem cell growth actor activity, hemalopolesis requisiting activity, tissue growth factor activity, immunoshalatury activit, and activity, activity activity, activity, activity, and activity, and activity, and hay be useful in the districts and treatment of cancer, teuboemia, nerveus system disorders, arthritis and
   Human, cytokine, cell proliferation, cell differentiation, see therapy, vaccine, peptide therapy, stem cell growth factor, harmatopolesis; Lissue growth factor, im-m-m-dulatory, one or lonkaemia, nervous system disorder, arthritis, inflammation.
  Ma Y;
  Note: Records for SE2 ID NO 2010 (AARSOSSI), 2111 (AARLUSE) and 4666 (AARMUSE) are emitted as the relevant pages from the sequence listing were missing at the time of publication.
   Mucjejo unida encedina palipagtides with cytokine like out rities,
  Tang YT, Liu C, Draanac RT, Abandi V, Shou F, Xu C, Cao Y, Chao QA, Wang D, Wang L, Sharq J, Pen F, Chen F, Wang ZW; Xue AJ, Yang Y, Wejhrman T, Goodrich P;
   claim 20; Page 3901-3906; 6221pp; English.
   useful in diagnosis and gene therapy -
   AAM78911 standard; Protein; 2473 AA.
  Human protein SEQ ID NO 1573.
   200008-0663561.
200008-0693325.
200008-0728422.
   05 - FEB - 2001; 2001WO - US04098
  06-NOV-2001 (first entry)
   WPI; 2001-476283/51.
  2473 AA;
  (HYSE-) HYSEQ INC.
217 nilrriwv 224
   N-PSDB; AAK52044.
   WC200157190 A2.
  inflammation.
   Homo sapiens.
   15 SEF:2000,
20-0CT-2000;
  C: NOA - 2000;
   09-AUG-2001
   AAM78911;
   Xue AJ,
   AAM78911
   RESULT
```

Sequence

1763 AA;

Sednence

```
The invention relates to polymerhootides (AAKSA485, and the tipe encoded polymerides (AAMSA23 AAMASA7) that exhibit polymerides (AAMSA23 AAMASA7) that exhibit polymerides of evidence of differentiation of which may induce production of other polymerides are useful in gene therapy, varyines or peptide therapy. The polymerides have various cyrokine-like activities, experience, stop of the application of peptide therapy. The pelypeptides have various cyrokine-like activities, activity, hasmalogolosis regulating activity lissue growth factor activity, immenomedialisty principle activity and activity and series as and a continuity in the diadress and activity in the diadress and activity and treatment of cancer, leukaemia, nervous system disorders architical and
   Human: eytokino: cell proliferation; cell differentistion; gene therapy; vacchie; peptide therapy, stem cell growth factor; haematopoiesis; tissue growth factor, immunomodulatory; caucer; leukaemia; nerous system disorder; arthritis; inflammation.
  Can Y, Ma Y;
  Note: Powerds for SEG ID NO 2116 (AAKS258)), 4111 (AAKL484) and Mere (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication
   Caps
  Nucleic acids enorable polypoptides with cytokino like activities useful in diagnosis and gene therapy.
   P. Asundi V. 2boy P. Xu C. Cao Y.
Eband J. Een E. Chen E. Wang (W)
F. Goodrich P.
   C
Shorr 41; PR 22; Tength 2473;
Pred. No. 75;
   0; Indels
                                       1; Mismatches
   Claim 20; Page 377-379; 6221pp; English.
   AAM79895 standard; Protein; 2668 AA.
   03 - FFFF 2000; 2000US - 0496914.
27 - APR - 2000; 2000US - 0560875.
20 - JUN - 2000; 2000US - 0598075.
19 - JUL - 2000; 2000US - 062032
01 - SEP - 2000; 2000US - 065337
15 - SEP - 2000; 2000US - 066337
   83 78;
87,58;
   Wejhrman T
  Human protein SEQ ID NO 3541.
  Drmanac PT.
  05-FEB-2001; 2001WO-US04098.
   รอิยธรรม รับบอบอิ
   3000 Budbud
  Wang D, Wang J,
  06-NOV-2001 (first entry)
                     Best Local Similarity 87.5
Matches 7, Conservative
   2001-476283751
  SEER AA
  927 nllfrillt
927 nllfrilwv 934
  HYSE ) HYSEQ INC.
   N-PSDB; AAK53028
  I NIJERKMWV 8
  Lin
   Yang Y.
   WO200157190-A2.
   01-SRP-2000;
15-SRP-2000;
20 oot 2000
  Homo sapiens.
   09-AUG-2001.
   100002-A0N-08
   intlammation
  AAM79895;
     Query Match
  Serprometers
   Panq YT.
  Clude OA,
   Xue AJ,
   £
   AAM79895
   RESULT
```

```
;
0
   ligase; hyperproliferative disorder; immunodéliciency disorder; autoimmune disorder; neurological disorder; metabolic disorder; inflammatory disorder; cardiovascular disorder; reproductive disorder; blood-related disorder; infectious disorder; cytostatic; anti arthritic; nephrotropic; anticoagulant.
   oxidoreductase engyme; transferase; hydrolase; lyase; isomerase;
                     0; Gaps
83.7%; Score 41; DB 22; Length 2668; 87.5%; Pred. No. 81;
                     0; Indels
                    1; Mismatches
  Novel human engyme polypeptide #679.
  AAU23593 standard; Protein; 112 AA.
  200008 0224519.
200008 0225213.
200008-0225214.
   17496.
  200005-0180628
  200.05 0195.75.
200008-0198123
   2000BS-0224518.
   . 4.58
   200 m/S m225759.
2000m/S 0.26279.
  17-JAN-2001; 2001WO US01239
  1000008 0184564
  January - 01369350
  2000US:0189874
   2000018-0205515
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  February 0.220963
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   2000008 0225267.
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   2000008-0226868.
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  18 DEC 2001 (first entry)
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  .co-socor
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   1122 nllrrlwv 1129
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  WO200155301-A2.
   24 FUR-2000,
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14 - 70L - 2000)
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   :0007-
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14 - AUG - 2000;
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2000018-0231243
  2000018-0232081
200018-0231958
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  2000001S 0.248477
  DRUG STORESHOOM
   Zero 25 Zero Stereora
   F90++76-Simon7
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17-NOV-2000;
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   29-SEP-
  -1,,,,,-7,,
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   20 001
   02-00T-
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The present invention relates to the isolation of novel human engine polygeptides, and the edge character AAS4 (84) and powers responses polygeptides of the invention are comparise the four timed character to the invention are useful in the diagnosts, treathers of the invention are useful in the diagnosts, treathers of a wide range of diagnosts, treathers from the area of the invention are useful in the diagnosts, treathers presented and/or prepared as wide range of the invention are useful in the diagnosts including hyperproliferative disorders (e.g. cancer), immandaging hyperproliferative disorders (e.g. disease), compared in the disorders (e.g. disease), arthritis, neurological disorders (e.g. disease), compared in the phenylevecuria), inflammatory disorders (e.g. arthritis), neurological disorders (e.g. attendatis), contributed (e.g. attendatis), inflammatory disorders (e.g. attendatis), and inferitual disorders (e.g. attendatis), and inferitual disorders (e.g. attendatis).

MASTAGE AAUZSELA represent the open head in the therapy.
   Note. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the wip inthoughthy betweeness.
   Recentric, traiting nearly, immune system, mescalur, reproductive, presenting, traiting nearly, immune system, mescalur, reproductive, politicative disorders and can erous
  = 1
  73.5%, Scare 36, 58.50; Length 112; 55.5%, Fred, No. 28; 1, Index: 1, Assmatches 1, Index:
  Claim 11, SEQ ID No 1589, 1180pp, English.
   Essen CA, Barash SC, Ruben SM
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2000US 0249217.
;unouts 9249218.
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2000008-0249245.
2000008-0249264.
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200008-0051990.
200008-0254097.
   (HUMA ) BUMAN GENOME SCI INC.
   200103 0759578
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Matches 6, Cosservative
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  [[[ |:|]
n]]erlw: 12
  1 NLLERMWV 8
  09 PEC 2000
08 PEC 2000
09 FEC 2000
11 PEC 2000
   NOV 1898
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NEC 2808
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NCV 2000;
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HCV-2010;
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   17 - NOV - 2200.
17 - NOV - 2200.
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  OGENY Match
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RESULT

ABC28776

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invention
              AAY51901;
  AAU37812;
  Sequence
   Query Match
   10
  Matches
   RESULT
  ŝ
  q
   polynocheridas are also used in diagnostics as expressed sequence tags for identifying expressed genes. (i) is useful in que bluedey techniques to restore notical activity of (II) or to tread disease states involving (II). (II) is useful for generating antibodies against if, detecting or quantificial a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) and (II) and (II) and (II) and (II) are useful for treating
   disorders involving aberrant probein expression or biological activity. The polypeptide and polynucieotide sequences have applications in diagnostics, forensits, gone mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human
   diagnostic amino acid sequences of the invention.
Note: The sequence data for this patent did not appear in the printed
specification, but was obtained in electronic format directly from WIPO
  polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCB) primers, aliquences, and for chromosome and gene mapping, and in recombinant production of (II). The
   0; Gaps
   diagnostics, forensits, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
  Human; chromosome mapping; gene mapping; gene therapy; forensic; tood supplement, medical imaging; diagnostic; genetic disorder.
  New isolated polynucleotide and encoded polypeptides, useful in
  71.4%; Score 35; DB 22; Longth 666; 75.0%; Pred. No. 2.5e+02; ive 1; Mismatches 1; Indels
  The invention relates to isolated polynucleotide (1) and
  at ftp.wipo.int/pub/published_pot_sequences.
  Claim 20; SFQ TP No 59195; 103pp; Eaglish.
  Novel human diagnostic protein #28767.
  AAY51901 standard; Protein; 329 AA.
ABG28776 standard: Protein; 666 AA.
   30-MAR-2001; 2001WO-US08631.
   31-MAR-2000; 2000US-0540217
  201618 SHUGUC
  18-FEB-2002 (first entry)
  6; Conservative
   WPI; 2001-639362/73
  Drmanac RT, Liu C,
  Best Local Similarity
  666 AA;
  (HYSE-) HYSEQ INC.
  1141 | 11:
137 nllrimwi 144
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  biodiversity
   11-ocr-2001.
  23 ATE: DOON
   Sednence
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  Query Match
  Matches
   AAY51901
   RESULT
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This invention describes a movel isolated nucleic acid (1) encoding ODE (uridine diphosphate) R acety/glucosaminyl.bctal, 4 or application of all an acid (1) encoding options among the containing the repeated disacremation most file for the containing the repeated disacremation most file acid (1) is useful for tecombinant expression of Worls, to alter adhesion and recognition properties of transfected cells and to produce glycoproteins
  New nucleic acid encoding a glucosaminy! transferase, used for in vivo
  substituted by polylactosaminealycens, when introduced into cells that express glycoproteins. Vectors containing (1) are used in gene therapy and for production of transgenic animals. Fragments of (1) are used to
  detect related sequences from other species and as antisense reagents. This sequence represents the human 36nl protein described in the
   UDP (uridine diphosphate)-N-acetylqlucosaminyl; betal,4 galactoside;
betal,3.N acetylqlucosaminyl transferase; 36mm; polylactosaminyl;
disacehatide production; cliqosaccharide production; qlycan;
   0; Caps
   Streptococcus pneumoniae cellular proliferation profein #241.
  or in vitro synthesis of glycan chains containing a specific disaccharide repeat element.
   Length 329;
   Score 34, DH 21, Length 32, Pred, No. 1,9e+02;
  glycoprotein; gene therapy; transgenic animal; human.
  0; Mismatches
  Disclosure, Fage 31-32, 34pp, German.
  AAU37812 standard; Protein; 750 AA.
  69.48,
85.78;
  99WO-CH00365.
   38CH-0001717.
15-JUN-2000 (first entry)
  14-FEB-2002 (first entry)
   6; Conservative
   Berger EG, Hennet T;
  2000 224707/19.
   (BERG/) REPORER E G.
   Hest Local Similarity
  329 AA;
  (HENNZ) HENNET T.
   N-PSDB; AAZ89455.
   WO200011190-A2
   1 NLI.RRMW 7
  œ
   Homo sapiens.
  2 nllrraw
  06-AUG-1999;
   20-ATG 1998.
   02-MAR-2000
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Sequence
  AAG65919;
  RESULT 12
   AAG65919
      ò
   X E X
   DT
  The invention relates to antisense inhibitors of genes essential to prokatyctic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokatyctes used are Escherichia coli, Staphylococcus and proteins and encoded and promoniae, Pseudomonas acuginose and Enterococcus faccalis. The forential coliferation of potential new targets in relating proteins used in proliferation of potential new targets to active development. The antisense nucleic acids can also be used to obtain antibodies expended to be included to the expressed proteins. The proteins can be used to serve of engineering to the expressed proteins. The proteins are sequenced in a state of a sequence is also useful to serven for homologous nucleic acids which are respired for cell protein in a wide variety of crisals.
   0
  Ohlsen KL, Zyskind JW, Wali D, Trawick JD, Carr GJ;
Xu 8H;
  Gaps
   0
   New polynuclectides for the identification and development of antibiotics, comprise sequences of antisense nucleic acids -
   Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic
   69.4%: Score 34; DB 22; Length 750;
55.6%; Pred. No. 4.3e+02;
Live 3; Mismatches 1; Indels
Antisense, prokaryotic cellular proliferation protein;
  essential prokaryotic cellular proliferation protein.
  Example 3, Seq 1D No 13405, 511pp, English.
  ftp.wipo.int/pub/published_prt_sequences
               antibiotic; antibacterial; drug design.
  Novel human diagnostic protein #19079
  ABG19088 standard; Protein; 798 AA.
   tormat directly from WIPO at
   23-001-2080; 2000US-242578P.
27-NOV-2000; 2000US-253625P.
22-PEC-2000; 2000US-25931P.
16-FEB-2001; 2001US-269308P.
   2000015-205727P
  21-MAR-2000; 2000US-191078P.
   21-MAR-2001; 2001WO-US09180
  18-FEB-2002 (first entry)
   Local Similarity 55.69
  Streptococcus pneumoniae
  (ELIT-) FITTPA PHAPM INC
   2001 631495770
   750 AA;
  :||:| |:|
109 sllgrfwit 117
  N-PSDB; AAS55671.
  1 NLI.RRMWVT 9
   WO200170955-A2.
  Haselbeck R,
   Yamamc⁺∩ PT,
  26 - MAY 2000;
  27-SEP-2001.
   Sequence
   ABG19088;
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XX
DT
XX
DE
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The invention relates to isolated polynucleotide (1) and polypeptide (11) sequences. (1) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oliqueness and for chromosome and gene image in the polynucleotides are also used in diagnostics as expressed sequence tags. Or for identifying expressed genes (1) is useful in gene therapy Lechniques to restore mernal activity of (1) or to treat disease states involving (1). (1) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a tood supplement. (11) and its binding partners are useful in medical imaging of sites expression (11). (1) and (11) are useful in treating disease expression (11). (1) and (11) are useful in treating disease. The polypeptide in the objective sequences have applications in disquestics, foreisies, generating sequences have applications in disquestics. Foreisies of other traits to assess biodipresity responsible to generate disorders or other traits to assess biodipresity.
   and to produce other types of data and products dependent on into and askine acid sequences. ABG50910-ABG39377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
  Saps
   New isolated polymacleotide and encoded polypeptides, maetu, in diagnostics, forensies, gene mapping, identification of mutations tespensible for greatly disorders or other traits and to assess
Human; chromosome mapping; gene mapping; gene therapy; forensic;
   Amino acid sequence of novel human arginine-rich protein (ARP).
                                      food supplement; medical imaging; diagnostic; genetic disorder
  69.4%; Score 34; DB 22; Length 798; 109.0%; Pred. No. 1.6e.00;
Live C; Mismatches G; Indels
  at ftp.wipo.int/pub/publish.d_pot_sequences.
  Claim 20, SEQ IL No 49447; 103pp; English.
  AAG65919 standard; Protein; 187 AA.
   Tang YE;
   30-MAR-2001; 2001WO-US08631.
  31 MAR 2006, 2000US-8540217.
23-AUG-2000, 2000US-0649167.
   (first entry)
   Ouery Match
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   Drimanac RT, Liu C,
   WPI; 2001-649462/73.
   798 AA;
  (HYSE ) HYSEQ INC.
  N-PSDB; AAS83275.
   111111
362 llrrmw 367
  WO200175067-A2.
  2 LLRRMW 7
   Homo sapiens.
   biodiversity
   11-OCT-2001.
  11-FEB-2002
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4 mrrmwat 10

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by decreasing anglogenesis in cancerous tunkais and treating myordridal infarction and promoting healing, by increasing anglogenesis. Iransgenic non-human animals, having disrupted arginine-rich protein (APP), are useful for determining the clinical stage of ovarian tuncrous, which is useful for determining it the tumour has potential for metastasis. ARP is useful in gene therapy and in diagnostic applications VEGFMA proteins are useful in the treatment of tumours, neoplasias, hemangiomas, rheumatoid arthritis, atherosclerosis, idiopathic pulmonary fibrosis, vascular restensis, hemophile joints, hypertrophic stats, Osier Weber advances, seleroderma vascular adhesion pathologies, synchlis, dermattis, endometriosis, diabetic retinopathy neovascularistis, endometriosis, diabetic retinopathy neovascularistic dermattis, endometriosis, diabetic retinopathy neovascularistic dermattis, endometriosis, diabetic retinopathy neovascularistic healing. The present sequence represents the amino acid sequence of human ARP.
  The invention relates to modulating angiogenesis and cell survival that involves modulating the arrivity of at least one vascular endulabelial growth lactor VBGP)-incolulated game polypepi ide the method is useful for modulating angiogenesis and cell survival, for treating tumour and cancer
                           arqinine rich protein; cardiant; antirheumatic; antiarthritic; human; antiatheroscierotic; vasotropic, gynecological; antidiabetic; vulnerary; antiuleer; dermatological; ophthalmological; antipsoriatic; apoptosis:
ARP; anglogenesis; vascular endothelial growth factor; VEGF; cytostatic;
   Modulating angiogenesis and/or apoptosis for preventing or treating cancer, myocardial infarction and promoting healing, by modulating the activity of vascular endothelial growth first restricts gene polypeptide.
  "nucleotides encoding these 2 residues are not indicated in the corresponding nucleotide sequence"
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   /note- "enroded by GAC"
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Misc-difference 16
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   21-MAR-2001; 2001WO-US09043.
   21-MAR-2000; 290048 191201P
   Rastelli LK, Gerber H;
   Misc-difference 50..51
   /note=
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   (CURA-) CURAGEN CORP
  WPI; 2001-649087/73.
  Misc-difference 48
   Misc-difference 49
  Misc-difference 17
  Sequence 187 AA;
   N-PSDB; AA167447
  W0200170174 - A2.
   qene therapy.
   Homo sapiens.
   27-SEP-2001.
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hybridisation assay; genetic mapping; gene expression control; promoter;
  Protein identification; signal transduction pathway; metabolic pathway;
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  AAG28778 standard; Protein; 204 AA.
  99US-0131449.
  99US-0132863.
   99US-0135124.
99US-0135353.
  25-FEB-2000; 2000EP-0301439
   99US-0126785.
  99US-0128244.
   99US-0129845
   99US-0130449.
  99US-0130510.
  99US-0132484
   99US-0132485.
   99US-0132487.
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  99US-0139454
  17-OCT-2000 (first entry)
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  08-APP-1999:
   16-APR-1999;
   21-APR-1999;
  23-APR-1999;
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  999;
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  MAY-
  11-MAY-
  14-MAY-
   19-MAY-
   03-JUN-
   19-APR-
  23-APR-
   28-APR-
   14 - MAY -
   14-MAY-
  I α-MAΥ-
  MAY
  -NUV-
   O-AFE
   28-MAY-
  -NOC-
   -NOC-9
RESULT 13
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1; Indels

1; Mismatches

5; Conservative

3 LREMWVT 9

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Sest Local Similarity

Matches

Query Mateh

67 3%. Somre 33. DH 22: Length 187; 71.4%; Pred. No. 1.60+02;

| 18. 01 3.09 4.0 4.0 4.0 4.0 4.0 4.0 4.0 4.0 4.0 4.0                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | 4018 0145084<br>9018 0145187<br>9018 01452187<br>9018 0145224<br>9018 0145224<br>9018 0145224<br>9018 0145241<br>9018 0145241<br>9018 014534<br>9018 0147328<br>9018 0147328<br>9018 0147333<br>9018 0147333<br>9018 0147333<br>9018 0147333<br>9018 0147333<br>9018 0147333<br>9018 0147333<br>9018 0147333                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       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  RESULT 14
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  원인 인경 전 등 일 또 한 전 용 인영 한 한 등 원 등 법 등 일 등 등 인원은 한 분 등 일 등 입원을 하면 일 등 또 등 표 명은 인본 등 은 도 등 본 수 만인 인인 일 만인 모
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AAB90765 standard; Protein; 234 AA.

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  16-JUN-1
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   23-APR-
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   OR-APR-
  -NDD-10
  NO5-32
   18-JUN-
  24 GUN:
Protein identification, signal transduction pathway, metaholic pathway, hybridisation assay, genetic mapping, gene expression control, promoter, termination sequence.
   The present invention provides the protein and coding sequences of a number of human shear stress response proteins. These are useful in the diagnosis, treatment and screening of vascular diseases caused by arteriosclerosis, including heart failure, post-PTCA restenosis and
   Nojima H., Yoshisue H., Obayashi M. Ota T., Kawabata A., Sakurada P.;
   0; Gaps
   DNA sequences, proteins encoded by them and antibodies against them useful in diagnosis and treatment of vascular disease caused by
   Human; shear stress-response protein; vascular disease;
   Arabidopsis thaliana protein fragment SEQ ID No. 34123
                             Human shear stress-response protein SEQ ID NO: 30.
  Sugano S.
  Claim 60; Page 258-259; 678pp; Japanese.
   AAG28777 standard, Protein, 258 AA.
  Sokine S. Nakamura Y.
   (KYOW ) KYOWA HAKKO KOGYO KK
   99JP-0280976.
   02-0CT-2000; 2000W0-JP06840
  25-FFP-2000; 2000EP-030;449
             15-JUN-2001 (first entry)
   17-OCT-2000 (first entry)
   5; Conservative
   Arabidopsis thallana.
   WPI; 2001-266308/27.
   Query Match
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   arteriosclerosis -
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   (NOUIZ) NOUIMA H.
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  hypertension.
  Homo sapiens.
  01-OCT-1999;
  12-APR-2001.
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Scarch completed: September 5, 2002, 15:26:29 Job time: 369 sec

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GenCore version 4.5 Capyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

September 5, 2002, 15:27:34 ; Search time 58:86 Seconds (without alignments) 3.735 Million cell updates/sec Run on:

US-09-744-804-37 45 1 NLFETPILA 9 Title: Perfect score: Sequence: BLOSUM62 Gapop 10 0 , Gapoxt 0 S Scoring table:

231628 seqs, 24425594 residues Searched: Total number of hits satisfying chosen parameters:

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Database :

Pred No is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

|          |                     | مو             |                 |              |                                 |                                       |
|----------|---------------------|----------------|-----------------|--------------|---------------------------------|---------------------------------------|
| Result   |                     | Query          |                 |              |                                 |                                       |
| ON       | Score               | Match          | Match Length DB | DB           | ID                              | Description                           |
| -        | 4.5                 | 100.0          | 3 V -           | 24           | US-0#-152-402B-12               | Seaucace 12. Appl                     |
| C        | ₽3<br><del>**</del> | 0 UST          | 533             | ٠,           | - 'A: 7                         |                                       |
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| Q        | 45                  | 100.0          | 197             | ۲,           | 115-00-162 402R 6               | Sequence C, Appli                     |
| 7        | 45                  | 100.0          | 465             | <b>C</b> 1   | 1                               | æ                                     |
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| σ        | 32                  | 71.1           | 1,4             | C 1          | US-08 152 4028-26               | 93                                    |
| 10       | 32                  | 71.1           | 590             | ດ•           | HS-08-756-317-12                | Sequence 12, Appl                     |
| 11       | 32                  | 71 1           | 36.72           | C 1          | US-08-822 445 12                | ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; |
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| 13       | 32                  | 71.1           | 3801            | C 4          | US-08-822 445 10                | Sequence 10, Appl                     |
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| 17       | 31                  |                | 103             | _            | US-08-111-939-25                | e Ci                                  |
| 18       | 31                  | 6.8            |                 | C4           | US-08-162-402B-13               | Sequence 13, Appl                     |
| 19       | 31                  |                |                 | 4            | US-09-077-675A-5                | Sequence 5, Appli                     |
| e e      | ۲.                  |                | ÚČE             | C.           | 63-5633 381 80-Sh               | c)                                    |
| Ć.       | 5.                  | 6.83           | <u>්</u><br>ස   | e a          | -08-623                         | C)                                    |
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| æ:<br>€1 | 31                  |                | 391             | ₹            | -08-384-                        | Sequence 11, Appl                     |
| 24       | 31                  | 6.83           | 463             | C1           | -08-162-                        | 7 '6                                  |
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Query Match 160.0%, Store 45, DB 2; Length 159; Rest Long. Similarity journs, Pred No. 0.038;

LEMOTH: 159 amino acids

TYPE: amino acid TTEANHIDHESS, JOHNSOWN TSTOLOGY, JOHNSOWN MOLECOLE TYPE: POPTIGE US-08-162 4028-12

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| พ.๊ผลัส ให้ผู้ผู้สุดให้ผู้ผู้ผู้ผู้<br>พ.๊ผลัส ให้ผู้ผู้ผู้ผู้ผู้ผู้ผู้ผู้ผู้ผู้ผู้ผู้ผู้                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              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APPLICANT: PETERSON, JERRY A.
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  OSA
  USA
   STRANDEDNESS:
   FILING DATE:
   90071
  ADDRESSEE:
  US-08-162-402B-3
   US-07-607-538C-2
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                 APPLICANT:
  COUNTRY:
   Quory Mateh
   TYPE:
  Matches
  RESULT
  POLYPEPTIDE WITH 46 DIFFERENTIATION ANTIGEN BINDING SPECIFITY AND CLOTTING
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  1900.0%, Score 45, DB 1, Length 217, 1000.0%; Pred. No. 0.055;
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   OPERALING SYSTEM: PC:DGS/MS-DGS 5.0
SOFTWARE: Patentin Release #1.0, Version #1.25
ADDITORION DATA:
  0; Mismatches
 0; Mismatches
   Amzel & Assoc.
5. 5455031th Broadway
   100-boode
   APPLICATION NUMBER: US/07/607,538C FILING DATE: 01-NOV-1990
   APPLICANT: Ceriani Dr., Roberto L.
APPLICANI: Peterson Dr., Jerry A.
   Sequence 3, Application US/U7607538C Patent No. 5455031
  : Sequence 3, Application US,08162402B
; Patent No. 5972337
  USF THERFOF
  IBM PC compatible
   APPLICANT: CERIANI, ROBERTO L.
  REGISTRATION NUMBER: 30,930
REFERENCE/OWNYET NUMBER: OPE
TELECOMMUNICATION INFORMATION:
  (510) 943-1931
  Larocca, David J
   INFORMATION FOR SEQ ID NO: 3:
  ATTORNEY/AGENT INFORMATION:
  Floppy disk
  (510) 943-1189
  217 amino acids
   SEQUENCE CHARACTERISTICS:
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9; Conservative
  single
   MOLDCULD TYPE, protein
FRAGMENT TYPE:
   CORRESPONDENCE ADDRESS:
   COMPUTER READABLE FORM:
  435
   Viviana Amzel
   Walnut Creek
   California
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TITLE OF INVENTION:
   2055 No.
  amino acid
   linear
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Bost Local Similarity
  GENERAL INFORMATION:
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   VSD
  STRANDEDNESS:
   MEDIUM TYPE:
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.
Z
   94596
  TELEPHONE:
  COMPUTER:
  US-0B 162-402B-3
   US 07-607-538C-3
  US-07-607-538C-3
   TOPOLOGY:
   COUNTRY:
  APPLICANT:
   TELEFAX:
  LENGTH:
  STREET
  STATE:
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 Matches
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  <del>1</del>
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TITLE OF INVENTION: POLYPEPIIDE WITH 46
JILLE OF INVENTION: DIFFERENTATION ANTION BINDING SEPTIITY AND CLOTHING
TITLE OF INVENTION: FACTORS V AND VIII LIGHT-CHAIN HOMOLOGIES,
TITLE OF INVENTION: PUSION PROFEIN, POLYNICLEOTIDE AND POLYRHO-
                 TITLE OF INVENTION: 46 KINLTON HUMAN MILK FAT
TITLE OF INVENTION: GLOBURF (HMPG) ANTHORN, PRACMENTS & FRICLON PROTEIN
  Gaps
   NUCLECTIDE ENCODING THE POLYPEPTIDE, ANTI-POLYPEPTIDE ANTIBODIES, KITS AND METHODS OF
  100 0%; Soore 4%; 194 2; Tength 217; 100.0%; Pred. No. 0.055;
   0; Indels
   SOFTWARE: FastSEQ for Windows Version 2.0 CUPPENT APPLICATION DATA:
AFFI (PAITOR NUMBER 18, 08, 742,4028
  CORRESPONDENCE ADDRESS:
CORRESSEE: Pretty, Schroeder & Poplawski
STREET: 444 South Flower St., 19th Floor
  0; Mismatches
   2055 No. 5455031th Broadway
  P66 38215
   APPLICANT: Ceriani Dr., Roberto L. APPLICANT: Peterson Dr., Jerry A. APFLICANT: Larcaca, David J. TITLE OF INVENTION: POLYPERITE WIT
   . Sequence 2, Application US/076075380
: Patent No. 5455031
  USE THEREOF
   Amzel & Assoc.
   30,930
   TELECOMMUNICATION INFORMATION:
LAROCCA, DAVID J.
  COMPUTER: IBM Compatible
   FILING DATE: 03-DEC-1993
   ATTORNEY/AGENT INFORMATION:
   TELEFRONE: 213-622-7700
TELEFFAX: 213-489-4210
  REFERENCE/DOCKET NUMBER:
  217 amino acids
  9; Conservative
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  V:viana
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MOLECULE TYPE: peptide
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MEDIUM TYPE: Diskett
  CORRESPONDENCE ADDRESS:
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   CIIY: Walnut Creek
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   NUMBER OF SEQUENCES:
   STREET: 444 CONTRACTOR LOS Angeles
  NUMBER OF SEQUENCES:
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  GENERAL INFORMATION:
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TITLE OF INVENTION: 45 CYALTON HUMAN MILE FAT
TITLE OF INVENTION: GEORGIE (BMFS) ANTIGEN, FRAGMENTS & FUSION PROFEIN
NUMBER OF SEQUENCES: 29
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   100.0%; Score 45; FH 2; Lenath 218;
100.0%; Pred. No. 0.055;
ive 9; Mismatches 0; Indels
  100.0%; Score 45; DE 2; Longth 387; 100.0%; Pred. No. 0.11;
   Indels
   ë.
   SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
   ADDRESSEE: Pretty, Schroeder & Poplawski STREET: 444 South Flower St., 19th Floor CITY: Los Angeles
   Mismatches
  REFERENCE/DOCKET NUMBER: P66 38215 TELECOMMUNICATION:
  APPLICATION NUMBER: US/08/162,402B
  Sequence 6, Application 08/08162402B
Patent No. 5972337
  APPLICANT: CERTANI, ROBERTO I..
APPLICANT: PETERSON, JERRY A..
APPLICANT: LAROCCA, DAVID J.
   ô
  30,930
   OMPUTER: Diskette COMPUTER: ibm Compatible OPERATING SYSTEM: DOS
  INFORMATION FOR SEQ ID NO: 2:
  03-DEC-1993
   ATTURNEY/AGENT INFORMATION:
   Gest Local Similarity 100.0%
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amino acid
 213-622-7700
  LENGTH: 387 amino acids
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   INFORMATION FOR SEQ ID NO:
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  APPLICATION NUMBER:
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  Best Local Similarity
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   1 NLFETPILA 9
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   STRANDEDNESS:
  FILING DATE:
  FILING DATE:
  90071
TELEPHONE:
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   THLEPHONE:
   TOPOLOGY:
   TOPOLOGY:
  US-08-162-402B-6
  US-08-162-402B-2
  US-08-162-402B-6
  COUNTRY:
   LENGIH:
   STATE:
  Query Match
   NAME
  RESULT
   Ś
  ó
  TITLE OF INVENTION: 46 KDALTON HUMAN MILK FAT
TITLE OF INVENTION: GLOBULE (HMFG) ANTIGEN, FRAGMENTS & FUSION PROTEIN
  Gaps
  ं
   100.0%; Score 45; DB 1; Length 218; 100.0%; Pred. No. 0.055;
  0, Indels
   Patentin Pelease #1.0, Version #1.25
   SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
  Mismatches
  E. Proffy, Schroeder & Poplawski
444 South Flower St., 19th Floor
   PC-DOS/MS-DOS 5.0
  P66 38215
   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/607 538C
  APPLICATION NUMBER: US/08/162,402B
FILING DATE: 03-DEC-1993
   100-004A
   Sequence 2, Application US/08162402B
Patent Mo. 5972337
   Incom
, Viviana
, viviana
  APPLICANT: CERIANI, ROBERTO L. APPLICANT: PETERSON, JERRY A. APPLICANT: LARGCCA, DAVID J.
             COMPUTER PFAINARLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
  0
  NAME: Viviana Amzel
REGISTRATION NUMBER: 30,930
   TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 943-1931
  REFERENCE/DOCKET NUMBER: P6
TELECOMMINICATION INFORMATION:
   TELEX: N.À.
INFORMATION FOR SEQ ID NO: 2:
  01-NOV-1990
   ATTORNEY/AGENT INFORMATION:
  IHM Compatible
   ATTORNEY/AGENT INFORMATION:
  (510) 943-1189
   218 amino acids
   REFERENCE/PROTKET NUMBER.
   !cral Similarity 100.0
es 9; Conservative
  SEQUENCE CHARACTERISTICS:
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  SOG
  single
  MOLECULE TYPE: protein FRAGMENT TYPE:
   PRIOR APPLICATION DATA:
   COMPUTER READABLE FORM:
   CORRESPONDENCE ADDRESS:
   NAME: Amzel, Viviana
PEGISTFATION NUMBER:
   CLASSIFICATION: 435
  APPLICATION NUMBER:
  STREET: 444 South
CITY: Los Angeles
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  OPERATING SYSTEM:
  OPERALING SYSTEM:
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  187 NLFETPILA 195
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   STRANDEDNESS:
   FILING DATE:
   MEDIUM TYPE:
  FILING DATE:
  COUNTRY: US
21P: 90071
   CA
  ADDRESSPE-
  TOPOLOGY:
  COMPUTER:
   COPTWARE.
   US-07-607-538C-2
  US-08-162-402B-2
   TELEFAX:
   LENGTH:
   Query Match
  Matches
  RESULT
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ò

Caps

```
APPLICANT: CERTANI, KOBEKTO I.,
APPLICANT: PETERSON, JERKY A.
APPLICANT: PETERSON, JERKY A.
APPLICANT: LAROCCA, DAVID J.,
ITLE OF INVENTION: GLOBULE (HMFG) ANTIGEN, FRAMENTS & FUSTON PROTEIN
TITLE OF INVENTION: GLOBULE (HMFG) ANTIGEN, FRAMENTS & FUSTON PROTEIN
  46 KLALLON HOMAN MITE FAT
GLOBULE (HMFG) ANTIGEN, FRACMENTS & FUSION PROTEIN
  O, Gaps
   100.0%; Score 45; DB 2; Length 465; 100.0%, Pred. Bc. 0.13;
  O, Indels
  SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
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  ADDRESSEE: Pretty, Schrooder & Poplawski
STREET: 444 South Flower St., 19th Floor
   APPLICATION NUMBER: US/08/162,402B
FILING DATE: 03-DEC-1993
FASSFEIGATION: 435
PRIOR APPLICATION DATA:
  P66 38215
   // Sequence 10, Application US/08162402B
// Patent No. 5972337
   Sequence R. Application HSZAR162402B
Patent No. 5972337
  GENERAL INPORMATION:
APPLICANT: CERTANI, ROBERTO L.
APPLICANT: PETERSON, JERRY A.
APPLICANT: PAROCCA, DAVID J.
TITLE OF INVENTION: 45 KIALION
TITLE OF INVENTION: GLOROLE (BA
  KEFEKBNYE/TWYKET NUMBEP: 166
TELEPOMMUNIOTION INFORMATION:
TELEPHONE: 213 622-7700
TELEPHAX: 213-489-4210
   30,930
   INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
  E: Diskette
IBM Compatible
  ATTORNEY/AGENT INFORMATION:
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   NAME: Amzel, Viviana
REGISTPATION NUMBER:
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  COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
   TITLE OF INVENTION: ON NUMBER OF SEQUENCES:
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   Onery Match
Best Local Similarity
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156 NLFETPILA 364
   11111111
434 NLFETPILA 442
  GENERAL INFORMATION:
1 NLFETPILA 9
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  USA
   STRANDEDNESS:
   90071
  FILING DATE
  US-08-162-402H-10
  COMPUTER:
  US-08-162-402B·8

    Acortrodou

   US-08-162-402B-8
  COUNTRY:
  LENGTH:
  STATE:
  PELEX:
  Matches
   RESULT
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APPLICANT: LAROCCA, DAVID J.
TITLE OF INVENTION. 46 KDALICN HUMAN MILK FAT
TITLE OF INVENTION. GLOBELE (HMFS) ARTICEN, FRAGMENTS & FUSION PROTEIN
  Gaps
  ..
  82.2%, Score 37, DB 2, Length 160; 77,8%, Fred. No. 1.8; tive 1; Mismatches 1; Indels
   CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/162 AOVVERING DATE: 03-DEC 15/08/162 AOVVERNMENT DATE: 03-DEC 15/08/162 ADVERNMENT DATE: 03-DEC 15/08/162 AD
  SOFTWARE: FASTSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US-CM.142,402H
FILLING DATE: 03-DEC-1943
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ALDRESS:
ADDRESSEE: PretLy, Schroeder & Poplawski
STREET: 444 South Flower St., 19th Floor
CITY: Los Angeles
  CORRESPONDENCE ADDRESS:
ADDRESSER: Pretty, Schrouder & Poplawski
STREET: 444 South Flower St., 19th Floor
   P66 38215
  Sequence 26, Application 08,08162402B
; Patent No. 5972337
  GENERAL INFORMATION:
APPLICANT: CERIANI, ROBERTO L.
  30,930
   APPLICANT: PETERSON, JERRY A.
   REFERENCE/DOCKET NUMBER: P6-TELECOMMUNICATION INFORMATION:
   INFORMATION FOR SEQ ID NO: 10:
   E: Diskette
JBM Compatible
   COMPUTER: IBM Compatible
   ATTORNEY/AGENT INFORMATION;
  TELEPHONE: 213-622-7700
TELEFAX: 213-489-4210
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  Ouery Match
Best Local Similarity 77.8°
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  Diskette
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00
00
   Amzel, Viviana
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   STRANDFDNFSS:
  90071
  FILING DATE:
   COUNTRY: US
ZIP: 90071
  US-08-162-402B-10
  CA
  US-08-162-402B-26
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   TOPOLOGY:
   COUNTRY:
  LENGIH
  STATE:
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Ouery Match 71.1%; Score 32; DB 2; Length 3672; Rest Local Similarity 75.0%; Prod No 7.79+02; Matches 6; Conservative 1; Mismatches 1; Indels
  Store 32; DB 2; Length 590;
Pred. No. 89;

    1::dela

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.... 7853 062 999
   1155 Avenue of the Americas
   Sequence 12, Application US/09396540; Patent No. 6310182; GENERAL INFORMATION:
   SOFTWARE: FastSEQ Version 2.0 CURRENT APPLICATION DATA: APPLICATION PAIR HE HE PARTY RESERVED.
   Pennie & Edmonds
  TELECOMMUNICATION INFORMATION:
  TELEFAX: 212-869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 12:
  Quir, Match
Bost Local Similarity 62.58,
Matches 7, Assessable
   COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
   21-MAR-1997
  ATTORNEY/AGENT INFORMATION:
  3672 amino acids
  NAME: Corummi, Laura A.
PEGISTRATION NUMBER: 30
  STRUCK JOSEPH ACMBER
   APPLICANT: Kaplan, Jerry
  SEQUENCE CHARACTERISTICS:
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  HOLFOULE TYPE: protein US-08-822-445-12
   NUMBEP OF SECUENCES: 3. CORRESPONDENCE ADDRESS:
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  HILK NOWN
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                    ; TOPOLOGY: linear
US-08-756-317-12
   New York
   2711
   CLASSIFICATION:
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| 443 NLFETAVL 450
   New York
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   COUNTRY: USA
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   US-09-396-540-12
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   71.1%; Score 32; DB 2; Longth 14; 71.4%; Pred. No. 1.1; tive 2, Mismatches 0, Indels
   APPLICANT. Clemente, Thomas E.
APPLICANT. Kishore, Ganesh M.
APPLICANT. Kishore, Ganesh M.
APPLICANT. Stark, David M.
TITLE OF INVENTION: Improved Rhodospirillum Rubrum
TITLE OF INVENTION: Dayle B Hydroxyalkonoute Synthase
CORRESPONDENCES: 15
CORRESPONDENCE AGGRESS.
  OPERATING SYSTEM: PCTEGE/MS-FGS
SOFTWARE: Patentin Fulease #1 0, Version #1 40
CURRENT APPLICATION DAIA:
  REFERENCE, DA CREET AUMBER. FOR 38-LIC
TELECOMOUNICATION INFORMATION:
IELEPHONE: 213-622-7700
TRIEFAX: 213-489-4210
   RECISTATION NUMBER: 33,062
REFERENCE/DOCKET NUMBER: MOBI:008
TELECOMMUNICATION INFORMATION:
  FILLING DATE: 25-NOV-1996
CLASSIFICATION: 536
  ADPRESSEE, Arnold, White & Durhue STREET: P.O. Box 4433
  ns 60,7007,693
   Sequence 12, Application US/08756317 Patent No. 5845894
  E: Floppy disk
IBM PC compatible
  NAME. Amin., Viriana
REGISTRATION NUMBER: 30,930
   NAME: Patterson, Melinda L. REGISTRATION NUMBER: 33,062
   (713) 787-1400
(713) 787-1440
  INFORMATION FOR SEQ ID NO: 26:
   INFORMATION FOR SPO ID NO. 12. SEQUENCE CHARACTERISTICS:
  FILING DATE: 29-NOV-1995
ATTORNEY/AGENT INFORMATION:
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   5; Conservative
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TOPOLOGY: unknown
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US-08-162-4028-26
CLASSIFICATION: 435
PRIOR APPLICATION DAIA:
APPLICATION NUMBER:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
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   amino acid
  amino acid
   GENERAL INFORMATION:
  Houston
  0.SA
   1 NLFETPI 7
   2 NLFDIPL 8
  FILING DATE
  ×
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   US-08-756-317-12
   TELEFAX:
  COUNTRY:
   LENGIH:
   Query Match
  IELEX:
   Matches
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Side
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   Sequence 12, Application US,08822145
Sequence 12, Application US,08822145
Patent No. 5952224
Patent No. 5952224
Patent No. 5952245
Patent No. 5952245
Applicant: Raplan, Jerry
Applicant: Peron, Charles
Applicant: Peron, Charles
TITLE OF INVENTION: COMPOSITIONS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF CHEDIAK-HIGASHI SYNDROME
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  New York
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   USA
  FILLING DATE:
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  SOFTWAPE
   COUNTRY:
  TOPOLOGY
  TELEFAX:
   LENGTH:
  STATE:
  RESULT 14
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               APPLICANT: Moore, Karen
TITLE OF INVENTION. COMPOSITIONS FOR THE DIAGNOSIS
TITLE OF INVENTION. AND TREATMENT OF CHEDIAK-HIGASHI SYNDROME
NUMBER OF SEQUENCES: 32
  TITLE OF INVENTION: COMPOSITIONS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF CHEDIAK-HIGASHI SYNDROME
  71.1%; Secre 32; DB 4; Length 3672;
75.0%; Prod. No. 7.7e+02;
1ve 1, Mismatches 1, Endels
  7853-062-999
  E. Pennie & Edmonds
1155 Avenue of the Americas
  ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
   APPLICATION NUMBER: US/09/396,540
   PRIOR APPLICATION DATA.
APPLICATION NUMBER- 08/822,445
  Sequence 19, Aprlication is/OBR22445
Patent Ne. 5952223
GENERAL INFORMATION:
  SOFTWARE: FastSEQ Version 2.0 CURRENT APPLICATION DATA:
  FastSEQ Version 2.0
  JORMA.
Laura A.
30,742
  REFERENCE/DOCKET NUMBER: 785
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-909
TELEFAX: 212-869-8864
TELEX: 66141 PENNIE
   INFORMATION FOR SEQ ID NO: 12:
   COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
  COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
  ATTORNEY/AGENT INFORMATION:
  LENGIH: 3672 amino acids
  APPLICANT: Kaplan, Jerry
APPLICANT: Perou, Charles
APPLICANT: Moore, Karen
APPLICANT: Perou, Charles
   SECTIONS CHARACTERISTICS.
  Query Match
Best Local Similarity 75.93
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US-09-396-540-12
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MEDIUM TYPE: Diskett
  CORRESPONDENCE ADDRESS.
   REGISTRATION NUMBER:
   NUMBER OF SEQUENCES:
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   amino acid
  New York
   10036/2711
  New York
   ||||||| :|
443 NLFHTAVL 450
  CLASSIFICATION:
   STPEET: 1155 Av CITY: New York
   New York
   Coruzzi,
  1 NLFETPIL 8
  USA
  USA
  MEDIUM TYPE:
  FILLING DATE:
   FILING DATE:
   TOPOLOGY:
  ADDRESSEE.
  US-08-822-445-10
  COUNTRY:
  SOFTWARE:
   COUNTRY:
  STATE:
  STATE:
   CITY:
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0; Caps
   TITLE OF INVENTION: COMPOSITIONS FOR THE DIAGNOSIS TITLE OF INVENTION: AND TREATMENT OF CHEDIAK-HIGASHI SYNDROME
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   7853-062-999
  PEPEPENCE/DOCKET NUMBER: 7853-062-999
   COMMESSER: Pennie & Edmonds
STREET 1155 Avenue of the Americas
UMBER: US/08/822,445
21-MAR-1997
  APPLICATION NUMBER: US/09/396,540
   Sequence 10, Application US/09396540 ; Patent No. 6310182
   08/822,445
   SYSTEM: DOS
PastSEQ Version 2 0
   /AGENT INFO.C.
Coruzzi, Laura A.
... minneRp: 30,742
   NAME: Coruzzi, Laura A. FEGISTRATION NUMBER 30,742
   PEPEPENCE/INVIESE NUMBER 789
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
   TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
   TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO· 10: SEQUENCE CHARACTERISTICS:
  TELEFAX: 212-869-8864
TELEX: 66141 PENNIE
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  IBM Compatible
  ATTORNEY/AGENT INFORMATION:
   ATTORNEY/AGENT INFORMATION:
  3801 amino acids
   LENGTH: 3801 amino acids
   APPLICANT: Kaplan, Jerry
APFLICANT: Perou, Charles
APPLICANT: Moore, Karen
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  GENERAL INFORMATION:
APPLICANT: Quertermous, Thomas
APPLICANT: Hogan, Brigid
APPLICANT: Hogan, Brigid
APPLICANT: Supancic, Thomas J.
TITLE OF INVENTION: DEVELOPMENTALLY-REGULATED ENDOTHELIAL
TITLE OF INVENTION: CELL LOCUS-1
NUMBER OF SPOIENCES: 29
CORRESPONDENCE ADDRESS:
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
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CORRENING SYSTEM: PC-FnS/MS-FnS
SOFTWARE: Patentin Polesse #1 0, Version #1.30
CURRENINA APPLICATION DATA:
APPLICATION NUMBER: US/38/480,229G
FILING DATE: US/38/480,229G
FILING DATE: US/38/480,229G
FILING DATE: US/38/480,229G
FILING SABATION: S36
ATTON NEY AGENT INFORMATION:
NAME: POISSANT, Brian M.
REGISTRATION NUMBER: 28,462
REGISTRATION NUMBER: 8907-0026-999
TELECOMMUTCATION INFORMATION:
TELECOMMUTCATION INFORMATION:
TELECOMMUTCATION INFORMATION:
   Search nompleted: September 5, 2002, 15:27:34
  ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
  RESULT 15
US-08-480-229C-2
; Sequence 2, Application US/08480229C
; Patent No. 5874562
  TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 Pennie
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
   CITY: New York
STATE: New York
CONMYRY: United States
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
  LENGTH: 85 amino acids
TYPE: amino acid
   TOPOLOGY: Unknown
MOLECULE TYPE: peptide
US-08-480-2295-2
MOLECULE TYPE: protein
  443 NLFETAVL 450
  |:|| | :|
67 NIFEKPFMA 75
  1 NLFETPILA 9
   1 NLFETPIL 8
   STRANDEDNESS:
        ; MOLECULE TYF
US-09-396-540-10
   Query Match
   qq
   ò
   ōλ
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Job time: 319 sec

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|--|--|---|
|  |  |   |

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GenCore version 4.5
Copyright (c) 1993 - 2000 Gempugen Etd.
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OM protein - protein search, using sw model

September 5, 2002, 15,20,29, granch time 198,43 Seconds (without alignments) 6,310 Million cell updates/see Run on:

US-09-744-804-37 45 1 NLFETPILA 9 Title: Perfect score. Seguence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Sooring table.

747574 segs, 111073796 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Listing first 45 summaries Post-processing, Minimum Match 09 Maximum Match 100%

Database

| <br>A_Grnogorg_032807 - *                                                                     |   |
|-----------------------------------------------------------------------------------------------|---|
| <ol> <li>ZELEST Stepdata Sheddegeta sergejere eserges intel [AA] 380 LLAT.</li> </ol>         |   |
| <ol> <li>(2) (2.1587) (404 late, 3.134 generally decreased prompt), AA1361.1 A1. *</li> </ol> |   |
| 31 (21781) Soviet Later the Orlegence of Species of Proceedings and CAM (2017) LATER          |   |
| <ul> <li>अस्ति विक्राम्य के जिल्लाक कुल कर्ना करका कुल कर्मा कर १ का ।</li> </ul>             |   |
| 5: Vilish gerjalata helid gerseen, gerseenge embi, AA1984.DAT:*                               |   |
| 6: /S10S1/gegdata/hold-genese-poperse-process-popers                                          |   |
| 7: /SIDS1/grgdata/hold-geneseg/genesegp-emb1/AA1986_DAT+*                                     |   |
| 8: /SIDS1/qcgdata/hoid-geneseq/geneseqp-emb1/AA1987.DAT:*                                     |   |
| 9: /Sitsl/qcgdata/hoid geneseq/qeneseqp-embl/AAi988.DAT:*                                     |   |
| 10: Shire in gradulation of demonstrate property and year DAL: *                              |   |
| 11: /SIDSI/Appdata/ducld-apmessari/Apmessarip-respir/ANI@ag.14A1:*                            |   |
| 12: /SIBSL/gogdata/fbold-geneseq/qeneseap-embl/AAlual DAT.*                                   |   |
| 13: /SIDS1/qcqdata/hold-genescq/geneseqp-emb1/AA1992.DAT:*                                    | _ |
| 14: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1993.DAT:*                                    | L |
| 15: /SIDS1/gogdata/land-geneseq/geneseqp-embi/AA1994_DAT:*                                    |   |
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| 18: /SIDST/Joydata/Judd-genesed/Jenesedp-code//AA1997 pA: *                                   | _ |
| 19: /STDS1/gcgdata/hold-genese//yeneseap-emb1/AA1998.DAL:*                                    | _ |
| 26. /SibSi/gogdata/Auld-geneseq/yeneseqpeembi/AA1999 DA: *                                    | _ |
| 21: /Slbs1/gcgdata/hold-geneseq/genesegp-cmb1/AA2000.DAT:*                                    |   |
| 22: /SIDS1/gegdati/Bolf geneseq, geneseqF emtl/AA2001 DAT *                                   |   |
|                                                                                               |   |

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by unalysis of the total score distribution.

## SUMMARIES

|        |       | æ         |                 |          |          |                     |
|--------|-------|-----------|-----------------|----------|----------|---------------------|
| Result |       | Query     |                 |          |          |                     |
| Ž      | Shore |           | Match Length DB | g)<br>C) | CT.      | Description         |
| -      | 4.5   | 100.0     |                 |          |          | Lactadherin (BA-46  |
| C1     | 455   | 100.0     |                 |          |          | HMFG 46 kDa antige  |
| m      | 45    | 100.0     | تا ه            | ۲.       |          | HMPG 46 kDa antige  |
| 4      | 45    | 100.0     |                 |          |          | HMFG 46 kDa antige  |
| 'n     | 45    | 100.0     | 387             | 21       | AAY94453 | Human lactadherin   |
| 9      | 3.7   | 0)<br>(1) |                 | c 1      | AAY82843 | Lattadher in (BA 46 |
| Ĺ      | 35    | 77.8      |                 | CI       | ABB62713 | prosophila melanod  |
| ж      | 35    | 77.8      |                 | 14       | AAR42839 | Urea amidolyase.    |
| gr.    | 34    | 75 6      | 171             | 21       | AAR41545 | Human OPFX ÓPF1309  |
| 10     | 34    | 75.6      |                 | 5        | AAR23032 | Human putative mit  |
| 111    | 34    | 75.6      | 306             | 22       | AAU44139 | Propionibacterium   |
|        |       |           |                 |          |          |                     |

| ABC1 protein exter<br>Propionibacterium<br>Decembils metanom | Arinetobacter sp.<br>Human HE6 receptor |      | ABC 1    | Himan ABC1 satant | VECT        | LYST    | LYSTI    |                    | Human ABC1 cholest | Human ATP binding | Human ATP binding | Human ATP binding | Human ABCl FHA-3 m | Human ARC1 cholest | Human ABC1 cholest | Human ABC1 cholest | Human ABC1 cholest | Herman ARCI cholest | Human ABC1 cholest | Human ABC1 cholest | Himan ABC1 cholest | Human ABC1 cholest | Human ABC1 cholest | Human ABC1 cholest | Haman APC1 cholest | manna ABC1 cholest | estat. Att binding | an ATP bind | 747 3 4 4 5 5 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 |
|--------------------------------------------------------------|-----------------------------------------|------|----------|-------------------|-------------|---------|----------|--------------------|--------------------|-------------------|-------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|---------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------|-----------------------------------------------|
| AAB62694<br>AAU46488<br>Abb60663                             |                                         |      | AAB62691 | AATTO 2184        | AACCC18     |         | AAW23596 |                    | AAB38108           | AAY79380          | AAE13021          | AAM50227          | AAB28107           | AAH28106           | AAB38082           | AAB 18104          | AAB 18105          | AAB38109            | AAB38110           | AAB38111           | AAB28112           | AAB38113           | AAB38114           | AAB38115           | AAB38116           | AABCB117           | AALL 9922          | AAMS 8      | AAM24555                                      |
| 26 22<br>302 22                                              |                                         |      |          | ::c               |             | 81      |          |                    |                    |                   |                   |                   |                    | E 0                |                    |                    |                    |                     |                    | 1 21               |                    |                    | 21                 |                    | _                  |                    | -                  | 7           | :<br>_                                        |
| 71 O F                                                       | 590                                     | 1038 | 1089     | 1144              | # UT        | 1531    | 2001     | 2532               | 214                | 2201              | 1077              | 2201              | CI<br>CI           | 22.6               | 377                | 2261               | 326                | 2261                | 1355               | 526                | 977                | 968                | 977                | 226                | ä                  | ÷.1                | -1                 | F1          | ÷;                                            |
| 71.17                                                        | 71.1                                    | 71.1 | 7.1      |                   | 4           |         |          | r: 1<br>r: 1<br>P: | F-1                | 71.1              | 71.1              | 71.1              | ۲.<br>۲.           |                    |                    | -1.                | 71.1               | 71.1                | 77.1               | 71.1               |                    | 71.7               | 1.1.               | 71.1               | 71.1               | 71.1               | 71.1               | 1.1         |                                               |
| 4 4 5<br>4 5 5                                               | 무무무                                     | 3.2  | 25       | , ,<br>, , ,      | 1 0         | <u></u> | <u></u>  | 2                  | C4<br>201          | 21                | <u></u>           | 51<br>20          | Ç                  | 즟                  | <b>₹</b>           | C1<br>25           | 35                 | C4<br>61            | 급<br>중             | ្ន                 | <u>.</u>           | Ž.                 | <del>2</del>       | 32                 | C 4<br>703         | 7                  | 7                  | 7           | ,                                             |
|                                                              | 15.                                     | 17   | œ ;      | <u> </u>          | ) —<br>1 —: | ( C4    | <u></u>  | 24                 | en<br>C4           | 92                | 5.7               | 28                | Ф.СТ               | ○<br>~             | 3.1                | C4<br>20           | 33                 | 34                  | ۳':<br>در          | 36                 | f: -               | a)                 | ÷                  | 40                 | . ·                | 7                  | 7.7                | - <b>;</b>  | -                                             |

### ALIGNMENTS

Lastadherin (88-49) peptide fragment (tummos: associated antigen). Imment assertated antigen peptide; iAA, cancer, careinoma; trealment, prevention; cure; anti tumour vaccine; metastases; breast, Elodder, prostate, prostate, syrif; thyraid, coton; stomach, carcinoma; MHC Class 1; HIA-A2; human; Major Histocompatibility Complex; utoplakin; prostate specific antigen; prostate specific mentane antigen; prestate and phesphatase, morin, lactadherin; teratocarcinoma derived growth factor; PSA; PSMA; PAP; CRIPTO-1. AAYR2842 standard; poptide; 9 AA. (YEDA ) YEDA RES & DEV CO LID. (BIOT ) BIO IECHNOLOGY GEN CORP. GRII - 0125508. 39WO-1L00417. 19 JUN 2000 (first entry) W0200006723-A1. Homo sapiens. 30-1111-1048; 29 - JUL - 1999; 10-FEB-2000. AAY82842; AAY82842 RESULT 

Carmon L, Tirosh B, Bar-halm E, Faz A, Fridkin M;

Eisenbach 5, Ca Fitzer-attas C;

:. O

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used in assays to determine the presence of a cancerous tumour of
  Sequence
  AAR77254;
   m
  Matches
   RESULT
  5
  Ü
  treatment, prevention and cure of cancer or cancer metastasss. The cancer may be breast, bladder prostate, pancreas, ovary, thyroid, colon, standard, head or neck cancer or a carcinoma. The tumour associated antiques are presentable to the immine system by HLA-A2 molecules and are quencially between 8 to 10 amino acids in length. The amino acids located at positions 2 and 9 of the tumour associated antiques are described in participate in the binding to MHC class I molecules, more specifically HLA-A2. More tumour associated antiques are described in GDNHSBQ records AAY82806-Y82882 Those Jumest associated antiques described in GDNHSBQ records AAY82806-Y82882 and AAY82855 Y82869 are derived from Uroplakin ib. Those described in GDPJAkin ib. Those described in records AAY8285 are derived from prostate specific antique records AAY82829 are derived from prostate specific antique (PSA). Those described in records AAY8285 are derived from prostate specific antique
   prostate specific membrane antigen (PSMA). Those described in records YY82846-AAX82849 are derived from prostate acid phosphetase (PAP). Those described in records AAY82841-Y82846 are derived trom Lactadherin (BA 46). Those described in records AAY82847-Y82884 are derived from Mucin and those described in records AAY82871-Y82883 are derived from Teratocarcinoma derived growth factor (CRIPTO-1).
   Tumor associated antiqen peptides, especially derived from uroplakin,
   Gaps
  HMFG: human milk fat globulo; antigen: immunogen; varring viruside;
epithelium; tumor; breast cancer; monoclonal antibody; MAb.
   46 kD apparent molecular weight human milk fat globule antigen
  .;
0
  useful as vaccines to prevent or cure cancers including breast, bladder, prestate, parefeas, exaty, thyreid, each and stemach
   Tumour associated antigen peptides (TAA) may be used for the
  100.0%; Score 45; DB 21; Length 9; 100.0%; Pred. No. 6.44*65;
  Indels
  c
  0; Mismatchos
  HMFG 46 kDa antigen C-terminal region.
   Ceriani KL, Larocca DJ, Peterson JA;
   (CANC-) CANCER RES FUND CONTRA COSTA.
  AAR77253 standard; Protein; 217 AA.
   Claim 17; Page 99; 113pp; English.
  9308-0162402
  94WO-US13967
  21-NOV-1995 (first entry)
   Guery March
Hest Local Similarity 100.5
Tec 9, Conservation
                WPI; 2000-205463/18.
   WPI; 1995-215151/28.
  1 NLFETPILA 9
  9 AA;
  Homo sapiens.
  05-DEC-1994;
  03-DEC-1443;
  08-JUN-1995.
  W09515171-A.
  AAR77254;
   Sequence
  ~
   AAR77253
  RESILT
   Š
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Gaps
  HMFG; human milk fat globulo; antigen; immunogen; vaccino; virucido; epithelium; tumor; breast cancer; monoclonal antibody; MAb.
   A partial cond clone BA46 i (AAQ31159) for the 46 kDa HMFG antigen, a major component of the apical surface of the normal breast epithelial cell, was obtained by PCR of cDNA from a lactating
  a major component of the apidal surrace of the normal breast epithelial cell, was obtained by PCR of tennA from a lactuating breast cDNA library. The C-terminal region of the encoded protein showed 43% identity to corresp. regions of human Factor-V and 38%.
  A partial cona clone BA46 1 (AAQ41194) for the 46 km HMHS antigon
   46 kD apparent molecular weight human milk fat globule antique used in assays to determine the presence of a cancerous tumour of epithelial origin, and in a vaccine against neoplastic tumours
   ó
epithelial origin, and in a vaccine against neoplastic tumours
   100.0%; Score 45; DR 16; Length 217; 100.0%; Pred, No. 0.37; ive 0; Mismatches 0; Indels (
  /label- N.qlycosylation_site
156..158
   /label- N-qlycosylation_site
  M qlycosylation_site
   /label N glycosylation_site
  Larocca DJ, Peterson JA;
   Example /; Page 38-40; 88pp; English.
   HMFG 46 kDa antigen partial sequence.
   (CANC-) CANCER RES FUND CONTRA COSTA.
  Location/Qualifiers
   AAR77254 standard; Protein; 218 AA.
                                 Claim 7; Page 41; 68pp; English.
   94WO-11513967
  93US-0162402.
  21-NOV-1995 (first entry)
  /label "
   Conservative
  WPI; 1995-215151/28.
  Query Match
Best Local Similarity
   217 AA;
  1 NLFETPILA 9
   N-PSDB; AAQ41149
  to Factor-VIII.
  Modified-site
   Modified-site
  Modified-site
   Modified-site
   05-pRC-1994;
  C3-DEC-1993;
   Homo sapiens
  W09515171-A.
   C8-JUN-1995.
  Ceriani RL,
   .
6
```

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11-SEP-2000 (tirst entry)
  Homo sapiens
   Binding-site
  EP1004664-A1
   24 - NOV - 1998;
   24-NOV-1998;
   31-MAY-2000.
  Sequence
 AAY94453;
  AAY82843;
   umors -
   Peptide
  Protein
  9
   AAY82843
   0;
  Ö
  Caps
   Gaps
   HMFG; human milk fat globule; antigen; immunogen; vaccine; virucide; epithelium; tumor; breast cancer; meneclosal antibody; MAE.
  used to prepare MAbs for use in immunotherapy, immunohistopathology, prognosis, diagnosis, imaging and therapy. Recombinant antigen can be expressed in Fishalyctic of (glycosylated) in cukaryctic cells.
  46 FP apparent molecular weight human milk lat globule untigen used in assays to determine the presence of a cancerous fumout of optimeistal origin, and in a vaccine against neoplastic tumouts
   A complete cDNA sequence for the 46 kDs iMFG antigen, a major component of the apical surface of the normal breast epithelial cell, was obtained by PCR and RACE methods. cDNA clones can be
  Ö
   0
  100.0%; Score 45; DB 16; Length 387; 100.0%; Pred. No. 0.68; tive 0, Mismatches 0; Indels (
  Score 45; DB 16; Length 218; Pred. No. 0.37;
  C; Indets
   Mismatches
  Larocca DJ, Feterson JA,
  (CANC-) CANCER PES FUND CONTRA COSTA.
  AAY94453 standard; Protein; 387 AA.
  AAR77252 standard; Protein, 387 AA.
   Claim 6. Page 46-47; 68pp; Fnglish
   100.0%; Scc
100.0%; Pre
   94WO-US13967
  93US-0162402
   21-NOV-1995 (first entry)
  Conservative
   Conservative
  Query Match
Best Local Similarity
9, Conserva
  WPI; 1995 215151,28.
breast cDNA library.
  HMFG 46 kDa antigen.
   Ouery Match
Best Local Similarity
  387 AA;
  356 nlfetpila 364
   1 NLFETPILA 9
  1 NLFETPILA 9
  N-PSDB: AAQ41198.
   05-DEC-1994;
   03-DEC-1993;
  Homo sapiens
   WO9515171-A.
  Ceriani RL,
  AAR77252;
   Sequence
                            Sequence
  Matches
  AAY94453
   AAR77252
   RESULT
 S X S
   δλ
  QQ
  à
```

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The protein is involved in the phagocytosis of particulate antiqens by denditive cells. Excasones produced by denditive cells exposed to tumour antiqens induce potent immune responses, lactadated to lactadate in may be used in the mediation of an immune response. Variants of lactadaterin may be used cor inflation of an immune response. Variants of uniquency be used in inflation of the phagocytosis of antiques by denditive cells. Compositions delived from instance response, more specifically a CTL cytoric or monitor and also be used to monitor an immune response, and estimated the phagocytosis of cytoricis and also be used to monitor and immune response, and also be used to monitor.
   Chimeric isolated (human) lactadherin polypeptide that tunctions as an adaptor of cross priming to eliminate pathogenic antigens, e.g. in
   hardadherin protein was found in exosomes produced by dendrific cells.
  Gups
   Lactadherin (BA-46) peptide fragment (tumour associated antiqen).
  150.00, Score 15, oB 21, Length 387, 100.0%; Pred. No. 0.68; 0; Indels live 0; Mismatches 0; Indels
   anti-tumour; immune response;
  (INRM ) INSERM INST NAT SANTE & RECH MEDICALE
  /label- Integrin_binding_site
  Secretion_signal
   Location/Qualifiers
   Lactadherin
   Example 3; Page 12; 20pp; English.
   AAY82843 standard; peptide; 9 AA.
   98EP-0402925.
   98EP-0402925.
  Human; lactadherin; MGF-E8;
   συς: γ Ματοί
Best Local Similarity 100.υ-
'es 9; conservative
  19-JUN-2000 (first entry)
Human lactadherin protein
  24..387
/label |
   exosome, dendritic cell.
  Mahol
  46..48
   lactadherin protein.
  WPI; 2000-352597/31.
   387 AA;
   356 nlfetpila 364
   N-PSDB; AAA27140.
  1 NLFETPILA 9
```

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0
   Tumour associated antigen poptides (TAA) may be used for the treatment, provention and care of canons or canons netastases. The cancer may be broast, bladder, pristate, pareceas, carry, thyroid, colon, stomach, head of neck cancer or a carcinoma. The tumour associated intigens are presentable to the immane system by BLA-A2 or molecules and are generally between 8 to 10 amino acids in legath. The amino acids located at positions 2 and 9 of the tumour associated at positions 2 and 9 of the tumour associated at positions which participate in the binding to antigens are the anchor residues which participate in the binding to a mid cause I molecules, more specifically BLA-A2. More tumour associated an incompassing records AAYB280-Y8280 to and AAYB285-Y82866 are derived from Uroplakin, such as Uroplakin 11, uroplakin 14, uroplakin 11, in and Uroplakin 10, Those described in records AAYB281-YR281-9 are derived AAYB281-9 specific and general from the cords AAYB281-YR281-9 are derived AAYB281-9 specific and described in records AAYB281-YR281-9 are derived AAYB281-9 specific and described in records AAYB281-9 are derived arom in the line of from the cords AAYB281-YR281-9 are derived arom in the line of described in the cords AAYB281-YR281-9 are derived arom in the line of derived
  Tumor associated antigen peptides, especially derived from uroplakin, useful as vaccines to prevent or cure cancers including breast, bladder, prostate, pancreas, crary, thyroid, colon and stomach .
   from Lactadherin (BA-46). Those described in records AAY82847-Y82854 are derived from Mucin and these described in peocyds AAY82871-Y92982
   0; Gaps
  records YY82836 AAV82839 are derived from prostate acid phosphotase (PAP). Those described in records AAY82840-Y82846 are derived
  Carmon L., Tirosh B, Bar-haim E, Paz A, Fridkin M;
  are derived from Teratocarcinoma derived growth factor (CRIPTO-1).
   teratocarcinoma derived growth factor; PSA; PSMA; PAP; CRIPTO-1
   Those described in
   Major Historompatibility Complex; uroplakin;
prostate specific antiqen; prostate specific membrane antigen;
prostate acid phosphatase; mucin; lactadherin;
                        Function associated antique peptide; TAA; cancer; carcinoma; treatment; prevention; ence; anti-function decisionses; breast; bladder; prostato; pancreas; ovary; thyroid; colon; stomach; carcinoma; MHC Class I; HLA-A2; human;
  Score 37, 5B 21, Length 9;
Pred. No. 6.4e+05;
1; Mismatches 1; Indels
   prostate specific membrane antigen (PSMA).
  ABB62713 standard; Protein; 1284 AA.
  Claim 17; Page 100; 113pp; English.
   (BIOT-) BIO-TECHNOLOGY GEN CORP.
  (YEDA ) YEDA RES & DEV CO LTD.
   82.28,
   981L-0125608.
   99W0-11.00417
  from Lactadherin (BA-46).
  Guery Match
Rest Local Similarity 77.0.
7: Conservative
   WPI; 2000-205463/18.
  1 NLFETPILA 9
  1 nitetpvea 9
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  W0200006723-A1.
  Homo sapiens.
  Eisenbach L,
  (49-1111 - 1444)
  30-JUL-1998;
   10-FEB-2000.
   Sequence
  ABB62714;
   АВВ62713
  RESHA
ŝ
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The invention relates to an isolated nucloic acid detection reagent capable of detecting 1000 or more genes from Prosophila. The invention is
   the sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ttp.wipo.int/pub/published_pet_sequences.
  New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elumidating cell signalling and cell-cell
  useful in developmental biology and in elucidating cell signalling and
   77.8%; Score 25; DB 22; Length 1284;
66.7%; Pred. No. 2.46°2;
tive 2; Mismatches 1; Indels 0; Gaps
   cell cell interactions in higher cukaryotes for the development of inserticides, therapeuties and pharmaceutical armas. The instrition discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840 ABL30515) and the encoded proteins
  Drosophila, developmental biology, cell signalling, insecticide;
   Disclosure, SEQ ID NO 14321, 21pp · Sequence Listing, English.
  Brosophila melanoqaster polypeptide SEQ 10 No 14931.
   Urea amidolyase: URL; yeast; recombinant plasmid.
  Li PWD, Myers EW;
   AAR42839 standard; Protein; 1835 AA.
  23-MAR-2000; 2000US-191637P.
   11-JUL-2000; 2000US-0614150.
   23-MAR-2001; 2001WO-US09231.
  Query Match
Pest Local Similarity ft.e.e.
Them 6; Conservative
             26-MAR-2002 (lirst entry)
  10-MAY-1994 (first entry)
   Saccharomyces cerevisiae
  Prosophila melanogaster
  Venter JC, Adams M,
   ecquences (ABL01840 A
(ABB57737-ABB72072).
  WPI: 2001-555860/75.
  (PEKE ) PE CORP NY.
  1284 AA;
  |:|| ||:|
|154 nvfevpita 162
   1 NLFETPILA 9
  N-PSDB; ABLÜÉB1É
   Urca amidolyase.
  pharmaceutical.
   W0200171042-A2.
   interactions -
  JP05244959-A.
  24-SEP-1993.
   27-SEP-2001
   | cell
  document
  AAR42839;
  AAR42839
   RESULT
0.7
   ď
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AAB23072
  Vulnerary; antiportatic; antiparkinsonian; noottopic; neuroprotective; or informatically antiparkinsonian; noottopic; neuroprotective; or informatically incurportective; or informatically incurportective; antipartico; antipart
   This sequence represents a protein which has urea amidolyase (UKL) and is derived from yeast. The DNA conseing this pritein ray because within a recombinant plasmid for the production of highly
   Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
   S. Cal 3
  DNA having the genetic information of urea amidolyase originated
   from Saccharomyces yeast out be used to prepare high parity urea amidolyase by culturing the transformant comprising the DNA
  77.8%: Score 35; DB 14; Length 1835;
100 0%: Pred. No. ( 50.02;
100 0%: Mismatches 0, Indils
   Human ORFX ORF1309 polypeptide sequence SEQ 1D NO.2618.
  Claim 2, Page 10-17, 17pp, Japanese.
  AAB41545 standard; Protein; 171 AA.
  77.00.
100.0*; Pre-
               92JP-0084531
  31-МАК-2000, 25000м0-и50м621
  99US-0127607
   99IIS-0127636
   05-APP-1999; 99US-0127728
30-MAP-2000; 2000HS-0540763
  927P 0084541
  08-FEB-2001 (first entry)
   7; Consermation
  thrombosis; contraceptive
  (CURA-) CURAGEN CORP.
   WPI; 1943-338925/43
  Query Match
Best Local Similarity
   Sequence 1835 AA;
  (TOYM ) TOYOBO KK.
  1418 tetpila 1424
  N-PSDB; AAQ49460.
   3 PETPILA 9
  WO200058473-A2.
               05-MAR-1992;
  31-MAR-1999;
  05-MAP-1992;
   02-APR-1999;
   05-APP-1999;
   05-0CT-2000
   AAB41545;
  pure URL.
   5
   Matches
  AAB41545
   RESULT
```

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AMILY AMONTATOR CHOOSE the proteins given in AABGURT to AABGRA.

Which represent the human OREX open reading frames 1 to 816. The OREX sequences have activities such as collection, hepatitic for the OREX sequences have activities such as collection incurrently antiportal anticonvolution. Incurrently immunosuppressant; anticonvolution antiarthritic; immunosuppressant; anticonvolution incurrently anticonvolution and anticonvolution. On the immunosuppressant; anticonvolution and antianeous of anticonvolution and antianeous. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an OREX-associated disorder. The nucleic acides can be used for express or or preventing or treat cancers, on uncleic acides can be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, and the proteins and nucleic acides may be used to treat cancers, proliferative disorders, neurodegenerative disorders, sylendicing any anticonvolution and continued anaemia, benefit thrombosis; and contraceptive.
  immune disolder, autoimmune disease, transplant rejection, allergy, ADDS, infoction, informatory disorder, arthritis, heamelopoicatic disorder; skin disorder, cardiovascular disorder, atherosclerosis, rectenosis, neurological disease, Alzheimer's disease, trauma; wounding; espinal coord injury, skeletal disorder, eyostatic; immunosuppressive; auti-HIV; anti-inflammatory, anti-arthritic; anti-arteriosclerotic; neuropropter; vulnegary; anti-alleratic; autimicrobial; cardiant;
  SECX protein, human, secreted, membrane-associated; cancer;
proliferation requlator; differentiation regulator; non-malignant tumour;
  Caps
   Movel macleic acids and pertides derived from open reading frame X, useful for treating e.g. cancers, prollierative disorders,
  75.6%; Score 34; DB 21; Length 171; 66.7%; Pred. No. 44; tive 2; Mismatches 1; indels
   neurodegenerative disorders and cardiovascular disease
  Human putative mitochondrial protein, SECM 1981339.
   Claim 11; Page 1863-1864; 5507pp; English.
  AAB23032 standard; Protein; 196 AA.
   dermatelogical, yene therapy.
  09-MAR-2000; 2000WO-USU6280.
  (first entry)
   Best Local Similarity 66.7
Matches 6, Consernative
Shimkets RA, Leach M;
   2000 602362,/57.
  Sequence 171 AA;
   1: |||||:
27 uimetpils 35
  N PSDB; AAC75754.
  1 NLFETPILA 9
  WC200053742 A2.
  Homo sapiens.
   16-JAN-2001
   14-SEP-2000.
  AAB23032;
  Query Match
   Matches
  RESULT 10
```

```
Sequences AAB23825 B23048 represent human SECX proteins. The SECX proteins of the invertion are either serrented or rembrane associated proteins and act as regulator of cellular proliferation and differentiation. SECX proteins on nucleotides are useful for diagnosing the presence of, or predisposition to, a disease associated with altered several softs proteins and nucleotides. The SECX proteins are also useful to serien compounds that modulate SECX activity or expression. The interaction of a SECX protein with other cellular proteins may be useful to modulate the activity of a partner protein cellular proliferation, cellular differentiation and cell survival. SECX nucleotides are useful for the recombinant expression of SECX gene. They may also be used to modulate sizex expression of SECX gene. They may also be used to modulate sizex expression for using antisense oignomicientes). SECX nucleotides of the result of the sections in the SECX gene. They may also be used to modulate sizex expression for using antisense oignomicientes or type in a biological sample, and in forensic biology. SECX primers or the procession can be resulted to the presence of SECX primers or the procession can be resulted to the presence of SECX primers or the procession can be resulted to the presence of SECX primers or the procession can be resulted to the presence of SECX primers or the procession can be resulted to the presence of SECX primers or the procession can be considered to the procession of the presence of SECX primers or the procession can be considered to the procession of the presence of SECX primers or the procession can be considered to the procession of the procession can be considered to the procession of the process
   Ö
  screening tissue cultures for contamination. Discases that may be treated or prevented using SECX proteins or aucleotides include cancer (e.g.,
  colorectal carcinoma, prostate cancer), benign tumeors, immune disorders (including autoimmune diseases, transplant rejection, allergies, AIDS), infections, inflammatory disorders, arthritis, haematopoietic disorders,
   SAPHO syndrome, synovitis, aene, pastulosis, hypertosis, osteomyelitis; uveitis, endepthalmitis, boac, joint, central nervous system, ELISA, intlammatory lesion, acne vulgatis, enzyme linked immicosorbent assay; dermatological; osteopathic; neuroprotectant.
  skin disorders, cardiovascular disorders, atheroaclerosis, restenosis, neurological diseases (e.g., Alzheimer's disease), Franca (e.g., surgical or traumatic weards, spinal cord injury), and skeletal
   0; Gaps
  polynucleotides useful for diagnosis, prevention and treatment of
pathological states such as cancer, immune, cardiovascular and
   Novel human membrane associated or secreted polypeptides and
  75.6%; Score 34; DB 21; Length 196; 75.0%; Pred. No. 51;
  1; Indels
  Propionibacterium acnes immunogenic protein #5035.
  Mismatches
   AAU44139 standard; Protein; 306 AA.
  Claim 1; Fig 4; 151pp; English.
                               990S-0123667
  08-MAR-2000; 2000US-0123667
  27-FEB-2002 (first entry)
  6; Conservative
  neurological disorders
   Propionibacterium armes
  (CURA-) CURAGEN CORE.
   WPI; 2000-594318/56
  Best Local Similarity
   196 AA;
  N-PSDB; AAA93619.
  1 NLFETPIL 8
                        09-MAR-1999;
  Shimkets RA;
   disorders.
   Sednence
  AAU44139;
  Query Match
   Matches
  AAU44139
   ŝ
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polypeptides. The proteins and their associated bnA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by E. acnes. The disorders include SAPHO syndrome (syndritis, acne, tustilesis, theperiosis and esteemychis), uveitis and endopthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the influencatory lesions associated with ache vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the preteins of the invention
  Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
   and determining the amount of bound protein in the sample. The polypoptides may be used as untiaons in the production of antibodies specific for P aches proteins. These antibodies can be used to downrequiate expression and activity of P. aches polypoptides and therefore treat P. aches intections. The antibodies may also be used as diagnostic agents for determining P. aches presence, for example, by energy of liked immunoscreent assay (BLISA).

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO.
  ABCI, antilipemic, cholesterol, inhibitor, low density lipoprofein; DDL
   0; Caps
   vaccinating against and diagnosing infections, especially useful for
treating ache vulgaris
   Propionibacterium acnes polypeptides and nucleic acids useful ton
  ABC1 protein external domain TM5 TM6 fragment (residues 795 820).
   75.6%, Score 34; DB 22; Length 306; 66.7%; Fred. No. 82;
   Wang SS, Bhatia A:
   1; indels
   Mitcham JL, Wand St
, Jen S, Carter D;
   at ftp.wipo.int/pub/published_pct_sequences.
   Pred. No. 82;
2; Mismatches
   Claim 3; SEQ 1D No 5334; 1069pp; English.
  AAB62694 standard; peptide; 26 AA.
   02-JUN-2000; 2000US-208841P.
07-JUL-2000; 2000US-216747P.
   ZU-APR-ZUG1; ZÜÖIWO-USIZ§65.
   21-APP-2000; 200005-199047P.
   maisonneuve J, Zhang Y,
  06-AUG-2001 (tirst entry)
   6; Conservative
   Persing DH,
   WPI; 2001-616774/71.
   (CORI-) CORIXA CORP.
   Sequence 306 AA;
   Local Similarity
   40 nimetpils 48
   N-PSDB; AAS59521.
   1 NLFETPILA 9
W0200181581-A2.
  Homo sapiens.
  C1-NOV-2001.
   Skeiky YAW,
  AAB62694;
   Query Match
   Matches
  AAB62694
   Best
   RESULT
    ó
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WO200132184-A2.

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ABB69663;
  ABB69663
  RESULT
   In the gut that comprises administration of an inhibitor of an Auch pretein The method is useful for lowering levels of LEL (low density lipoprotein) chelesteral by reducing the activity of ABC protein in the intestinal cells and the abendance of the ABC protein in the individual by inhibiting the activity of the protein, identifying drups that can blower serum choisererol and LDL levels comprises assaying the drup to rest if it one bind to an APCI protein; testing LBL choisererol lowering agents, and for modulation of ABCI biological activity. Sequences ABB62522-37 represent predicted external domain of ABCI protein.
  SAPHO syndromic; synovitis, agne; pustulosis, hypertools, osteomyelitis; uveitis; end-phthalentis; hone; joint, central nervous system; ELISA; inflammatory lesion; agne vulgaris; encyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
  The invention relates to a new method for inhibiting cholesterol uptake
   New method for inhibiting cholesterol uptake in the gut comprises administration of an inhibitor of an ARC1 protein .
   Cook M, Gray Keller MF, Hayden MR, Finstone S;
   71.1%; Score 32; DB 22; Longth 26; 71.4%; Pred. No. 15; U. C. C. Missatthes 0, Indels
  L, Wang SS, Bhatia A;
Caiter D;
  Propionibacterium acnes immunogenic protein #7384.
   Skeiky YAW, Fersing DH, Mitcham JL,
  Jen S,
   (WISC ) WISCONSIN ALUMNI RES FOUND.
   AAU46488 standard; Protein; 302 AA
   Disclosure, Page 9; 41pp; English.
   20-APR-2001; 2001WO-US12865.
   21-APR-2000; 2000US-199047P.
   99US-0162803.
   JUL-2000, 2000US-208841P.
JUL-2000, 2000US-216747F.
                                 01-NOV-2000; 2000MO-NS (0104
   30 JUN-2000; 2000TS-0215564
  Zhang Y,
  (first entry)
   Ouery Match
Best Local Similarity 71.4
Matches 5: Conservative
   Propionibacterium acnes.
   (CORI-) CORIXA CORP.
   WPI; 2001-335779/35
  L'maisonneuve J,
   Brooks-Wilson A;
   14 nlfespv 20
  W0200181581-A2.
   1 NLFETPI 7
   01-NOV-1999;
  27-FEB-2002
 10-MAY-2001
   01-NOV-2001
   Sednence
   Attic AD,
  AAU46488;
  RESULT 13
   AAU46488
```

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polypoptides. The proteins and their associated DNA sequences are used in the freahment, presention and diagnesss of aedical conditions caused by P. across. The disorders include SAPHO synchrome (synovitis, acros, pustulosis, hypertosis and osteomyelitis), uvoitis and cudophthalmitis. P. across is also involved in infections of boxe. Joints and the central nervous system, boxever it is particularly involved in the inflammatory lesions associated with acre vulgatis. A method for detecting the presence or absence of P. across in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention
   Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunoqenic
  Note. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fip.wipo.int/pub/published_pct_sequences.
  and determining the amount of bound protein in the sample. The polypeptides may be used us an intervalent of authories specific for E. across proteins. These antibodies can be used to discretific for E. across proteins. These antibodies can be used to discretific for E. across proteins. The antibodies may also be used adjanuatic expression and attifity of E. across projectifies and disances intervalent by across prosence, for example, by engage inked immuniscrbent assay (BLISA).
  vaccinating against and diagnosing intections, especially useful for
treating acme vulgaris -
   Propionibacterium acnes polypeptides and nucleic acids useful for
   Promorbila, developmental bickey, cell sipalling, inserticides
  0
  71.1%; score 32; nm 22; Longth 302; 77.1%; Pred. %. 2<-92; Live 0; Mismatches 2; Indels
  Drosophila melanogaster polypeptide SEU 1D NO 35781
  Example 1; SEQ ID No 7683; 1069pp; English.
   Li PWD, Myers EW;
  ARB69663 standard; Protein; 343 AA.
  23-MAR-2001; 2001WO-US09231.
   23-MAR-2000; 2000US-191637P.
   26-MAR-2002 (first entry)
   Query Match
Bost Lwul Similarit, 77.87
Matches 7, Conservative
   Drosophila melanogaster.
   Venter JC, Adams M,
   WFI; ZUOI-с5с86U/75.
N-PSDB; ABL13766.
2001-616774/71.
   (PEKE ) FE CORE NY
   Sequence 302 AA;
  176 nlfetqtla 184
  N-PSDB; AASS9532.
   I NI.FETPII.A 9
  WO200171042-A2.
  pharmaceutical.
   27-SEP-2001.
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invention also relates to a process for preparing clarified sphingans

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   The invertor relates to an isolated socketor reid detection reagent
emphate of detecting 1000 or more genes from broophila. The invention is
useful in developmental biology and in elumidating real signalling and
cell-cell interactions in higher eukaryotes for the development of
  Polyhydroxybut, rate synthase, PHB, splingun, food product; dessert qel;
Jelly; Jam: beverage; dairy product; gelling agent; rheological modifier;
   The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at Itp.wipo.int/pub/published_pct_sequences.
New isolated nucleic acid detection reagent for detecting 1666 or more genes from Drosephila and for elucidating edl signalling and cell cell
   Meissner D;
   Saps
   insecticides, therapeuties and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
   <:
   bischesure, SEQ ID NO 35781, 21pp + Sequence Listing, English.
  Acinetobacter sp. RA3849 polyhydroxybutyrate (PBB) synthase.
   Length 333;
   71.1%; Score 32; DB 22; Length 33
85.7%; Pred. No. 2.2c+02;
Live 1: Mismatches 0, Indels
   Schneider JC,
  sequences (ABL01840-ABL16175) and the encoded proteins
  Patel YN,
   AAE10893 standard; Protein; 590 AA.
   Harding N,
  02-MAR 2001; 2001WO-US07010.
   02-MAR-2000; 2000US-186433P.
  (first entry)
   Conservative
  Acinetobacter sp. RA3849.
  (KELC ) OP KELCO US INC.
  Bezanson R;
  industrial application.
   WP1; 2001-589870/66.
   (ABB57737-ABB72072).
   Best Local Similarity
  Burke E,
  3.53 AA;
   WO200164897-A2.
  2 LPETPIL 8
   interactions -
  18-DEC-2001
  07-SEP-2001,
  Morrison N,
  Sequence
   AAE10893;
   Query Match
   BOWET S,
   RESULT 15
   Matches
  AAE10893
```

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have a mutation in the gene encoding a protein involved in internal storage polymer polyhydroxybutyrate (PHB) synthesis that allows the mutant strains to produce PHB delicient sphindans. Sphindans are capsular polysaccharides secreted by bacteria of the genus Sphingomonas. The

The invention relates to mutant strains of Sphingomonas species which

Example 1; Page 84-86; 98pp; English.

polyhydroxybatyrate synthesis

Mutant strain of Sphindomonas species useful for producing sphingan, has a mutation in the gene encoding a protein involved in

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:
(
   as theological modifier in industrial applications such as oil field drilling and cementitions systems. The present sequence is Administrated by Strain FA3849 polyhydraxykutyrate (FHR) synthase which is used for the generation of Sphingomonas elodea phaC tragment, phaC DNA
                    which are useful as gelling agents in a variety of tood applications for ingroving the tasks, texture, stability and appearance of food products such as dessert gels, contectionery jellies, james, dairy products, beverages, films and coatings. The sphingans are also useful
   0; Gaps
  fragment encodes polyhydroxybutyrato (PBB) synthase protein.
  Score 32; DB 22; Length 590;
Pred. No. 4.1e+02;
3; Mismatches 0; Indels
   Scarch completed: September 5, 2002, 15,26:30 Job time: 370 sec
   71.18;
62.58;
   Best Local Similarity 62.5 Matches 5; Conservative
  Sequence 590 AA;
  239 nvyqtpil 246
  1 NLFETPIL 8
   Query Match
8888888888
```

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
```

OM protein · protein search, using sw model

September 5, 2002, 15:20:50 ; Scarch time 69.78 Seconds (without alignments) 12:393 Million cell updates/sec Run on:

US-09-744-804-37

1 NLFETPILA 9 BLOSUM62 Scoring table: Sequence:

Perfect scare.

283138 seqs, 96089334 residues Gapop 10 0 , Gapext 0.5 Searched: Total number of bits satisfying chosen parameters:

Maximum DB seq length: 2000000000 Minimum DB seq length: 0

Listing first 45 summaries Maximum Match 100% Post-processing, Minimum Match 0%

1: pirl: \* 2: pir2: \* 3: pir3: \* 4: pir4: \* PIR\_71:\* Database

Pred. No. is the number of results predicted by chance to lave a score greater than or equal to the score of the result being printed, and is derived by analysis of the retal score distribution.

SUMMARIES

|           |          | ø          |                |           |        |                    |
|-----------|----------|------------|----------------|-----------|--------|--------------------|
| Result    |          | Query      |                |           | :      |                    |
| . CN      | score    | Match      | Length         | 90        | 1D     | Description        |
| 1         | 4.5      | 100.0      | 218            | CI        | A47285 | milk fat globule p |
| 7         | 36       | 80.0       | 612            | C4        | T11830 | deh,               |
| 3         | 36       | 80.0       | 669            | 7         | T48466 |                    |
| 4         | 36       | ó          | 705            | △         | T48464 |                    |
| Ŋ         | 35       |            | 404            | ~         | T11743 | pP47 protein - piq |
| 9         | 35       |            | 1283           | ~         | T13799 | xin IV - 1         |
| 7         | 35       | 9.77.      | 1835           | e i       | 546082 | urea carboxylase ( |
| 80        | 34       | Ġ.         | 142            | C         | A12479 | hypothetical prote |
| S         | 34       | 75.6       | 250            | Ca        | A70554 | probable dehydroge |
| 10        | 3:4      |            | ~1°            | c.        | A12848 | ribuse phosphate p |
| 11        | 34       |            |                | C1        | 497625 | prsa (AE206059) (i |
| 12        | 33       | <u>.</u> : |                | C 3       | A11303 | dihydroorotase deh |
| 13        | 33       | 5.5        | 304            | ۲.        | AITETE | dibydrcoretase deh |
| 14        |          | <u>~</u>   | 363            | 7         | 137716 | actin-interacting  |
| 15        | 33       | ٣,         | 401            | C 1       | 865138 | glycoprotein anti- |
| 16        | 33       | ۲.         | 457            | C .       | 874211 | PAS-6/7 protein pr |
| 17        | 33       | ش          | 464            | ~         | T16889 | hypothetical prote |
| 18        | 33       | ς.         | 535            | _         | S76953 | IJ.                |
| 19        | 33       | ٠,         | 572            | C)        | T32636 | _                  |
| ()<br>(1) | en<br>en | 73.3       | 658            | C 1       | T40107 | _                  |
| 5         | ar<br>ar | 73.3       | 694            | с.        | 123325 | hypothetical prote |
| C 3       | <u>;</u> | 71.1       | -4<br>-4<br>-4 | €1        | G71111 | hypothetical probe |
| 53        | S        |            | £.13           | <b>(3</b> | 383363 | hypothetical prote |
|           | C1<br>C0 |            | 208            | C 1       | B71031 | _                  |
| C1<br>U1  | CT.      |            | 212            | C 3       | - 1    | hypothetical prote |
| 92        | CI<br>Ci |            | 2555           | C a       | н83326 | probable short cha |
| 27        | CI<br>CI | 71.1       | 268            | C 1       | 597394 | undecaprenol kinas |
| C1        | Ç.       | <br><br>   | 568            | C 1       | AF2612 | baritazia resista  |
| 53        | 32       | 71.1       | 268            | C4        | AH3541 | bacitracin resista |

| melybdenum transpo | nicotinate phospho | nicotinate phospho | nicotinate phospho | probable tolylpoly | conserved hypothet | sodium dependent c | propable permease | hypotherical prote | induly displaying | 59K transcription | probable dihydroli | ichalita, and all disconnections | probable replicati | protein PS202.7 [i | hypothetical prote |
|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|-------------------|-------------------|--------------------|----------------------------------|--------------------|--------------------|--------------------|
| F87289             | D82725             | F83099             | E83040             | T50165             | F81706             | H83699             | AC0133            | S62484             | T41892            | WZBEF5            | H70786             | 183551                           | C84496             | 089473             | 864993             |
| c a                | CI                 | C1                 | 7                  | 7                  | C-1                | ~                  | C1                | C 3                | ۲٦                | _                 | ~                  | <b>(</b> )                       | C4                 | C 1                | C1                 |
| 278                | 194                | 86¥                | 868                | 417                | 425                | 439                | 494               | 00<br>00<br>00     | 530               | 532               | 553                | C.                               | 670                | 757                | 779                |
| -1.                | 71.1               | 71                 | 71.1               | 71.1               | 71.1               | 71.1               | 71.1              | 71.1               | 71.1              | 71.1              | 71.1               |                                  | 71.1               |                    | 71.1               |
| 32                 | €1<br>27           | C1<br>65           | 32                 | 3.2                | (T)                | 32                 | 77.5              | 32                 | 32                | 3.2               | 32                 | (4<br>(2)                        | 32                 | 35                 | 32                 |
|                    |                    |                    |                    |                    |                    |                    |                   |                    |                   |                   |                    |                                  |                    |                    |                    |

### ALIGNMENTS

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A47285
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milk fat. globule protein – human (tragment) C;Species: Homo sapiens (man) C;bute: 3: Dec-1993 #sequence\_tevision 3: Dec-1993 #text\_change 28-May-1999

Concession: A47285
Ellatocca D., Petersan, J.A., Urrea, F., Kuniyeshi, J., Ristrait, A.M., Ceriani, K.L. Cancer Res. 51, 4994-4998, 1991
Anticle A. M. F. V. 4994-4998, 1991
Anticle A. M. F. V. 4994-4998, 1991
Anticle Comber A47285
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Anticle Competence Comber A47285
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Anticle Competence Competence A47285
Anticle Competence

0; Gaps 100.0%; Score 45; DB 2; Length 218; 100.0%; Pred. No. 0.067; 0; Indels 0; Mismatches Ouery Match Best Local Similarity 100.v-5. Conservative

187 NLFETPILA 195 1 NLFETPILA 9 qq

T11830

NADH dehydrogenase (ubiquinone) (PC 1.6.5.3) chain 5 - Atlantic evi mitrehondrion

Cyspecies, mitachendries dadus morthus (Atlantic cod)
Cyspecies, mitachendries dadus morthus (Atlantic cod)
Cyspecies, mitachendries ascending for 19 1999 atoxit\_change 20 1900
Cyspecies, S. Bakke, I.
Mol. Marine Hiol. Riotechnol. 5, 204-214, 1996
A.Title. The codelete mitachendrial DNA sequence of Atlantic acd, Cadus markus. Relev.
A.Reference number, 21731. MUID.96414925
A.Recession: T11830
A.Recession: T11830
A.Recession: T1830
A.Recession: T1

C. Reymon Bar membrane associated respect to the electrical RAL, existed to people platter

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R.Baumgartner, S., Littleton, J.T.; Broadie, K.; Bhat, M.A.; Harbecke, R.; Lenqyel, J. Cell 87, 1059-1068, 1996
A.Title: A Drosophila neurexin is required for septate junction and blood-nerve barril A, Reference number. #17762, MUID.9713213
A, Recession: T18799
A, Status: preliminary; translated from CR/FMRI/DDBJ
  ArItle: Molecular cloning and characterization of P47, a movel toar sperm associated A;Reference number: 217325; MUID:98206817
A;Accession: T11743
  R:Ensslin, M.; Vogel, T.; Calvete, J.J.; Thole, H.H.; Schmidtke, J.; Matsudu, T.; Foe
Biol, Reprod. 58, 1057-1064, 1998
  A bescription and be involved in membrane remodeling and for tunoffer as a consequence
  A, bescription, is required for NSX in the formation of septate jonetion septa and int
   AlBesidues: 1.409 <ENS>
A. Chess references: PMRI Y11683, HTD q2652927; PTDN-CAAP2 09 1; PTD-q2652928
                    p947 protein - pig (fragment)
C)Species: Sus scrofa domestica (domestic pig)
C)Bate. 16 Jul 1999 #sequence_revision 16.Jul 1999 #text_change 21.Jul-2000
C)Acession: T11743
   A,Residues. (11283 :BAU).
A,Cress-references. EMBL.X86685: WIL:91518220; PIDN:CAA60783.1; PiD:91518221
  C.Bute. 13 Aug 1999 Asequence_resister.13 Aug-1999 #fest_change 17 Nos 2000
C.Accession: T13799
  C.Species: Savcharomyces cerevisiae
C:Date: 26 Aug 1994 #Sequence_revision 05 Sep 1994 #teat_shampe 11 Jan 2002
C:Accession: S46082; S46081; S46080; S31341; S34930; S34043
  urea carbexyluse (PC 6.3.4.£) yeust (Sarcharomyees rerevisioe)
NyAlternate names: protein YBR1449; protein YBR208c; urea amidolyase
   Query Match
Best Local Similarity 66.78, Pred. No. 69;
Matches 6, Conservative 2, Mismatches 1, Indels
   Score 45: DB 2: Length 409;
Pred. No. 18:
1: Mismatches 1: Indels
   C.Superfamily: unassigned EGF related proteins, EGF komolony F.f. 40/Pemain. EGF homelogy 79GFs
   submitted to the Protein Sequence Database, August 1994
  A; Status: preliminary; translated from CB/EMBL/DDBJ
   neurexin IV - fruit fly (Drosophila melanoquster)
  Ajfross references FlyBase-FBgn0013997
  77.8%;
75.0%;
  Query Match
Best Local Similarity 75.00
6. Conservative
   A; Experimental source: testis
   A; Reference number: 845734
  153 NVFEVPIIA 161
   1:1111 1
378 NMPETPFL 385
   1 NLFETPILA 9
   A: Molecule type: mRNA
  A; Molecule type: mRNA
   1 NLFETPIL 8
  A; Accession: S46082
  Penetics:
   A;Gene: nrx
  C:Function:
  9
   7
   R;Rieger,
   RESULT
  846082
  qq
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  ΟŽ
  δŏ
   Cyarcession: T48466
KSBevan, M.; Terryn, N.; Ardiles, W.; Buysshaert, C.; Dasseville, B.; De Clerck, R.; De ewes, B.W.; F.B.; S.; Cert, F.; Mayer, F.F.;
Schmer, B.W.; F.B.; S.; Cert, F.; Mayer, F.F.;
Schmer, B.W.; F.B.; S.; Cert, F.; Mayer, F.F.;
Asherical to the Protein Sequence Database, April 2000
A.Reterence number: 72449;
A.Aeression: T48466
  N ; Ardiles, W.; Buysshaert, C ; Basseville, P ; De Clerck, P ; De
  0
  ö
  hypothetical protein TLB3.60 - Arabidopsis thaliana
C:Species. Arabidopsis thaliana (mouse war cress)
C:Date: 20 Apr.2000 #sexponenteration 20 Apr.2000 #text_change 28 'ul 2000
  hyperberical protein TIE4.40 - Arabidopsis thallana
C.Species: Arabidopsis Unitana (mouse ear cress)
C.Date: 20-Apr-2060 #seepernollevisies 26 Apr. 1963 #rext_change 10 Apr. 1963
  Gaps
   Gaps
  0
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.
   C;Superfamily: Arabidopsis thaliana hypothetical protein T1E3.60
   80.0%; Seare 36; PH 2; Longth 705; 75.0%; Pred. No. 21; Live 2; Mismatches 0, Indels
   Ouery Match
Best Local Similarity 75.0%; Pred. No. 20;
Matches C. Chestration 2, Mishalthes C. Indels
  80.0%; Score 36; DB 2; Length 612;
   0; Indels
  A; Experimental source: cultivar Columbia; BAC clone T1E3
   A; Experimental source: cultivar Columbia; BAC clone T1E3
   C,Accession: T48464
E:Bevan, M.: Terryn, N.: Ardlles, W.: Buysshaer, C.: F
cwes, H.W.; Rudd, S.: Lencke, K.: Mayer, K.E.X.
Assubmitted to the Trotein Sequence Database, April 2000
A;Reterence number: Z24491
  A; Int.rons - 72 (1 - 226/1) 287 (1) 307/1 - 322 (1) 465/3
                       Pred. No. 18;
2; Mismatches
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   A;Cross-references: EMBL:AL162972
   A)Cross-references: EMBL:AL162972
                          75.0%;
   6, Conservative
   6; Conservative
Onery Match
Best Local Similarity
  Query Match
Best Local Similarity
  A; Residues: 1-669 <BEV>
   A:Residues: 1 705 <BEV>
   479 NLFKTPVL 486
   112 NLYETPLL 119
   ||:|||:|
| 99 | NLYETPLL || 106
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  A;Status: preliminary
  1 NLFETPIL 8
  1 NLFETPIL 8
   1 MLFETPIL 8
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   A; Molecule type: DNA
  A; Accession: T48464
   A;Map position: 5
A;Introns: 59:1 2:
A;Note: TIE3:40
   A; Map position: 5
   A; Note: T1E3.60
  C; Geneties:
  4
  Matches
  Matches
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  RESULT.
  T48464
   Q.
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C.Spanius. Mysokaterium imberculosis
C.Sato. 17-Jul 1998 #sequence_revision 17 Jul 1998 #text_chunge C? Pur.2000
C.Accession. A70554
E.Coix. S.I., Eussch. E.: Parkhill. J.: Garnier. T.: Churcher. C.: Harris. D.: Gordon
F.Coix. S.I., Enseth. E.: Parkhill. J.: Garnier. T.: Churcher. C.: Harris. D.: Gordon
F.Coix. S.I. Davies. E.: Portin, K.: Petwerll, T.: Gentles, G.: Humlin, M.: Holroyd.
Pajandream. M.A.: Ecopors. J.: Futter, S.: Seeger, R.: Skelton, S.: Squates, S.
Nature 393, 537-544, 1998
   A)Authors, Squies, E., Suiston, J.E., Taylor, K., Whitehead, S., Barrell, B.G. A, Title Farifield in Finley of Myrelarical in therein six from Farifield and A. Reference number. A70509, MOID, 98295987
A)Accession. A70554
A)Accession preliminary, nucleic acid sequence not shown translation not shown A)Molecule type: DNA
A)Molecule type: DNA
A)Residuce: 1.250 <COL>
   Tibose-phosphate pyrophosphokinase [imported] - Agrobacterium tumefaciens (strain CS8 C;Species: Agrobacterium tumefaciens C;Species: Agrobacterium tumefaciens C;Latt. Juni 2002 #sequence_revision 11-Jan-2002 #sext_change 91 Feb-2002 (Screesion: AT2848 #sequence_revision 11-Jan-2002 #sext_change 91 Feb-2002 R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woodrage, G.; Glillet, W.; Grant, G.; Grentliner, D.; Puryamin, T.; Levy, R.; Li, M.; McCB science 294, 2317 2323, 2001
Nakaraki, N., Shimpo, S., Sugimete, M., Takarawa, M., Yanada, M.: Yasuda, M.; Tabata DNA Rex. 8, 265-213, 2001
A,TILL: Complete Schools Sequence of the Filamentons Nitroges fixing Syanabacterium Astronomer namber: Astronomer Number 155985; PMID:11759840
   A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kam
   A,Cross-references: GB:255584; GB:AL123456; NID:93261774; FIEN:CAR99032.1; PID:421171
   ster, E.W.
A.itle: The Compass of the Autural Contile Engineer Agrebacterium tumefaciens C58.
A.Reference number: AR2577; PMID:11743193
A.Acceppien: AI2848
  C. Saper Country, athered deby Aregenase, short chain alvolot dehydrogenase homelony
P. C. 1877, Smith about their absolut deby dregenase benefoly. GAMB.
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   A)Cross-references: GB:HA000020; PIDN:BAB78101.1; PID:q17135555; GSPDH:GN00180
A,Experimental source: Strain FCC 7120
C;Genetics:
  sdr:
   0; Gaps
  Ö
  probable dehydrogenase - Mycobacterium tuberculosis (strain H37FV)
  75.6%; Score 34; DB 2; Length 142; 75.0%; Pred. No. 8.8;
  75.6%; Soure 24; DB 2; Length 250;
75.0%; Pred. No. 17;
tive 2; Mismatches 0; Indels
  1, indeis
  i, Mishatches
  A.Experimental source: strain H37Ev
C,Genetics:
  6, Constivative
   Johnsonvallive
   Query Match
Best Local Similarity
   A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-142 <KUR>
  Querr Match
Bust Loval Şimilarit;
  ||:||:||
| 188 LFDTPLLA 195
   2 LFETPILA 9
   1 NLFETPIL 8
   A; Genome: plasmid
   ٠.
   A;Gene: alr7017
  A; Gene. Rv1144
  Matches
   Matches
   RESULT
A12848
   q
   CiAccession: A12479
P:Kaneko, T.: Nakamura, Y.: Welk, G.P.: Kuritz, T.: Sasamoto, S.: Watanabe, A.: Iriquehil
  A;Tile: Yeast Sequencing Reports, A 12.8 Nb sequent, on the right aim of chromosome II A;Reference number: $34025; MTIP: 9327417
A;Accession: $34930
   hypothetical protoin alr7017 (imported) - Amabaena sp. (strain PCC 7120) plasmid pCC7122
  A.Molecule type: DNA
A.Residucs: 1-95,70,707-258,707-258,707-259-458,707-469-829,787,831-1394,787,1396-1835
A.Cross-references FMRI MG4926; NID.3173121, PIDN.AAC41643.1, PID:3173122
E.Bussarreau, P.: Mailet, E.: Gaillan, E.: Jucquet, M.
   CiSpecies: Anabaena sp.
A:Note: Anabaena sp. (Strain PCC 7120) is a synonym of Nostoe sp. strain PCC 7120 C:Date: 14-Dec 2001 #sequence_textion 14-Dec 2001 #text_change 11 Jan 2002
   AbCross-references: EMBL-221487; NIB-3311665, PIBN-GAA79695 ), PIB,3311684
AbExperimental source: strain S2880
  O; Gaps
   DNA Soq. 2, 19-32, 1991
AJTitle: The urea amidolyase (CUE),2) gene of Saccharomycus curerisiae.
A/Reference number: S31341; MOID:92159240
A/Accession: S41341
  77.8%; Score 35; DB 2; Length 1835; 100.0%; Pred. No. 1c.02; ivo 0; Mismatches 0; Indels
   F;1798/Rinding site: bictin (Lys) (covalent) #status predicted
   R.Feldmann, H.: Mannhaupt, G.; Schwarzlose, C.; Vetter, I. submitted to the Profesin Sequence Database, August 1994
  submitted to the Protein Sequence Database, August 1994
   A;Molecule type: DNA
A;Residues: 873-1835 <FEL>
A;Cross-references: BBB::Z36077; MIPS:YBR208c
A;Experimental source: strain S288C
R;Bussereau, F; Demolis, N.; Jacquet, M.; Mallet, L.
   A:Cross-references: SGD:SAMAN12; MIPS:YBR208c
                           A)Residues: 1-893 /PIE>
A)Cross-references: EMBL.226077, MIPS:YBB208c
A)Experimental source: strain $2890
   A.Molecule type: DNA
A.FrestLacs. 1487 1835 - BUS.
A.Cross-references: EMBL-34677; MIPS:YBR208c
A.Fxperimental source: strain 5298s.
  A; Status: translation not shown
   RiGenbauffe, F.S.; Cooper, T.G.
DNA Seq. 2, 19-32, 1991
   7; Conservative
   A;Molecule type: DNA
A;Pesidues: 1487 1835 FRE
   A; Reference number: S45927
  A; Reference number: $46054
  Best Local Similarity
Matches 7; Conserv
   A; Molecule type: DNA
  3 FETPILA 9
   A;Accession: S46081
  A;Accession: S46080
   A; Gene: SGD: DUR1, 2
  Query Match
  RESILLT
  AI2479
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A:Status: preliminary A: Molecule type: DNA

RESULT 11

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C, Superfamily. dihydrocrotate oxidase

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Gaps

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Cyaccession: Alloyous Alloyous Alloyous Alloyous Alloyous Alloyous Alloyous Law, Rates, E.; Buchieser, C.; Amend, A.; Baquero, E.; Bercho, P.; Blobero, B.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsiht, D.; Jones, L.M.; Karst, U. Science 294, M44-857, 2001
A.Authors: Kreft, J.; Kuhn, M.; Kunst, P.; Kurapkat, G.; Madueno, E.; Maifournam, A.; Ok, C.; Schlueter, T.; Simos, N.; Teierez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla A.Reference number: ABIO77; MUD:21537279; PMID:11679669
A.Ression: Allo75
A.Riatus, Preliminary
A.Molecule type: DNA
A.Residues. 1304-C2L*
A.Cress reference: GB-ALE92802; FIFN.CAC97177.1; FIB:414449; GSEPB-GNR0178
A.Experimental source: strain Clip11262
   dibydroorotase debydrogenase bomolog pyrD (imported) - Listeria innocua (strain Clipt
  actin-interacting protein bud6/Aip3p protein SPAC15E1.01 [imported] - fission yeast (
   Ajdross-references: EMEL:ALlu9/70; FIEN:CABS24z0.1; GSFEB:GN00066; SPDB:SPAC15E1.01
AjExperimental source: strain 972h-; cosmid e15E1
   C;Species. Schizosaccharomyces pombe
C;Date 15:Sep-2000 #seg.energrevision 15:Sep-2000 #fext_charge 15 Sep 2000
C,Accession: T37716
  C.Species: Listeria innocua
C.Date: 27 New 2001 #Sequence_revision 27 New 2001 #text_change 14 Dec.2001
  RiMurphy, L.: Harris, D.: Barrell, B.G.: Rajandream, M.A.: Lyne, M.H. sabmitted to the EMBL Eata Library, August 1999
A.Reference number. 221739
A.Accession. T37716
   Ouery Match 73.3%; Score 33; DB 2; Length 504; Best Local Similarity 85.7%; Pred. No. 34; Matches 6; Conservative 1; Mismatches 0; Indels
   73.3%; Score 33; DB 2; Length 363; 62.5%; Pred. No. 42;
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Pred. No. 34;
  0, Indels
  0: Indels
  A:Status: preliminary: translated from Ge/EMBL/DDBJ
  1; Mismatches
   Fred. No. 42;
3; Mismatches
  A, Cene. SPAC15A10.15, SFDB.SPAC15E1.01
   C; Superfamily: dihydroorotate exidase
                               73.3%,
   Post Local Similarity 85.7%
Matches 6: Conservative
   Bost Local Similarity 62.5%
Matches 5, Conservative
  1-363 <MUR>
  282 NIYETFIV 289
  1 NLFETPII, 8
   92 FETPLIA 98
   A, Molecule type: DNA
A; Residues: 1-363 <M
  C; Accession: AI1675
  3 FETPILA 9
   3 FETPILA 9
   A; Map position: 1
                                   Query Match
   Query Match
  A; Gene: pyrD
   C; Genetics:
  RESULT 14
   CP
  Widtherson, P., Franceul, E.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, J. Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Lussurget, O.; Entian, K.D.; Fsihi, H. D.; Jones, L.M.; Karst, J.
Science 294, 845-852, 2001
A;Authors: Krett, J., Kuhn, M. Kunst, F.; Keraphat, G.; Maduene, E.; Maiteuram, A.; Maharines: Krett, J., Kuhn, M.; Therebat, G.; Maduene, E.; Maiteuram, A.; Maharines: Outparadive genomics of Listeria species.
A;Title: Comparadive genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
   dibydrorotase dehydrogenase bemodog pyrD (imported) - Listeria memocytugenes (strain Ed
Cisperies: Listeria monocytoacnos
Cipato: 27-Nov 2001 msequenco_revision 27 Nov 2001 mtext_change 14-Dec-2001
Ciarcession: Altan
   C:Species: Agrobacterium fumefaciens
C:Date: 30 Sep 2001 #Sequence_revision 30 Sep 2801 #text_change 11.Jun.2002
C:Accession: 697625
R:Goodner, B.; Hinkle, G., Gattung, S.; Miller, N., Blanchard, M., Qurollo, B., Goldman, A.; Liu, P.; Wollom, C.; Allinger, M.; Doughty, D.; Scott, C., Laggas, C., Markelz, R. Science 294, 2323-2328, 2001
   A:Title: Genome Sequence of the Plant Pathogen and Pictochnology Agent Agrebacterium Lud
A:Reterence number: A97359; PMID:11743194
A:Aeression: G97625
   ċ
   A)Cross-references: GB:NC_003210; FIDN:CAC99911.1; FID:q16411287; GSPDB:GN00177
  A) Cross references: GB: AE007869; PTDN: AAKR7960.1; PID: 915157366; GSPDB: GN00169
C: Geneties:
                               A)Cross-references: GB:AE008668+ PIDM-AAL43207 1; PID-917740668); GSPPR-GNO0186
  prsa (AR006059) [imported] - Agrobacterium tumefaciens (strain C58, Cereon)
  Gaps
  Gaps
   ·.
   A:Map position: circular chromosome
C:Superfamily: ribose phosphate pyrophosphokinase catalytic chain
  C, Superfamily: ribose-phosphate pyrephosphokinase catalytic chain
   75.6%; Score 34; DB 2; Length 310; 77.8%; Pred, No. 22;
  75.6%; Score 34; DB 2; Length 318; 77.8%; Pred. No. 22; 21;vc 0; Mismatches 2; Indels
   2; Indels
   0; Mismatches
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  A, Experimental source: strain EGD-c-C, Genetics:
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  Query Match
Rost Local Similarity 77.89
Matches 7; Conservative
   Conservative
   Overy Match
Rest Local Similarity
7, Conserv
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A; Residues: 1:410 < KUR>
  141 NLFAAPILA 149
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A;Residues: 1-304 <GLA>
  149 NLFAAPILA 157
  I NLFETPILA 9
   1 NI.FETPILA 9
   A;Status: preliminary
  A; Accession: All303
  Ardene: AGR_C_4031
   Cyclenetics:
Ayclene: prsA
  A;Gene: pyrh
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RESULT 12

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A.Note, sequence extracted from NCBL backbone (NCBLE:131457)
(Superfamily, mix fait globale protein, discodin famina terminal homology, EGF homology
(Stepwards, 4)yooptotein
(Fil.32,Yoomale: FGF homology (fragment) -EGI:
(Fil.32,Yoomale: FGF homology (fragment) -EGI:
(Fil.32,Yoomale: FGF homology (Fragment) -EGI:
(Fil.32,Yoomale: GGF homology -FG2)
(Fil.32,Yoomale: GGF homology -EGI:
(Fil.32,Yoomale: GGF homology -EGI:
(Fil.32,Yoomale: GGF homology -EGI:
(Fil.32,Yoomale: GGF homology -EGI:
(Fil.33,Yoomale: GGF homology -EGI:
(Fil.34,Yoomale: GGF homology -EGI:
(Fil.34,Yoomale: GGF homology -EGI:
(Fil.35,Yoomale: GGF homology -EGI:
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  541.5
  ` ے
   Query Match 73.3%; Score 33; DB 2; Length 401; Best Local Similarity 66.7%; Pred. No. 48; Matches 6: Conservative 1; Missatches 2; Hobels
  Search completed: September 5, 2002, 15:28:51
  A,Reforence number: A48344, MIII)-93250576
A;Accession: 048394
A;Batus: preliminary
A;Molecule type: protein
A;Residues: 207-220 <MAT>
   A; Experimental source: milk
  |:|||| | 1
370 NIFETPFQA 378
   1 NLFETPILA 9
  Job time: 356 sec
RESULI
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GenCore version 4.5 Cepyright (c) 1993 - 2000 compugen 1.5d.

OM protein - protein search, using sw model

September 7, 2002, 15.31.40 , Search time 43 G. Accads (Without alignments) 10.252 Million cell sphates/sec Run :n.

US-09-744-804-37 45 1 NLFETPILA 9 Title: Perfect score: Sequence: BLOSUM62 Gapop 10 0 , Gapext 0.5 Scoring table:

105224 seqs, 38719550 residues Searched.

105224 Total number of hits satisfying chosen parameters:

Minimum DR seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08 Maximum Match 1008 Listing first 45 summaries

SwissProt\_40:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the soure of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

|                     |            | 32 गुवतमङ   |               |            | P32528 saccharomyc |            | vlostl czeporhażdi | P74745 synechocyst | 013735 schizosacch | _         | QOARAS Schilles not | _              | _          |            | P41233 mus musculu | ٠,         | metha      | 018404 drosophila |            |             | 191      | P21956 mas masculu | ofp/75 schoosacch |             |            | P55153 lactobacili |            | Q08385 rhodobacter | E25996 barillus su | 0259       | 384         | Q59072 met.handanan | P58595 ralstonia s |
|---------------------|------------|-------------|---------------|------------|--------------------|------------|--------------------|--------------------|--------------------|-----------|---------------------|----------------|------------|------------|--------------------|------------|------------|-------------------|------------|-------------|----------|--------------------|-------------------|-------------|------------|--------------------|------------|--------------------|--------------------|------------|-------------|---------------------|--------------------|
| QI                  | MFGM_HUMAN | NITSM_GADMO | MFGM_PIG      | NPX4_DROME |                    | MFGM_BOVIN | YSV5_CAREL         | SPKC_SYNY3         | FAT1_SCHPO         | BLM_MOUSE | YAD7_SCHPC          | ICPO_HSVER     | ODO2_MY@T9 | ABC1_HUMAR | ABC1_MOUSE         | LYST_HIMAN | Y528_METJA | HCD2_DROME        | BIOB_HAEIN | GHSP_PTG    | MFGM_PAT | MEGM_MOUSE         | SIN1_SCH!         | TIL70_HCMVA | YO33_SKEOO | DLTC_LACCA         | RSEA_HAEIN | MOPA_EHOCA         | PYF?_RACSU         | FM10_YEAST | YPPPA_CARFT | YG78_METTA          | EPF1_RALSO         |
| Length DB           | 387 1      | 213         | $\overline{}$ | 1284 1     | 1835 1             | 427 1      | 464 ]              | 53                 | 1385 1             | 1416 1    | 527 1               | 532 1          | 553 1      | 13261 1    | 2261 1             | 3801 1     | 98<br>1    | 255 1             | 333 1      | 366 1       | 427 1    | 463 1              | 665 1             |             | f.4 ]      | 81                 | 195 1      | 265                | 311 1              | 322 1      |             | 396                 | 418 1              |
| %<br>Query<br>Match |            |             | 77.8          | 77.8       | 77.8               | 73.3       | 73.3               | 73.3               | 73.3               | 73.3      | 71.1                | 71.1           | 71 1       | 71.1       | 71.1               | 71 1       | 9.89       | 6.89              | 6.89       | σ<br>«<br>« | 68.3     |                    | 68.3              | x.          |            | 66.7               | 66.7       |                    | L                  | œ.         | ٠.          | 66 7                | 66.7               |
| Score               | 45         | 36          | 35            | 32         | ሆ<br>ም-            | 33         | 33                 | 33                 | 33                 | 33        | 35                  | <del>ر</del> ۳ | 32         | 32         | 32                 | C.         | 31         | 31                | 31         | .3          | 31       | 31                 | e 4               | 3.1         | O c        | 30                 | 3.0        | 30                 | o<br>K             | c.         | J.          | 30                  | 30                 |
| Result<br>No        | 1          | ca o        | <b>*</b> 0 •  | 4          | LC:                | 9          | 7                  | œ                  | 6                  | 10        | 11                  | 12             | 13         | 14         | 15                 | 16         | 17         | 18                | 19         | 20          | 21       | C1                 | ci.               | 24          | C1<br>ru   | 56                 | 27         | 58                 | ر.<br>(1           | 30         | 31          | e<br>E              | 33                 |

| P46153 rattus norv | Q61169 mus musculu | Ç92908 homo sapien | v83i72 treponema p | 028164 archaeoglob | Q10898 myrobacteri | P40492 saccharomyc | Fried Superior |          | P33871 mariola vir |            | _          |
|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|----------------|----------|--------------------|------------|------------|
| GAT6_RAT           | GAT6_MOUSE         | GATE_HUMAN         | Yise_trepa         | GATB_ARCFU         | Y104_MYCTH         | YIJ7_YEAST         | VET LVALLE     | VP1VACCE | VF12_VAEV          | YD84_HUMAN | PALY BROFI |
|                    |                    | r 1                | ,                  |                    | <b>,_</b> ,        | 1                  | _              |          | _                  |            | -          |
| 441                | 444                | 113                | 485                | 492                | 504                | 516                |                | t,       | 635                | 652        | 703        |
| 66.7               | 66.7               | 66.7               | 66.7               | 66.7               | 66.7               | 66.7               | 1.1. 7         | 1. 1.4.3 | 66.7               | 66.7       | 66.7       |
| 0                  | 30                 | 3.0                | 30                 | 30                 | 30                 | 30                 | ij             | 30       | 33                 | 30         | 30         |
| cr                 |                    |                    |                    |                    |                    |                    |                |          |                    |            |            |

## AL. I GNMENTS

| 튀           | HOWAN STANDARD, PRT; 387 AA.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
|-------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| AC OT DT 01 | QU8431,<br>01-OCT-1996 (Rel. 34, Created)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
| DT 03       | 01 NOV 1997 (Rel. 35, Last sequence update)<br>16-oct-2001 (Bol. 40 Tast amonation update)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
|             | ctadherin precursor (Milk fat globule-EGF factor 8) (MFG-E8) (HMFG)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
|             | Medin].                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
| NO WE       | MFGEB.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
|             | omo ompisto (naman).<br>Persentato (naman).                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
|             | Mammalia; Futheria; Primates; Catarrhin; Hominidae; Homo.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
|             | $NCBI_TaxID = 9606;$                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
|             |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
|             | SEQUENCE FROM N.A.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
|             | 1158UE-Breast, and Breast cardinoma;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
|             | DELINE FOR INSTITUTE FOR A STATE OF CONTRACT DISCUSSION OF CONTRACT |
| EA EA       | "Cloning and sequence analysis of himan breast enithelial antiden                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
|             | rousing and ordered marifold of rounds presented on an epidermal                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
|             | growth factor-like domain.";                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
|             | A CALL RIOL, 15.281-286(1996).                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
|             |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
|             | WEGINERY F. LUI-ART, F. FOM N. A.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
|             | TISSUE=Mammary gland;<br>Mrst two_als71351: Pubms4-1606623:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
|             | detance district, Muchael 1909952)<br>mondo D. Doforson I.A. Hrres P. Kurinseki I. Bistraio A.M.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
|             |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
|             | Mr 48,000 number milk hat alobase protein that is highly expressed                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
|             | in human breast tumors contains factor VIII-like domains.";                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
|             | incer Res. 51:4994-4998(1991).                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
|             | [3]                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
|             | PARTIAL SEQUENCE, AND CHARACTERICATION.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
|             | SSUE-MILK;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
|             | PRINE 98194921, Pubmed 9531276;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
|             | uffrida M.G., Cavaletto M., Giunta C., Conti A.,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
|             | Godovac: Ziminermann J.;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
|             | "Isolation and characterization of full and transacted forms of human                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
|             | east careinoma protein BA46 from human mix lat globure memblanes.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
|             | J. Profein Chem. 17:143-148(1998).                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
|             | )<br>THENEVE OF THE 217 AND TERMITETOARTON OF MEDITA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
|             | MEDI.INE-9934-2076 F: PNM-3-104-11933:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
| FA He       | Hawayayist B., Nacslund J., Sletten K., Westermark G.F., Mucchiano G.,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
|             |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
|             | eding an integral fragment of abitic smooth muscle celliproduced                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
|             | of other in forms the most element burger amploid. To                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
|             | Proc. Nati Acad. Sol. 8 & A Shrahma-Rh74 (1999).                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
|             |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
|             | AKAGTERIZATION.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
|             | MEDITURE (27405XHS) PLAMED SECONDS,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
| FA T.       | policy March Charles Charles Or Proceedings W. Fr. Perfection C. A.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
|             | "Tactadheric (fermerly BA46), a membrace associated glycoprotein                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
|             | aressed in buran milk and treast cardinemas, premetes Arardly-Asp                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
|             | And I to Carry and a language with the same and the same |

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Sadus morbua (Atlantic cod).
                 Mitochondrion.
  P79385;
   MFGE8
  Matches
  MFGM_PIG
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   entities requires a license agreement (See http://www.isb.sib.ch/announ.e.).
   ö
  -t- TISSUE SPECIFICITY: MAMMARY EPITHFLIAL CELL SUFFACES AND AGETTE
MEDIA, OVEREXPERSED IN SEVERAL CARCINOMAS.
-t- PTM: MEDIN HAS A RAGGED N-TERMINUS WITH MINOR SPECIES STARTING AT
                 -1: FUNCTION: MAY BE INVOLVED IN PROSPHOLIPID BINDING, EINDS SERCIPE/GALLY TO E-TAYINGS AND UNIBELS IS REPLICALLON.

-1: FUNCTION: MEDIA IS THE MAIN CONSTITUENT OF ACKID MEDIAL AMYLOTD
-1: SUBCELLUTAR ENTRY PERIPHERAL MEMBERNE PROTEIN.
   5.15
   CELL ATTACHMENT SITE (POTENTIAL).
BY SIMILARITY.
N-LINKED (SLUNAC. . . ) (POTENTIAL).
   Ċ
  Repeat, Billike desain; Amyloid
   100.0%; Score 45; DR 1; Length 3R7;
196.0%; Pred 85; 0.062;
  0, Indels
   268657118083783D CP064,
  LACTAURERIN; SHOFT POPM
  NOTE STATES OF STANDARD STANDA
  SIMILARITY CONTAINS 1 BOR-LIKE DOMAIN. SIMILARITY: CONTAINS 2 PEZE TYPE 3 18:MAINS
  0, Mismutches
  F5/8 TYPE C 1.
F5/8 TYPE C 2.
  LACTADHERIN.
DNA COLL Biol 16-861-869(1997)
  SMART; SMO0181; FGF; 1
SMART; SMO0281; FGF; 1
PHOSTITE; PSO0180; EGF_2; 1
PHOSTITE; PSO1286; EGF_2; 1
PHOSTITE; PSO1286; FASRC_1; 2
SIGNAL; GLYCOPTOLEIG, MILE, FMY
SIGNAL
   Pfam; PF00754; F5_F8_type_C; 2
   InterPro; IPR000561; EGF-like.
InterPro; IPR000421; FA58_C.
   43123 MW,
  EMRL; 1158516; AA050549,1; -.
EMRL; S56151; AAR19771 1; -
  AMINO ACID 264 AND 273
   Conservative
   STANDAPP:
  317
67
225
387
   Pfam; PF00008; EGF; 1.
  350
387 AA,
  Best Local Similurity
Matches 9; Conserv
   356 NLFETPILA 364
   1 NLFETPILA 9
  212
230
238
328
325
  24
268
268
24
230
230
27
27
   MTND5 OR ND5.
   MIM: GREERS:
   NU5M_GADMO
  DISULFID
   Ouery Match
  DISULFID
  DISULFID
  DISULFID
  CARBOHYD
  CARBOHYD
  CAPROHYD
  CARBOHYD
  DISULFID
  DISULFID
   SEQUENCE
  DOMAIN
DOMAIN
  DOMAIN
  CHAIN
  CHAIN
   NU5M_GADMO
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   a
C
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   Submitted (NGV-1997) to the EMRL/GenRank/EDBJ databases.
  Gaps
Eukaryota, Merazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
Arrinoprerygii; Neoprerygii; Teleostei; Euteleostei, Neoteieostei;
Aranthomotyba; Parazanthopterygii; Gadiformes, Gadoidei; Gadidae;
   กับพับจัจจี (หย่างรี, อาคมาคน)
15-มีน.1908 (Pol 36, Last sequence update)
จับ-MY-2000 (หย่างจี Last amoutation update)
เลยโลป์คะมีก (Milk fat globellar Farth fatth (MFG-E8) (MFGM) (Sperm
   Eukaryeta, Metissa, Chondata Standata, Vertebrata: Puteleostomi,
Mammailia: Eutheria, Cetartisdactyla; Suina, Suidae, Sus
   Johanson S., Bakke I.; "The complete of Atlantic Food (Gadus "The complete mitochood taxonomic studies among codfishes."; mortus Mar. Riel Hinderhood. 5:203-214(1996).
  -!- CATALYTIC ACTIVITY: NADH + ubiquinone - NAD(+) + ubiquinol.
  0
  Oxidoreductaso, NAD, Hbiquinone, Mitochondrion, Transmembrane.
SELUENTE - 617 AA, 64544 MW, 4A6344 EF51EGAL94 CRO64;
  -!- SÜRCFLÜLAR LOCATION- PFRIPHERAL MEMBRANE PROTEIN.
-!- TISSUE SPECIFICITY: MAMMARY EPITHELIAL CELL SURPACES AND
  Query Match
Rest Local Similarity 75 0%; Pred No. 7.7;
  0; Indels
   -!- SIMILAPITY: CONTAINS 2 FGF-LIKE DOMAINS.
-!- SIMILAPITY: CONTAINS 2 F5,78 TYPE C DOMAINS.
  2; Mismatches
  or send an email to licensewish-sib ch).
  STRAIN=NORWEGIAN COASTAL 1;
MEDGINE-546414325; FURMAJ-8817335;
   Pfam; PF00662; cxidored_q1_N: 1.
PRINTS; PR01434; NADHDHGNASE5.
   surface protein SP47) (PP47).
   Pfam, PF00361, oxidored_q1;
   6; Conservative
   STANDARD;
   BINDING PROTEIN.
  SEQUENCE FROM N.A.
   SECTENCE FROM N A
   Sus serofa (Pig).
  SPERMATOZOAN.
  479 NLFKTPVL 486
   NCRI_TaxID=8049;
   NCBI_TaxID=9823;
   1 NLFETPIL 8
   TISSUE=Testis;
   Ensslin M.A.;
   MFGM PTG
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   Baumgartner S.W., Littleton J.T., Broadie K., Bhai M.A., Harbecke R., Lengyel J.A., Chiquef-Ehrismann R., Prokop A., Rellon B.J.; "A Drosophila neuraxin is required for septate junction and blood-nerve barrier formation and function.", Cell 87:1059-1068(1996).
  Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilldae, Drosophila.
   Caps
  BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-ITMPED (GLCNAC. ..) (FOTENTIAL).
BOFOTAPROD29927A CPF64.
  Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
   He demain.
EGFLIRE 1.
EGFLIRE 2.
ES/8 TYPE 0.1.
FS/8 TYPE 0.2.
CELL ATTACHMENT SITE (POTENTIAL)
   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
  Score 35; DR I; Longth 409;
Pred. No. 8.2;
   1; indels
   094887; c9vTU5;
01-MAR-2002 (Pcl. 41, Greated)
01-MAR-2002 (Pcl. 41, Last sequence ipdate)
01-MAR-2002 (Rcl. 41, Last amnotation update)
  PRT; 1284 AA.
   BY SIMILARITY.
   SIMILARITY. SIMILARITY.
   Mismatches
   Drosophila melanogaster (Fruit fly).
   MEDLINE=97133213; Pubmed 8978610;
  MEDLINE=20196006; PubMed=10731132;
   Pfam; PF00008; EGF: 2. Pfam; PF00749; PF.P8-1;F6-C: 2. SMAPT; SMO0231; FASBC; 2.
  InterPro; IPR000561; EGF-like.
InterPro; IPR000421; FA59_C
  PROSITE: PS00022; ECF_1; 2, PROSITE: PS01184; PCF_2; 2 PROSITF; PS01184; PA59C_1; 2, PPOSITF; PS012284; PA59C_2; 2 Clymprotein; Popoat; PA59C_2; 2
   45725 MW;
   EMPL: Y11683; CAA72379.1; -.
  Query Match
Best Local Similarity 75.0%;
   Conservative
  STANDARD;
  88
247
409
   Popoa*;
  Neurexin IV precursor
   HSSP; P00740; 1EDM.
  409 AA:
   SEQUENCE FROM N.A.
  SEQUENCE FPOM N A
   378 NMFETPFL 385
  STRAIN-Canton-S;
  1 NLFETPIL 8
   NCBI_TaxID=7227;
  STEAIN-Berkeley;
  41
   Glycopretein;
DOMAIN
   NRX OR CG6827
  NRX4_DROME
  DISULFID
   DISULFID
  DISULFID
   DISULFID
   CARBOHYD
  CARBOHYD
   SEQUENCE
   DOMAIN
   DOMAIN
  POMAIN
   NKX4_DROME
  Matches
   SITE
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  Foster C., Gabrielian A.E., Garq N.S., Gelbart W.M., Glasser K., Glods A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Hostin B., Houskon, K.A., Howaland T.J., Wei M. H., Iboqwan C., Jaiali M., Kalush F., Korpen G.H., Korf, Kornicon I.A., Kaltak C., Larkis E., Larkis C., Larkis C., Larkis E., Larkis C., Larkis E., Larkis C., Larkis C., McLeod M.P., McPherson D., Merkulov G., Mishina N.V., Moberty C., Morris J., Moshreil A., McLei M., McHishia N.V., Moberty C., Morris J., Moshreil A., McHant C., Musch, L., Walley D.M., Nelson D.L., McHant C. M., Hasskern D.R., Parleb J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
                    Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Feiffer E.D.,
W.E. & Gaerre Y. H.G., Blazej R.G., Champe M., Feiffer E.D.,
W.E. & M. Los G.L.G.,
Abril J.F., Aubayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Rallew R.M., Rasu A., Baxenhale J., Bayrakiaroglu L., Beasley E.M.,
Heeson K.Y., Benes P.V., Rerman R.P., Rhandari D., Britchar E.,
Borteva D., Bortchan M.B., Reviek J., Reokstein P., Brottier E.,
Cheri, J.M., Gamin D.A., Buller H., Cadieu E., Center A., Chandra I.,
Theri, J.M., Gamin D.A., Buller H., Gadieu E., Center A., Chandra I.,
Shodson K., Seig I.F., Ewwiss M., Ludan E., Sunkey E.C., Found P.,
Soddon K., Seig I.F., Ewwiss M., Ludan E., Sunkey E.C., Found P.,
Bortlish K.G., Evander A., Devilas E., Sunkey E.C., Found P.,
Bortlish K.G., Skandellish R., Ferlas C., Ferlas S., Sunkey E.C., Ferlas C.,
Bortlish K.G., Skandellish A. B., Ferlas C., Ferlas S., Sunkey E.C., Ferlas S.,
Bortlish K.G., Skandellish A. B., Stankey E.C., Ferlas S.,
Bortlish K.G., Skandellish A. B., Ferlas C., Ferlas S., Sunkey E.C., Ferlas S.,
Bortlish K.G., Skandellish A. B., Stankey E.C., Ferlas S.,
Bortlish K.G., Skandellish A. B., Stankey E.C., Ferlas S.,
Bortlish K.G., Skandellish A. B., Stankey E.C., Ferlas S.,
Bortlish K.G., Skandellish A. B., Stankey E.C., Ferlas S., Stankey E.C., Ferlas S.,
  Reinert K. Remington K. Saunders R.D.C., Scheeler F. Shen H., Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R. Sun B., Wang A.C., Stapleton M., Strong R., Sun B., Wang X., Svitskas F. Tertor C., Turner B., Venter E., Wang A.H., Wang X., Wang Z. Y., Wassariman D.A., Weinsteck G.M., Weissenbach J., Yer F. F., Strong E., Yang S., Yao Q.A., Yer Yer F. F., Strong E., Chang S., Yao Q.A., Yer Yer F. F., Strong E., Strong S., Yao Q.A., Yer Y., Whers E.W., Rubin G.M., Venter J.C.; Shu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; Shu X., Smith H.O., "The genome sequence of Drosophila melanogaster.";
   Ward R.E. IV, Lamb R.S., Pehon R.G.; "A conserved functional domain of Drosophila coracle is required for localization at the septate junction and has membrane-organizing
   SUBCELLULAR LACATION: Type I membrane protein (Potential).
11SSUE SPECHFICLTY: FOUND IN SEPTATE JUNCTIONS OF EPITHELIAL AND
   -!- SUBDNIF: THE C-TERMINAL REGION INTERACTS WITH CORACLE. INTERACTS
  FUNCTION: SERMS TO PLAY A ROLE IN THE FORMATION AND FUNCTION OF SEPTATE JUNCTIONS. IS REQUIRED FOR THE BLOOD-BRAIN BARRIER
   Bhat M.A., Izaddoost S., Lu Y., Cho K.O., Choi K.W., Bellen H.J.;
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.
   "Disas lost, a movel maiti Fin domain protein, establishes and
  SIMILARITY: CONTAINS 4 LAMININ G-LIKE DOMAINS. SIMILARITY: BELONGS TO THE NEUREXIN FAMILY.
  SIMITARITY: CONTAINS 2 EGF LIKE DOMAINS.
SIMITARITY: CONTAINS 1 F5/8 TYPE C DOMAIN.
   INTERACTION WITH DISCS LOST.
MEDLINE 99200394, Pubmed-10162271;
  Cell Biol. 140:1463-1473(1998).
  MEDLINE 98177173; PubMed 9508778;
   maintains epithelial polarity.";
Cell 96:833-845(1999),
   WITH DISCS LOST IN CLS FORM.
  science 287:2185-2195(2000).
  INTERACTION WITH CORACLE.
  GLIAL CELLS.
  FORMATION.
  activity.
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SEQUENCE OF 873-1835 FROM N.A.
   3 FETPILA 9
  NH(3)
   CONFLICT
  Query Match
   ONIS_NP
BINDING
  CONFLICT
  CONFILICT
  Biotin;
  Best Luca
Matches
  HSSb;
 NEW TOOLS OF THE PROPERTY AND DESCRIPTION OF THE PROPERTY AND 
   01-oCT-1994 (Rel. 30, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Urea amidolyase [Includes: Urea carboxylase (Ri 6 3 4 6); Aliephanate
hydrolase (Rc 4.5.1.54).
  Sdep
   MEDLINE 92193240; PubMed 1802034;
Genbaulte F.S., Cooper I.G.;
"The urea amidolyase (PUPL,2) gene of Saccharemyces corevisiae.";
   Saccharomycos octovisiae (Baker's yeast).
Bukaryota: Fungi; Ascomycota; Saccharomycotisa: Saccharomycotes;
  ·:
   UB 1; Length 1284;
  Glycoprotein; Cell adhesion; Signal; Transmembrane; Repeat.
  1; Indols
  P -> MSA (IN REF. 1).
> D (IN REF. 1).
9372C71AC70E3D56 CEC64;
   Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
  EXTRACELLULAR (POTENTIAL)
   CYTOPLASMIC (POTENTIAL).
P5/8 TYPE C.
   Saccharomycetales; Saccharomycetaceae; Saccharomyces.
  LAMININ G LIKE 1.
   EGF-LIKE 2.
LAMININ G-LIKE 4.
  LAMININ G LIKE 3.
  PPT; 1835 AA.
  2: Mismatches
   Score 35; DB Fred No 27;
  NEUREXIN IV.
  EGF-LIKE 1.
  POTENTIAL.
  POTENTIAL.
   SMART: SM00181; EGF; 2.
SMART; SM00211; FA58C; 1.
SMART; SM00282; LamG; 4.
PHOSTIE; PS01022; EGF_1; FALSE_NEG; PHOSTIE; PS01184; ESF_2; FALSE_NEG.
PROSTIE; PS01184; ESF_2; FALSE_NEG.
   PROSITE; PS01286; PA58C_2; 1.
PROSITE; PS50025; LAM_C_DOMAIN; 4.
   MRPP
  Ptam; PF00008; EGF; 2,
Ptam; PF00754; F5_F8_type_C; 1.
Ptam; PF00054; laminin_G; 2.
   InterPro; IPR000561; EGF-like
InterPro; IPR000421; FA58_C.
InterPro; IPR001791; Laminin_G.
   01-OCT-1993 (Pol. 27, Created)
              AEU03542; AAF49951.1; -.
   DURL, 2 OR YBRZ08C OR YBR1448.
   77.8%;
66.7%;
  14547
  SEQUENCE OF 1-893 FROM N.A.
   IPR003585; 4.1m.
   PlyBase, Plejnoof3997, Brs.
EMBL; X86685; CAA60383.1;
  Conservative
  STANDARD
   SMART; SM00294; 4.1m; 1.
SMART; SM00181; EGF; 2.
   579
962
999
1183
   1217
1238
1284
  1284
  DNA Seq. 2:19-32(1991).
  1284 AA;
                                P00740; 1EDM.
  Best Local Similarity
   154 NVFEVPIIA 162
  SEQUENCE FROM N.A.
  1 NLFETPILA 9
  NCBI_TaxID=4932;
   47
  STRAIN S288C;
  . 9
  DUR1_YEAST
  InterPro;
   DOMAIN
TRANSMEM
DOMAIN
  CONFLICT
CONFLICT
SEQUENCE
   Query Match
   Rieger M.
  DOMAIN
DOMAIN
DOMAIN
  SIGNAL
   DOMAIN
  CHAIN
  Matches
  DURLYEAST
  ŝ
   <u>-</u>2
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   Yeast 9:797-806(1993).
-1- FUNCILON: HYDEOLYSIS OF UREA TO AMMONIA AND COZ.
-1- CATALYTIC ACTIVITY: ATP + urea + CO(2) = ADP + phosphate + urea :1-
   Bussereau F., Mallet L., Gaillon L., Jacquet M.; "A 12.8 kb segment, on the right arm of chromosome II from Saccharomyces cerevisiae including part of the DURL, 2 qene, contains five putative new genes.";
   Caps
  TO OTHER BIOTIN CARBOXYLARES C-TERMINI. 
 P \rightarrow R (IN REF. 1). 
 LKK \rightarrow KKN (IN REF. 1).
   PATHWAY: ALLANTOIN AND ARGININE METABOLISM.
SUBUNIT: MONOMER.
INDUCTION BY ALLOPHANATE OR 1TS NON METABOLIZED ANALOG
OXALURATE. REPRESSED IN THE PRESENCE OF READLY USED MITHEORIEM
   Ligase; Hydrolase; Multifunctional enzyme; Arginine metabolism;
   77.8%; Score 35; DB 1; Length 1835;
  0; Indels
Feldmann H., Mannhaupt G., Schwarzlose C., Vetter I.;
Soleifred (Anv 1994) i the EMRL/Senfank, TORI databases.
  F52B0DD00FB42CD65 CRC64;
  carboxylate.
-!- CATALYTIC ACTIVITY: Urea-1-carboxylate + H(2)c
  -> M (IN REF. 1).
-> K (IN REF. 1).
-> E (IN REF. 1).
  ATF (POTENTIAL).
   39;
   0; Mismatches
  Pred. No.
  BIOTIN.
   laterFre, IPR001882; Biotin.
InterPre, IPR000089; Biotin_lipoyl.
   ¥ - . I
  Plam; PP01425; Amidasc; 1.
Plam; PP02785; Hiotin, carb. C; 1.
Plam; PP00286; Biotin, lipoyl; 1.
Plam; PP00289; CPSasc., chain; 1.
Plam; PP02286; CPSasc., chain; 1.
Plam; PP02286; CPSasc., chain; 1.
Plam; PP02682; DP183; 1.
   MEDITINE=93377417; PubMed=8368014;
   201831 MW;
   SEQUENCE OF 1487-1835 FROM N.A.
   PROSITE, PS00188; BIOTIN: 1.
PROSITE, PS00866; CPSASE_1; 1.
PROSITE; PS00867; CPSASE_2; 1.
  EMBL, M64926; AAC41643.1; -. EMBL, 236077; CAA85172.1; -. EMBL, 221487; CAA79695.1; -.
   InterPro; IPPequel20; Amidase
   InterPro, IPR003833; DUF213.
   100.08;
   InterPro; IPROO0901; CPSase.
InterPro; IPROO3778; DUP183.
  7; Conservative
  129
  830
1395
  1835
  ; P24182; IBNC.
Sound412; PHP1, 2.
   -! - COFACTOR: BIOTIN.
   PIR; S46082; S46082.
  ATP-binding.
   AV:
   Lucal Similarity
   1798
   1779
  96
   STRAIN-S288C;
  SCURCES
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  entities requires a license agreement (See http://www.ish-sib ob/announce, or send an email to licensegisb-sib.ch).
  MEDLINESGROUP, FubMed 8485470, Mather I.B., Banghart L.B., Lane W.S.; The major fat-globule membrane proteins, boding compressed spirit and guinearpid op 55, are bonologous to MOS-EB, a murine digrophyclein sequences.";
   Biochem. Mol. Biol. Int. 29:545-554(1993).
-!- FUNCTION: PROBABLY ASSOCIATES WITH PHOSPHOLIPIDS ON THE SURFACE OF
MAMMARY EPITHELIAL CELLS AND MILK FAT GLOBULES. ZONA PELLUCIDA-
  --- TISSUE EPECIFICATY: MILK AND SPERMATOZDAM.
--- PIN: THE Z O-LINEED GLYDANS CONTIST OF SAL, GLUNA: AND FUC, WITH PROPERTY: VAR PEDICING TERMINAL SUGAR.
---- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
--- SIMILARITY: CONTAINS 2 E5/8 TYPE C DOMAINS.
  ALTERNATIVE PRODUCTS: 2 ISOFOHMS: A LONG FORM (SHOWN HERE) AND A SHORT FORM: ARE PRODUCED BY ALTERNATIVE SPLICING. THE SHORT FORM LACKS 53 AMINO ACIDS WITHIN THE F5/8 TIPE C 1 LOMAIN.
  095114; 027959; P79344; 01NOV-1997 (Rel. 35, Greated) 01-NOV-1997 (Rel. 35, Greated) 01-NOV-1997 (Rel. 35, Greated) 01-NOV-1907 (Rel. 40, tast sequence update) 16-OCT-2001 (Well 40, tast ancotation update) (MCD-1901 (Rel. 40, tast ancotation update) (MCD-1901 (Rel. 40, tast ancotation update) (MCD-1901 (Rel. 40, tast ancotate) (MFSM) (Species 3.0ffere protection SP47) (BP47) (Components 15/16).
   SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND CARHOHYDPATE-LINKAGE SITES
   Characterization of glycoprotein PAS 6,7 from mombrones of bowine
   "Malectoral of this of gipt protein and tens MGFC, by recommised by appointed and Bordess maked spatiest by the Milh Eut globable
  Bukarysta, Matazaa, Chordata, Craniata, Vertebrata, ButeleostoMi,
Mammalia: Eutheria: Cetartiodactyla; Ruminantia: Pecora, Bovoidea.
  Hvarreqaard J., Andersen M.H., Berglund L., Rasmussen J.T.,
  Fishi M., Taniguchi Y., Adachi T., Nakamura R.,
   Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
   SECCENCE OF 110 148; 174+187; 233-235 AND 422 427.
   427 AA.
  Biochim, Riophys, Acta 1245:385-391(1995),
   STPAIN-HOLSTEIN; TISSUE-Mammary Tland;
MEDLINE:97008954; Pubmed-RRSGO64;
  Rur. J. Biochem. 240:628-636(1996).
   TISSUE-Mammary qland;
MEDLINE-96125736; PubMed=8541316;
   SEQUENCE OF 18-427 FROM N.A.
   SEQUENCE OF 19-427 FROM N.A.
   STANDARD;
   Bovidae, Bevinae, Bos.
  BINDING PROTEIN.
  Bos taurus (Boyine).
   milk fat globules.
   NCBI_TaxID=9913;
   TISSUE=Testis;
  Petersen T.E.;
  Ensslin M.A.
  Matsuda T.:
   MFGM_BOVIN
  membrane.
  Ankin,
RESULT 6
MFGM_BOVIN
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) (HYPETT) (IN FAS-6
  . .) (HIGH MANNOSE) (IN
   Caps
  Eukarycta, Mctazoa; Nematoda: Chromadorea; Ehabditida; Phahditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
  01-NOV-1997 (Rel. 35, Greated)
NNV 1797 (Rel. 45, Last sequence update)
16-021-2601 (Rel. 40, Last amountation update)
Hypothetical 51.9 Kbs protein T1903.5 in chlomosome III presursor.
   BGF-LIKE 1.
BGF-LIKE 2.
BGF-LIKE 2.
PF-SF TYPE 2.
PF-SF TYPE 2.
CELL ATTACHMENT SITE (POTENTIAL).
   ) (IN DAS-6).
  Score 33, 28-1, Length 427;
Pred. No. 22;
   2; Indels
   Pulfon 1.5
Scientif (FIN-1995) to the EMML/AbdBJ databases.
---SIMILANITY SOME, TO THE REPOSEEP/REPOSEIP PANILY.
   MISSING (IN SHORT ISOFURM).
   4CBBEE3AlDC4EB24 CRC64;
   A \rightarrow F (IN REF. 1).
L \rightarrow Q (IN REF. 1).
   N LINKED (GLONAG.
PAS-6).
   BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
   PRT; 464 AA.
   1; Mismatches
   I ACTAPHEETN.
  47411 MW;
           EMBL: X91895; CAA62997.1; -. EMBL: S80643; AAR35894.2; -. EMBL: Y11719; CAA72406.1; -.
  Owery Match
Rest Local Similarity 66.7%;
Matches 6, Conservative
   STANDARD;
   Caenorhabditis elegans.
   18
427
59
   33
44
77
77
77
77
77
77
74
74
74
  106
265
427
   87
   Aiternative splicing.
   19
28
427 AA;
  496 NIFFTPF0A 404
   STRAIN-BRISTOL K2;
   SEQUENCE PROM N.A.
  1 NLFFTPILA 9
  NCBI_Tax1D: 6239;
   20
62
103
270
85
   YSV5_CAEFI.
  DISULFID
DISULFID
DISULFID
  CARBOHYD
   DISULFID
   CONFLICT
  DISHTED
   DISULFID
   CAPPOHYD
  DISULFID
   VARSPLIC
  SEQUENCE
   DISULFID
  CARBOHIE
  DOMAIN
POMAIN
DOMAIN
   T19C3.5
   SIGNAL
  DOMAIN
   CHAIN
  010011
   YSV5_CABEL
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  between the Swiss Estitute of Bishhormatics and the FMM or station the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See Mith grown as sub-dy-incomes) or send an email to licensewisb-sib.ch).
   This SWISS-PROT entry is copyright. It is produced through a collaboration
  Kaneko T., Salo S., Kotani H., Tanaka A., Asamidu E., Nukamura Y.,
Miyajima N., Hirosawa M., Suqiura M., Sasamoto S., Kimira T.,
Hosowchi T., Mateuro A., Murabi A., Nukataki N., Mateura S.
Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
   0) Gaps
  Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.";
   "Sequence analysis of the genome of the unicellular cyanobacterium
  Kamei A., Ikeuchi M.; "A noveles active Ser/The protein kinase in the "A novel grap, SpK", serveles active Ser/The protein kinase in the most Le cyanobacterian Synochecystis sp. Pr. 6603 ". Submitted (JOL-2000) to the PMRL/GenRank/PDRT databases.
  Res. 3:109-136(1996).
SIMILARITY: BELONGS TO THE SPRZTHR FAMILY OF PROTEIN KINASES.
   HYPOTHETICAL PROTEIN T19C3.5. : 4029CFD72F65E67F CRC64;
   73.3%; Score 34; DB 1; Length 464;
   0; Indels
  Probable serine/threonine-protein kinase C (EC 2.7.1.-).
  Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
  16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
   535 AA.
   0; Mismatches
   SMART: SM00329; HP12; 1.
PROSITE: PS00400; LBP_BPI_CETP: FALSE_NEG.
  Pred. No.
  POTERTIA:
   PRT;
   Sympochocystis sp. (strain PCC 6803)
  InterPro; IPR001124; IBP_BBPL_CETP.
Prom; PF02886; IBP_BBPL_CFTP. 1.
Prom; PF02886; IBP_BBPL_CFTP_C: 1
SMART; SM00328; BPIT; 1.
  MEDLINE-97061201; PubMed:8905231;
   16-00T-2001 (Rel. 40, Greated)
  FIGRE MW:
   Hypothetical protein; Signal.
  100.0%;
  EMBL; U28412; AAC46546.1;
WormPep: T19C3.5; CE02056.
   Conservative
   STANDARD
   464
  SEQUENCE 464 AA;
  Best Local Similarity
   SEQUENCE FROM N.A
   SPECIFICATION N A
   NCBI_TaxID-1148,
   SPKC OR SLR0549.
  134 NLFETP 139
  1 NUFFITP 6
   SPKC_SYNY3
P74745:
   Query Match
  SIGNAL
  SPKC_SYNY3
   CHAIN
   Matches
  DNA
  q
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EMBL; AB046599; BAB17035.1; -

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   between the Swiss Institute of Bioinformatics and the EMBL outstation
   Sdrip in
  pathway mediates localization of the orll polarity pathway ".
   MAÎ BEAL MAÎ ÎNÎ ÎNÎ 447-641(2000).
-!- FUNCTION: INVOLVED ÎN THE ORGANIZATION AND/OR FUNCTION OF THE
   Marphy L., Harris D., Barrell B.G., Pajandream M.A., Tyne M.H., Schmitted (Aug-1994) to the EMBC Actualistic databases.
  Murphy L., Harris D., Wood V., Barrell B.G., Rajandream M.A.;
Submitted (JON-1997) to the EMBL/Gembank/DDBJ databases.
   риовтру, рефіюв, рротети_KINASE_ST; 1.
Transferase, Serine/threonine-protein kinase; ATP-binding;
  Score 33; DB 1; Length 535;
  e, imbels
   1009 1096 COLLED COLL (POTENTIAL).
1385 AA; 154325 MW; ABB3D40CC4FF7537 CKC64;
   BY SIMILARITY,
533CD9FC0E3D23D8 CRC64;
   Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes, Schizosaccharomycetales, Schizosaccharomycetaceae,
  FECTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
   36, Created)
40, Last sequence update)
40, Last annotation update)
   PRT; 1385 AA.
  O, Mishatathes
   Schizosaccharomyces pombe (Fission yeast).
  PROSITE, PSSOOII: PROTEIN_KINASE_DOM: 1.
PROSITE: PSOOIIS: PROTEIN_KINASE_ATP: 1.
   Pred. No.
                  Interpro; TPR006719; Euk_pkinase.
Interpro; TPP002290; Sor_th_FPinase.
Pfam; PF00669; pkinase; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM;
  Actin interacting protein 3 homolog.
PAT1 OF SPACISA10 15 OF SPACISF1.01.
   MEDLINE-20143585; PubMcd-10679021;
Jin H., Amberg D.C.;
  SEQUENCE OF 1023-1385 FROM N.A.
  58141 MW:
   IDENTIFICATION, AND GENE NAME
  - ! - SIMILARITY - TO YEAST RUDA
  100.0%;
EMBL; D90917; BAA18865.1; -.
   SEQUENCE OF 1-1033 FROM N.A.
  EMBL; 297208, CABIO112.1; -.
   73.3%;
   FMH: Allow/7... "AHS/473.1;
Coiled coil; Cytoskeleton.
   Conservative
   STANDARD;
   142
  ACTIN CYTOSKELETON
  regulator Aipap/Rud6p
   142
535 AA:
   Schizosaccharomyces,
   Query Match
Best Local Similarity
  Complete proteome.
   FAT1_SCHP0 STAN
013735; Q9UT10;
15-JUL-1998 (Rel. 3
16-OCT-2001 (Rel. 4
   16-OCT-2001 (Rel.
   NCBI_TaxID=4896;
  396 NLFETP 401
   The secretory
  1 NLFETP 6
   STRAIN-972;
   STRAIN=972;
   SEQUENCE
   ACT_SITE
  SECUENCE
   ONIS JN
   BINDING
  DOMAIN
   RESULT 9
FAT1_SCHPO
   Matches
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   This SWISS-PPOT entry is copyright, it is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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   Biochim Riophys. Acta 1398:377-381(1998).
-- FUNCTION: PARTICIPATES IN DNA BEPLICATION AND MAY PARTICIPATE IN REPAIR. EXHIBITS A MAGNESIUM-DEPENDENT ATP-DEPENDENT DNA-HELICASE ACTIVITY THAT UNMINDS SINGLE. AND POTRIE-STPANCED DNA IN A 3'-5'
  Gaps
  -1- SURCELLUTAP LOCATION, NUCLEAR (B<sub>f</sub> SIMILIALILY).
-1- TISSUB SPECIFICITY: HIGHLY EXPRESSED IN TESTIS 12-14 DAYS AFTER BIRTH (COPPESPONDING TO THE PROTUTTENE PHASE) AND AT MECH LOWER LIPELS IN REALIN, HEART, KIVER, LUNG, THYMUG, KIDNEY AND SPIEEN.
-1- SIMILARITY: CONTAINS TO THE HELICAGE FAMILY. RECO, SURPAMILY.
-1- SIMILARITY: CONTAINS I HORC DOMAIN.
  Seki I., Wang W.-S., Okumura N., Seki M., Katada T., Enomoto T., "CDNA closing of mouse BLM gene, the homologue to human Bloom's syndrome gene, which is highly expressed in the testis at the mRNA
  Mne muchilus (Mouse).
Enkaryota, Metadoa, Chordata, Craniata, Vertebrata; Eutricoptomi;
Mammalia: Eutheria: Redentia; Sciucognathi; Muridue; Murinae; Mus
  Bahr A., de Graeve F., Kedinger C., Chatton B.;
"Pount mutations causing Bloom's syndrome abolish ATPase and DNA
hellease activities of the BLM protein.";
Operagene 17:2265-2571(1998)
                                     73.3%; Score 33; DB 1; Length 1385; 62.5%; Pred. No. 77; Urve 3; Mismatches 0; Indels
  SEGUENCE FROM N.A., AND TISSUE SPECIFICITY.
STRAIN-BALB/C; TISSUE=Testis, Spermatocyte, and Brain;
MEDLINE-98322127; PubMed-9655940;
  BLM_MCUSE STANDARD; PRI; 1416 AA. 088700; 088198; 15-DEC-1998 (Rel 37, Created) 15-DEC-1998 (Rel 37, Last sequence update) (1-MAR-2002 (Pri 41, Last annotation update) Hoom's syndrome protein homlogy (RE 3.5.1.-) (MBLM).
  SPOTENCE FROM N A., FUNCTION, AND MUTACENESIS.
   MODE MOLETA ALONA, MARCHANA MOLETANA, IPROCESSO, IEROZAGS, IEROZAG
  PROSITE: PS00690; DEAH_ATP_HELICASE; 1.
   MEDLINE-99054654; PubMed-9840419;
   InterPro; IPRÚÚl65U; Helicase_C.
   Pfam, PF00270, DEAD, 1.
Pfam, PF00271, helicase C; 1.
Pfam, PF00570, HRDC; 1.
  EMBL: 298263; CAR10933-1;
EMBL: AB008674; BAA32001.1;
   SMARI; SM00487; DEXDC; 1.
SMARI; SM00490; HELICC; 1.
SMARI; SM00341; HRDC; 1.
Ouery Match
Best Local Similarity 62.55
Free 5: Conservative
  MGD; MGI:1328362; Blm.
   DE 1304 NIVETPIV 1311
  NCB1_Tax1D-10990;
  1 NLFETPII, 8
  DIRECTION.
   evel
  RESULT 10
   BLM_MOUSE
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   Buddock E., Churcher C.M., Burrell B.G., Kujindream M.A., Walsh G.V., S.Amiftel (CTT 1917) . The PWELTA DESCRIPTION OF SERVICES (SECTION OF SERVICES) . SEMILARITY CAME, TO THE RNA METHYLIRANSTERASE TRMA FAMILY.
   NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
  Gaps
Helicase, ATP-binding, DNA-binding, Nuclear protein;
  . (
   Q->P: REDUCED ATPASE AND HELICASE
   K->A: REDUCED ATPASE AND HELICASE
  REDUCED ATPASE AND HELICASE
  C->S: REDUCED ATPASE AND HELICASE
  Score 33; DB 1; Length 1416; Pred, No. 78;
  1; Indels
  -> A (IN REF. 2).
> N (IN RDF. 2).
-> L (IN RDF. 2).
- 44709110A775DD42 CRC64;
   01-FFB-1996 (Pol. 34, Last sequence update)
16-OCI-2001 (Rel. 40, Last annotation update)
Hypothetical 59.6 Kha protein 6468.076 in chromosome I.
   Schizosaccharomyces pombe (Fission yeast).
Eakatyota, Eurji, Ascomposta, Schibosaccharomycetes,
Schirosaccharomycetales; Schirosaccharomycetaceae;
   [ . > P (IM RBF. 2).

E > E (IN RBF. 2).

V > M (IN RBF. 2).

WH : RT (IN RBF. 2).

MISSING (IN RBF. 2).
   ATP (BY SIMILARITY).
  527 AA.
  Mismulches X
   ACTIVITIES.
   ACTIVITIES.
  ACTIVITIES.
  ACTIVITIES.
                             POLY-GLU.
   DEAH BOX.
   POLY-ASP.
  POLY-GLU.
  PET
   158365 MW;
  01-FEB-1996 (Rel. 33, Created)
   InterPro; IPR002792; DUF90.
InterPro; IPR000051; SAM_bind.
  IPR001566; TRMA_1.
   Pfam; PF01938; TRAM; 1, PROSITE; PS01230; TRMA_1; 1.
  75.0%;
  EMBL; 256276; CAA91208.1;
  STANDARD;
  Conservative
                             2331
574
1317
704
806
1297
1348
   1063
   703
  5.58
   121
229
535
  Schizosaccharomyces.
   ٧
   Query Match
Best Local Similarity
Matches 6, Conserv
  SEQUENCE FROM N.A.
  490 NLFERPLL 497
                DNA replication.
DOMAIN 219
  1217
   1063
   NCBI_TaxID=4896;
   7.03
  1 NLFETPIL 8
   803
   647
  YAD7_SCHPO
Q09833;
   STRAIN-972;
  SPAC4G8.07C
 Hydrolase,
   InterPro;
  CONFLICT
  DOMAIN
DOMAIN
NP_BIND
  CONFLICT
  SEQUENCE
  CONFLICT
   CONFLICT
  CONFLICT
  MUTAGEN
   MUTAGEN
  DOMAIN
DOMAIN
   MUTAGEN
  MUTAGEN
  YAD7_SCHPO
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   Effetetes
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   PROSTIE: PS00518: ZF RING.1: 1.
PROSTIE: PS5089; ZF.RING.2: 1.
Transcription requiation. Trans acting tactor. Activator. Zinc finger;
DNA-binding: 80-structure.
   "A novel arrangement of zine binding residues and secondary structure in the C3HC4 motif of an alpha herpes virus protein family.";
J. Mol. Biol. 234:1038-1047(1993).
  Gaps
  MEDLINE-94087718; Pubmed-8263911;
Everett R.D., Barlow P.N., Milner A., Luisi B., Orr A., Hope G.,
   MEDLINE-94172642; PubMed 8126744; Barlow P.N., inisi B., Mihner A., Elliott M., Everett R.D., "Structure of the C9464 domain by 1H nuclear magnetic resonance specificsnapy. A new structural class of line-finger.".
   .
C
   Secret 32, 148-1, Length 527
   2: Indels
                 Hyperhotical protein; Hydrojase; Nuclease; Trinsferase;
Methyltransferase
   MEDIJINE 9229586; Pubmed-1318606;
Telford E.A.R., Watson M.S., McBride K., Davison A.J.;
"The DNA sequence of equine herpesvirus-1.";
   527 AA; 59613 MW; ACCERTONEPHA77F CRC64;
  -:- SIMILARITY: CONTAINS I HING-TYPE ZINC FINGER, -:- SIMILARITY: TO OTHER HERPESVIRUSES ICPO PROTEIN.
  Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
  Equine herpesvirus type 1 (strain Ab4p) (EHV-1).
  01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last Sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Irans-acting transcriptional protein ICPO.
   PY SIMILARITY
   Mismatches
  or send an email to license@isb-sib.ch),
  RING TYPE.
  Pred No
  PRT;
   ZINC 1.
  Alphaherpesvirinae; Varicellovirus.
  Mol. Biof. 237:201-211(1994).
   PDB; lCHC; 30-APR-94.
InterPro; lPMGO1841; Znf_rinq.
Ptam; PFO0097; zf-C3HC4; l.
SMART; SM00184; RING; l.
PROSITE; PS01231; TRMA_2; 1.
   71 18,
66 78;
  EMBL; M86664; AAB02498 1: -
   Virology 189:304-316(1992).
   6; Conservative
   STRUCTURE BY NMR OF 1-63.
  STANDARD;
  STRUCTURE BY NMR OF 1-63
  479
  47
  136801; WZBEF5.
   Query Match
Best Loral Similarity
  SEQUENCE FROM N.A.
   1 NLFETPILA 9
  NCBI_TaxID 31520,
   479
  ICPO_HSVEB
   ACT_SITE
  SECUENCE
   ZN_FING
METAL
   P28990;
   Lyon P
  ICPO_HSVEB
  Matches
  KESHLI
   3
   FINAL PROPERTY OF COURSE CONTRACTOR CONTRACT
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MEDLINE-9825987; PubMed-9614230; Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Barkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Barkhill F., Cas S., Barry C.E., III, Tekaia F., Eavies R., Besham D., Frown D., Chillinqworth T., Connor R., Eavies R., Devils K., Feltzell T., Gentles S., Hamiin H., Holroyd S., Hornsky T., Jaşels K., Krech A., McLean J., Monle S., Murphy L., Stuter S., Scoger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G., Taylor K., Whitehead S., Barrell B.G., Taylor K., Whitehead S., Barrell B.G., Mondete Genome Sequence."
  SIFAIN=The TSG / Oshkosh;
Fletschmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeRoy R., Podson R., Gwinn M. L., Haft D., Hickey E.,
Kolonay J.P., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
   OVERALL CONVERSION OF 2-OXOGLOTARATE TO SUCCINVL-YOA & CO(2), IT
CONTAINS MULIFIE COPIES OF 3 ENZYMATIC COMPONENTS: 2-OXOGLOTARATE
DEHYDROGENASE (E1), DIHYDROLIPOANIDE SUCCINYLTRANSFERASE (E2) AND
LIPOAMIDE DEHYDROGENASE (E3) (BY SIMILARLYY),
CATALYTIC ACTIVITY: Succinyl-COA + dihydrolipoamide - COA + S-
  0; Gaps
   1- FUNCTION: THE 2-OXOGL/TARATE DEHYDROGENASE COMPLEX CATALYZES THE
  Actinomycetaies, Colymebarterineae, Myrobarteriaceae, Myrobarterium.
NCBL_TaxiD-1773;
  "Whole genome comparison of Mycobacterium tuberculosis clinical and
  01-0cT-1996 (Rel. 34, Last sequence update)
16-0cT-2001 (Rel. 40, Last annotation update)
Ehydrotipoamide succinyltransferase component of 2-oxoqlutarate dehydrogenase complex (RC 2.3.1.61) (E2).
SHOR OP PV2315 CP MT2272 OP MTCY190.26.
  Score 32; DB 1; Length 532;
Pred. No. 46;
  1; Indels
   laboratory strains.";
Submitted (APR-2001) to the FMH,/GenHank/NDHJ databases.
   Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
   58629 MW; B4CB7E16FA26FDFA CRC64;
   553 AA.
  0; Mismatches
  71.1%; Score 32;
87.5%; Pred. No.
ZINC 1.
ZINC 2.
ZINC 2.
ZINC 1.
ZINC 2.
  .OCT-1996 (Rel. 34, Created)
   Mycobacterium tuberculosis.
  Conservative
   STANDARD
 532 AA;
   Local Similarity
   SEQUENCE FROM N.A.
   SEQUENCE FROM N.A.
  136 LFETPELA 143
   2 LFETFILA 9
   STRAIN-H37kV;
   ODOZ_MYCTU
C10381:
  Bishai W.;
   SEQUENCE
  Query Match
   LOMA I N
  STRAND
   STRAND
  STPAND
  HELIX
   METAL
METAL
  METAL
  ODOZ_MYCTU
 METAI,
                               METAL
  RESULT 13
  METAL
   TUPN
   IURN
  Matches
  90
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  c`
   Safe
  yeolysis: Transferase, Acritransferase; Lipoyl, Complete protecome.
NDING 43 43 LIPOYL (POTENTIAL).
NDING 162 162 LIPOYL (POTENTIAL).
  Santamarina-Polo S., Peterson K.M., Knaffer C.L., Giv Y.,
Freeman L.A., Cheng J.-F., Osorio J., Penalay A.T., Yang X.-P.,
Haudenschild C.C., Pradis Z., Pilmini G., Blackhou, P.E.,
Francols T.L., Duverger N., Rubin E.M., Rosier M., Deneile P.,
Fredrickson D.S., Brown H.R. Jr.,
Complete genomic sequence of the human ABCA1 quene: analysis of the
human and mouse ATF binding cassette A promoter."
Proc. Natl. Avad Svi U.S.A. 97-7982-7992(2009).
   SUBUNIT: FORMS A 24-POLYPEPTIDE STRUCTURAL CORE WITH OCTAHEDRAL SYMMETRY (BY SIMILARITY).
  095477; Ognuna; Ognuna; Ognuna; Ognuna; Ognuna; Ogarra; Ouassa; 16-007-2001 (Rel. 40, Last sequence update)
01-MR-2002 (Rel. 41, Last annotation update)
ATP-binding cassette, sub family A, member 1 (ATP-binding cassette transporter 1) (ATP-binding cassette transporter 1) (ATP-binding cassette transporter 1) (ATP-binding cassette transporter 1) (ATP-binding cassette transporter 2) (ATP-binding cassette 2) (ATP-binding cassette 3) (ATP-binding 
  Bukaryota, Metazoa, Chordata, Craniata, Vertebrutu, Buteleostomi,
Mommalia, Eutheria, Primatos, Catarrhini, Bominidue, Homo,
  SIMILARITY: BELONGS TO THE 2-OXOACTD DEHYDPOGENAGE PAMILY
succinyldihydrollipoamide.
-!- COFACTOR: COFACTOR INP COVALENTLY-BOUND LIPOYL COFACTOR
   71.1%; Score 32; DB 1; Length 553; 85.7%; Pred. No. 48;
   0, Indels
  54B6E70D23B804A7 CRC64;
  SIMILABITY FONTAINS 2 LIFFYL RINFING LOMAINS
  2261 AA
  BY SIMILARITY.
BY SIMILARITY.
  1; Mismatches
  PRT;
  MEDLINE=20345099; PubMed=10884428;
   IPROGORS; Biotin_lipoyl
  Pfam: PF00198, 2-oxoacid_dh; 1, Pfam: PF00364; blotin lipoyl; 2, Pfam: PF02817; e3_binding; 1, Proteom: P5041115; 2oxoacid_dh; 1, PROSITE: PS00189; LIPOYL; 2,
  Tubergulist; Rv2215; ...
InterPro; IPR001078; 20xoacid_dh.
  IPR004167; e3_binding.
   AE007072; AAK46557.1; -. P07016; 1E20.
  57087 MW;
   IPPOURATE; Lipoy!
   6; Conservative
   270283; CAA94286 1;
  STANDARD;
   requiatory protein).
ABCA1 OR ABC1 OR CERP.
  Homo sapiens (Human).
   553 AA;
   Query Match
Best Local Similarity
  SEQUENCE FROM N.A.
  474 LFDTPIL 480
  NOBI_TaxID-9606;
  (POFENTIAL)
   2 LPEIPIL 8
  TIGR; MT2272;
   ABC1_HUMAN
095477; 090
   InterPro;
   InterPro;
  ACT_SITE
ACT_SITE
  SEQUENCE
   BINDING
   ABC1_HUMAN
  Matches
   ô
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MEDIANE-20001430, PubMed-10533863; Marril M., Rendes Wilson A., Chan S.M., Rende K., Thang T. H., Yu L., Collins J.A., van Dam M., Molhuizen H.O.F., Loubser O., Onelette B.F.F., Sensen C.W., Fichter K., Mott S., Geris M., Boucher B., Pimstone S., Genest J. Jr., Kastelein J.J.P., Hayden M.R.; "Mutalions in the ABC1 gene in familial HDL deficiency with defective cholesterol efflux.";
   MEDINE-99194549; PubMed-10092505; Caromann T., Rlucken J., Reil M., Liebisch G., Luciani M.F., Chimini G., Kaminski W.E., Schmitz G.; "Molecular cloning of the luman ATP binding cassette transporter I (hABC1); evidence for sterol dependent regulation in macrophages.";
   MEDELTE 9936411, FabMed 10431236,
Procks-Wilson A., Marcil M., Clec S.M., Phand I.-H., Pecup K.,
van Dam M., Ya.L., Brewer C., Collins J.A., Molbuisch H.O.F.,
Loubser O., Ouelette B.F.F., Fichter K., Ashbourne-Excoffon K.J.D.,
Senger C.M., Scherer S., Mott S., Denis M., Martindale D.,
  "The seme encoding AIP-binding cassette transporter 1 is mutated in
Tangier disease.";
  VARIANTS ID ILE 929, ARC 907 AND ARG-1477, AND VARIANTS FUA LEU-693 DEL; TUR 1091: 1893-GLU-ASP-1894 DEL AND LEU-2150.
  VARIANTS ID SER-590; SUP 935 AND VAL-937, AMY VARIANTS ALA 299 AND
   SEQUENCE FROM N.A.

Tails A F , Me. D. Lower G , Archinks F , Different F., Eldera A.,
Kicka N., Amachi T., Yokoyama S., Ueda K.;
A new topological model of functional human AMCAI-signal peptide clearage and glycosylation of a large extraocliniar domain.";
Submitted (FEB-2007) L. The TMME, Genham K, PHPL databases.
   "ABCA1 gene expression and apoA 1 mediated cholesterol efflux are
   SEQUENCE OF 21 2261 FROM M.A. MEDILNE=99364413; FubMed 10431238; East S., Fusier M., Forker H., Erai J., Amoura E., Piette J.-C., East S., Fusier M., Forker H., Erai J., Amoura E., Piette J.-C., Transport J.-F., Brewer H.B., Duverger N., Denefle P., Assmann G.; Transport disease is caused by mutations in the gene encoding ATP binding cassette transporter 1.", Nat. Genet. 22:352-355(1999).
  Froblich J., Morgan K., Koop B., Pimstone S., Kastelein J.J.P.,
Hayden M.R.;
   "Mutations in ABC1 in Tangier disease and familial high-density
  Qiu Y., Caveller L., Chiu S., Yang X., Rubin E., Cheng J.-F.;
"Buran and make APCAL comparative sequencing and trinsponesia
studies to calling accel retained; sequences.";
Amounts 23.65.76(2001).
  Hodzioch M., Orso E., Klucken J., Langmann T., Boettcher A., Diobonk W., Barlage S., Buechler C., Porsely gevenerunear M., Kaminski W.E., Hahmann H.W., vette K., Pothe G., Aslanidis C., Tackner K.J., Schmitz G.,
   VARIANTS TD ARG-597 AND ARG-1477, AND VARIANT FHA LEU-693 DEL
   requilated by LXR.";
sobstitted (TT-2003) to the TMRG Genbank, Mtb. ditabases.
  VARIANTS FHA THR-1091 AND 1893-CLIT-ASP-1894 DEL.
   Blochem. Blophys. Res. C.Ammu. 257.29-33(1999).
  FISSUE Skin;
Schwartn K., Lawn R.M., Wade D.P.;
  MEDLINE-21251904; PubMed 11352567;
Qiu Y., Caveller L., Chiu S., Yang
  MEDLINE-99364412; PubMed 10431237;
   lipoprotein deficiency.";
Nat. Genet, 22:336-345(1999).
   SEQUENCE OF 21-2261 FROM N.A.
  Conct. 22:347-351(1999)
  Lancet 354:1341-1346(1999).
   SEQUENCE FROM N.A.
|Z|
SEQUENCE FROM N.A.
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"Age and residual cholesterol efflux affect HDL cholesterol levels and
  "Common variants in the gene encoding ATP binding cassette transporter
   Huang W., Moriyama E., Kega L., Hua E., Ageta M., Fawadata S., Mawatari K., Imamura T., Eto T., Kawamura M., Teramoto T., Sasaki J., "Novel mutations in ABCAl gene in Japanese patients with Tangier disease and Tamilial high density lipoprotein deficiency with coronary heart disease."
   I in men with low HDL cholesterol levels and coronary heart disease.",
Atheroscierosis 154:507-611(2001).
   Brousseau M.E., Bodzioch M., Schäefer E.J., Goldkamp A.L., Kielar D., Probst M., Ordovas J.M., Aslanidis C., Lackner K.J., Bloomfield Rubins H., Collins D., Robins S.J., Wilson P.W.F.,
   the ABGA1 gene and its application in genetic analysis of a new patient with familial high-density lipoprotein deficiency syndrome."; Biochim. Biophys. Acta 1537:42-48(2001).
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Van Ecrdeweqh P., Goldkamp A.L., Thurston L.M., FitzGerald M.G.,
Vasck McKenda D., O'Meill G., Eberhart G.P., Weifftenbach B.,
Ordovas J.M., Freeman M.W., Brown R.H. Jr., Gu J.Z.;
"Novel mutations in the quie encoding AFP binding cassette l in four
tangier disease kindreds.";
   "Homogeneous assay based on 52 primer sets to scan for mutations of
  VARIANTS LYS-219, ALA-399, MET-771; PPG-774; ASN-776; ILE-825; MET-883; ASP-1172; LYS-1587 AND CYS-1731.
MEDIANE 21138-79; Pubm-6 11288-26;
Clee S.M., Zwinderman A.H., Engert J.C., Zwarts K.Y.,
Melhulzen H.G.F., Poeney K., Jukema I.W., van Wijfand M., van Dam M.
Hudson T.J., Brooks Wilson A., Genest J. Jr., Kastelein 555,7.
   Wang J., Burnett J.R., Near S., Young K., Zinman B., Hanley A.J.G.,
Connolly D.W., Harris S.B., Hegele R.A.;
"Common and rare ABCAL variants affecting plasma HUL choiestetol.";
Arterioscler Thromb Vasc Rich Divided -1989(2000)
   MEDLINE-21369429, PubMed 11476961;
Lapicka-Rodzioch K., Rodzioch M., Kruell M., Rielar D., Probst M.,
Kiec B., Andrikovics H., Boettcher A., Hubacek J., Aslanidis C.,
   Heriolini S., Pisciotta L., Seri M., Cusano K., Cantalora A., Calabreni L., Peraneschini G., Barazmalo R., Calandra S., Appoint mutation in ABC1 gene in a patient with severe premature coronary heart disease and mild clinical phenotype of Tangler
                 Cloe S.M., Kastelein J.J.P., van Dam M., Marcil M., Roomp K.,
Zwarts K.Y., Collins J.A., Boelants R., Tamasawa N., Stule T.,
Suda T., Cessa R., Boncher R., Rondeau C., DeSouich C.,
Frieks Wilses A., Melhides H.O.F., Profileb J., Senest J. Jr.,
   VARIANT TO ASP 1046. VARIANT FIIA CYS-230, AND VARIANTS 1YS-219.
  VARIANTS TO ASN-1289 AND TEP-2081, AND VARIANT LYS 219. MEDLINE 21369433; Pubmed 11476965;
   corolary artery disease in ABCAl heterolygotes.",
J. Clin. Invest Postlas (1278 (2000)
   VARIANT TO TRP-587, AND VARIANT LEU-2168.
MEDITME 21157002; PubMed 11257260;
  Biochim, Biophys, Acta 1537:71-78(2001).
   VARIANTS 128-219; MET-883 AND ASP-1172.
MEDLINE 21157003; PubMed 11257261;
   ILE-825; MET-883 AND LYS-1587;
MEDLINE-20396633; Pubmed-10938021;
  PubMcd 11257261;
  VARIANTE TO ASN-1289 AND HIS-1800.
MEDLINE 20540002; PubMed 11086027;
   Atheroselerosis 154:599-605(2001).
  MEDITINE 20171964; PubMod-10706591
  Lipid Res. 41:433-441(2000).
  Suttorp N., Schmitz G.;
  VARIANT TO LEG-1506.
   Hayden M.R.;
  Hayden M.R.;
   Schmitz G.
  disease.
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-1- DISEASE: DEFECTS IN ABCAL ARE A CAUSE OF HIGH DENSITY LIPOTROTRIN DEFICIENCY TYPE I (HDLDI), ALSO KNOWN AS TANGLER DISEASE (TD). TO IS A RECESTIVE TRISECENCY CHARACTERIZED BY ANGRED OF HIGH DENSITY LIPOTROTEIN (HIGH DENSITY FROM PLASMA, HERALESTERM BEACH STEWN BEACH BY ANGRADIE.)

PERIPHERAL NEUROPATHY, AND FREQUENTLY PREMATURE CORONARY ARTERY
  "Expression and functional analyses of movel mutations of ATP-binding cassette transporter-1 in japanese patients with high-density
           Hipoprotéin levels and a modified risk for coronary arrory disease."; Cifewlation 193-1198-1205(2001).
   TPANSPOPTEP KEY CATEKEEPER INFLHENCING INTRACELLULAR CHOLESTEROL

    -!- DISEASE: Defects in ABCAl are a cause of high density lipoprotein

   Nishida Y., Hisano K., Tsukamoro K., Nagamo M., Hkodami C., Pesemp K., Ishihata M., Sakano N., Throq. T., Tsiji K., Matsuyama A., Ohamu T., Matsura E., Ishihamai M., Sakai N., Hiraoka H., Hattori H., Wellington C., Yoshida Y., Misuqi S., Hayden M.R., Equshira T., Yamashita S., Matsurawa Y.;
  0; Gaps
  EACH CONTAINING AN HYDROPHOFIC MEMBRANE-ANCHORING DOMAIN AND AN AIP BINDING CASSETTE (ABC) DOMAIN.
  MILITITIONAL POLYPEPTIDE WITH TWO HOMOLOGOUS HALVES,
  P41233;
21 FEB 1995 (Rel. 31, Created)
21 FEB 1995 (Rel. 40, Last sequence update)
31 MAR-2002 (Rel. 41, Last annotation update)
Atk-binding cassette, sub-family A, member 1 (ATk binding cassette transporter 1) (ATk-binding cassette)
  STEAIN-PRA/2; TISSUF-Macrophage; MEDLINE-94275009; PUDMED-9699292; Lichard M.F., Denizot F., Saviny S., Mattel M.-G., Chimini G.; Tilching W. Two novel AMS Transporters mapping on human chromosome
  -!- TISSUE SPECIFICITY: WIDELY EXPRESSED IN ADULT TISSUES. HIGHEST
   Eukaryota, Metazoa, Chordata, Graniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Bodentia, Sciuroquathi, Muridae, Murinae, Mus
   SSHE SPECIFICITY: WIDELY EXPRESSED, BUT MOST ABUNDANT IN
"Common genetic variation in ABCA1 is associated with altered
   tongth 2261;
   71.1%; Sevic 42; PH 1; Longth 226; 71.4%; Fred, No. 2.16+02; 0; Indels
   AMP VAPIANT ATHEPOSCIPPOSIS ASP-1611
   Oiu Y., Cavelier L., Chiu S., Rubin E., Cheng J.-F.:
   PFT; 2261 AA.
   MEDLINE=21645894; PubMed=11785958;
  THANSFORT (BY SIMILARITY).
   Genomics 21:150-159(1994).
  Lucal Similarity 71.4 nes 5; Conservative
   lipoprotein deficiency.";
   S'l'ANDARD;
   Mus musculus (Mouse).
   VARIANT TE THE Dee,
   SEQUENCE FROM N.A.
   DISEASE (CAD).
  SPOURNCE FROM N.A.
   NCHI_TaxID=10090;
   808 NIFESPV 814
  MACROPHAGES.
   STRAIN=C57BL/6J;
  1 NLFETPI 7
   TRANSPORT
   ARCAL OR ARCI
  POMATN:
   ARC1_MOUSE
  Query Match
   RESULT 15
  Matches
   ABC1_MOUSE
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LEVELS ARE FOUND IN PREGNANT UTERUS AND UTERUS.
DOMAIN: MULLIFUNCTIONAL POLYPEPTIDE WITH TWO HOMOLOGOUS HALVES,
EACH CONTAINING AN HYDROPHOBIC MEMBRANE-ANCHORING DOMAIN AND AN
ATP BINDING CASSETTE (ABC) DOMAIN.
SIMILARITY: RELONGS TO THE ARC TRANSPORTER FAMILY: ABCA SUBFAMILY.
  ATP (POTENTIAL).

N-LINKED (GLUNAC. ) (POTENTIAL).
  FAE62B21F51509F9 CRC64;
  Pram; PF00005; ABC_iran; 2.
Pram; PF00687; DUF214; 1.
Pram; PF00488; SRP54; 1.
SMART: SM0382: AAA: 1.
PROSITE; PS00211; ABC_IRANSPORTER; 1.
ATP-binding; Glycoprotein; Transmembrane; Transport.
TRANSMEM 26 42 POTENTIAL.
   (POTENTIAL).
   MISSING (IN REF. MISSING (IN REF.
  POTENTIAL.
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   EMBL, X75926; CAA53530.1; ALT_INIT.
EMBL, AF287263; AAG39073.1; ALT_INIT.
MGD; MGI:99607; Abcal.
  InterPro; IPR003593; AAA.
InterPro; IPR003439; ABC_transportr.
InterPro; IPR001687; ATP_GTP_A.
InterPro; IPR003838; DUF214.
  254011
   InterPro; IPR000897; SRP54.
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  CARBOHYD
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   CARBUHYD
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1 NLFETPI 7
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Gaps

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0, indels

2; Mismatches

Conservative

Best Local Similarity Matches 5; Conserv

Query Match

71.1%, Score 32, DB 1, Length 2261; 71.4%; Pred. No. 2.1e+02;

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|||||:|:
808 NLFESPV 814
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Search completed: September 5, 2002, 15:31:41 Job Lime: 476 sec

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GenCore version 4.5
Copyright (c) 1993 2000 Compugen Ltd
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OM protein - protein search, using sw model

Run on: September 5, 2002, 15.31.01 , Search time 122.86 Scoulds (Without alignments) 12.673 Million cell updates/see

Title: US-09-744-804-37
Perfect score: 45
Sequence: 1 NLFETPILA 9

Sequence: | NLFETPILA 9 Scoring table: BLOSEM62 Gapop 10 0 , Gapext 0 5 Sourched: 562020 segs, 170994929 recidues

Total number of hits satisfying these parameters (1000

Minimum DB seg length: 0 Maximum DB seg length: 2000000000 Post processing Minimum Match 03 Maximum Match 1008 Listing first 45 summaries

sp\_unclassified:\* sp\_invertebrate:\*
sp\_mammal:\* sp\_virus:\*
sp\_vertebrate:\* sp\_rvirus:\* sp\_bacteriap:\* sp\_organelle:\* sp\_phage:\* sp\_bacteria:\* sp\_archeap:\* sp\_rodent:\* sp\_archea:\* sp\_plant:\* sp\_human:\* sp\_fundi:\* SPTREMBL\_19:\* sp\_mhc:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the local score fixetible.

## SUMMARIES

| Description                   | gerials completely |                                                                      |        | 091227 arabidopsis | State Collection | Que544 mycobacteri | Ofraka nostoc sp. | 275814 human immun | 092ah5 listeria in | 044508 caencrhabdi | 074798 schizosacch | 021225 caenorhabdi | Q9bv54 homo sapien |        | uludana ana Opuego | Ognega2 dictyosteli |
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| ID                            | 99RTL9             | به 1 د د د د                                                         | ことこともご | Q9L227             | P34 229          | 0.006544           | OGPAH3            | 075814             | Q92AH5             | C44508             | 074798             | 021225             | Q9RV54             | Q9Y4B4 | 05N660             | 29NG02              |
| DB                            | 4                  | ų.                                                                   | ۲.     | 1.0                | <                | 9                  | c.                | 4                  | 16                 | п,                 | 'n                 | นา                 | ব                  | ₹      | 11                 | 5                   |
| %<br>Query<br>Match Length DB | 335                | 3.6.3                                                                | E a    | 699                | 700              | 250                | 1244              | 245                | 304                | 0.70               | 658                | 169                | 1162               | 1241   | 1466               | 2205                |
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| Score                         | 45                 | 6.<br>6.                                                             | 36     | 36                 | 3.6              | 34                 | 34                | ۲,                 | 33                 | 33                 | 33                 | 33                 | 33                 | 33     | 33                 | ££                  |
| Result.<br>No.                |                    | CI                                                                   | m      | 4                  | 5                | 9                  | 7                 | œ                  | 6                  | 10                 | 11                 | 15                 | 13                 | 14     | 15                 | 16                  |

| P78328 bomo sapien<br>OS8495 pyrococens<br>gakp24 "ibrio chol<br>e69231 pyrococens | CL                                       | 99aba4 caulobatim at<br>99aba4 caulobatter<br>998hw3 rhizobium l<br>099803 human immun | Cycoca numun<br>Cycocy drosophila<br>Oypedl xylella las<br>Oybw26 pseudomonas | 0.49254 årabidopsis<br>Ochep4 pseudomenas<br>Ochitdo schizosacch<br>P87562 equine herp | Copyris chlamydia m<br>Corf. bacilius ha<br>Corf. garobacturi<br>Coff. 3 arobidopsis | Q964p0 halobacteri<br>Q967h64 acinetobact<br>Q92qm7 arabidopsis<br>Q12168 saccharomyc<br>P71076 bacillus su |
|------------------------------------------------------------------------------------|------------------------------------------|----------------------------------------------------------------------------------------|-------------------------------------------------------------------------------|----------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------|
| 4 P78328<br>17 058495<br>16 998121<br>17 059241                                    | 16 09A1C1<br>2 09AHY1<br>16 0910T0       | 16 09000<br>16 098HW3<br>16 098HW3<br>15 098G03                                        | 15 098083<br>5 09VN80<br>16 09PED1<br>16 09HW26                               | 10 039254<br>16 24HUP4<br>3 09UTD0<br>12 F876C2                                        | 16 Q9PKg6<br>26 VRIST<br>2 G529/3<br>10 G9PF23                                       | 1 090420<br>2 050154<br>10 0920M7<br>3 012168<br>16 P71076                                                  |
| 1.1 78<br>11.1 121<br>11.1 173<br>11.1 208                                         | 245                                      | 11111                                                                                  | 1.1<br>1.1<br>3933<br>1.1<br>394                                              |                                                                                        |                                                                                      | 1.1 586<br>1.1 586<br>1.1 590<br>1.1 779<br>1.1 879                                                         |
| 32 71<br>32 71<br>32 71<br>32 71<br>32 71                                          | 32 32 32 32 32 32 32 32 32 32 32 32 32 3 | 2                                                                                      | 32 71<br>32 71<br>32 71                                                       |                                                                                        | \$3553<br>EEEE                                                                       | 32 22 32 32 32 32 32 32 32 32 32 32 32 3                                                                    |
| 118<br>188<br>100                                                                  | ଅପ୍ୟ                                     | 10101010<br>+ m & r- 0                                                                 | 20<br>20<br>31                                                                | ധയയ<br>വേധയാല<br>വേധകവ                                                                 | ტ F - 88 ტ <<br>ტ M - 88 ტ <                                                         | > ⊏ श्राल <b>क्ष</b>                                                                                        |

## ALIGNMENTS

```
Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Entereostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  Sobe 311.4 (EFF 2001) 'O PE FROTTS HEAD JULIANSES. -1-BIMILARITY: CONTAINS 1 F5/8 TYPE C DOMAIN. EMBL; BC003610; AAH03610.1; -1
   20E84E5DB78E8E25 CRC64;
  01-JUN-2001 (TFEMBLrel. 17, Created)
(1-JUN-2001 (TFEMBLrel. 17, Last sequence update)
(1-DPC-2001 (TFEMBLrel. 19, Last annotation update)
SIMILAR TO MILK FAT GLOBULE-EGF FACTOR 8 PROTEIN.
   PRI; 335 AA
   THENOWN_1.
  Interpro; 188006561; EGP-11ke, Interpro; 18800438; EGF_11, Interpro; 188000421; EGF_11, Interpro; 188000421; EASB_C, PHINE; PROONO19; EGFBLOOD, SWAFT, SWOOP91, EGFBLOOD, SWAFT, SWOOP91, EGFBLOOD, EGFBLOOD, EGFGLOOD, EGFGLOOD, EGFGLOOD, EGFGLOOD, EGFGLOOD, EGFGLOOD, EGFGLOOD, EGFGLOOD, EGFGLOOD, EGGGLOOD, 
   37523 MW,
   PRELIMINARY:
   HSSP; P08709; 1BF9.
   · t. VV
  SEQUENCE FROM N.A.
   TISSUE MELANOMA.;
   NCBI_TaxID-9606;
   Strausberg R.;
   SECTENCE
  Q9BTL9;
   QSBTL9
RESULT 1
                                     Q9BTL9
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Query Match
100.0%; Score 45; DB 4; Length 345;
Best Local Similarity 100.0%; Prod. Mo. 0.19;
Matches 9; Conservative 0. Mismatches 0. Indols 0. Gaps

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Q9LZ27;
  091227
  09LZ29;
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   Kawarabayasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M., Sekin- M., Baba S.-I., Aukai A., Kosugi H., Hosoyama A., Fukui S., Nagai Y., Nishijima K., Otsika R., Nakazawa H., Takamiya M., Kato Y., Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oquchi A., Aoki K.-I., Misuda S., Yanaqii M., Nishimura M., Yamagishi A., Oshima T., Kikuchi H.,
   Gaps
  Eguns caballus (Horse).
Eukaryotu, Metazoa; Chordata; Craniata; Vertebrata, Euteleostomi,
Mammalla: Puthoria: Perissodactyla; Equidac, Equas.
  Archaea; Crenarchaeota; Sulfolobales; Sulfolobaceae; Sulfolobus.
   ċ
  86 74. Gorn 34. HR 6. Longth 363. 77.88; Pred. No. 3.9;
   "Complete genome sequence of an aerobic thermoacidophilic
Crenarchaeon, Sulfolobus Lokodaii strain?.";
   1; Indels
  Gentzel M., Toepfer-Petersen E.;
Submitted (Aug.1998) to the EMRL/GenBank/PDRJ databases
EMBL: A010121: CAA09010.1; T. HSSP: P00740: 1EDM.
  363 AA; 40744 MW; 1F8B6395AF32338D CRC54;
  01-DEC-2001 (TremBLrel. 19, Last annotation update) SPERM-MEMBRANE ASSOCIATED PROTEIN P47 (FRAGMENT).
  01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL PROTEIN ST1017.
   01-NOV-1998 (TrEMBLrel, 08, Last sequence update)
  36.3 AA.
   531 AA.
   1; Mismatches
  01-DEC-2001 (TrEMBLrel. 19, Created)
  PPT;
  01-NOV-1998 (TrEMBLrel. 08, Created)
   PRT;
   PROSITE: PSU0022; EGF_1; UNKNOWN_2.
PROSITE; PSU1186; EGF_2; 2.
PROSITE; PSU1285; FA58C_1; 1.
   Interpro; IPR000561; EGF-11ke.
Interpro; IPP000421; FA58_C
Fram; PF00004; EGF, 1.
Fram; PF00754; F5_F8_L;pc_C; 2.
SMART; SM00731; FA58C; 2.
   ESF-like domain; Clycoprotein.
   Conservative
   PRELIMINARY;
   DNA Res. 8:123-140(2001).
   PRELIMINARY;
   STRAIN JCM 10545 / 7;
PubMed: 11572479;
  Omory Match
Rost Local Similarity
7; Conserva
   Sulfolobus tokodaii.
   SEQUENCE FROM N.A.
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304 NLFETPILA 312
   339 NMPETPFLA 347
  NCBI_TaxID=111955;
  SEQUENCE FROM N.A.
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  NORL TRAIL 4746;
  36.3
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  Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Trachcophyta,
Spermatophyta, Magnollophyta; eudicotyledons, core eudicots; Rosidae;
eurosids II, Mrassicales, Brassicaees, Arabidopsis.
   Sequence features of the regions of 1,191,918 bp covered by seventeen physically assigned PI clones.":
  0; Gaps
  Gaps
   Nakamura Y., Sato S., Kaneko T., Kotani H., Asamiru E., Miyajima N.,
Tabata S.;
  Bevan M., Terryn N., Ardiles W., Baysshaert C., Dasseville R., De Clerck R., De Keyser A., Neyt P., Rouze P., Van Den Daele B., Villaroel R., Gielen J., Van Montagu M., Bancroft I., Mewes H.W., Budd S., Lemeke K., Mayer K.F.X.;
Submitted (APR-2000) to the EMBL/GenBank/Bubt databases.
  "Structural analysis of Arabidopsis thaliana chromosome 5, 111.
   ċ
   01-0CT-2000 (TrEMBLEEL 15, Created)
01-0CT-2000 (TrEMBLEEL 15, Last sequence update)
01-0EC-2001 (TrEMBLEEL 19, Last annotation update)
PYPOTHETICAL 75 % KDA PROTEIN (GENOMIC DNA, CHROMOSOME 5, PI
   80.0%; Score 36; DB 17; Length 541; 66.7%; Pred. No. 26;
  80.0%; Score 36; DB 10; Length 669; 75.0%; Pred. No. 32;
   1; Indels
  0; Indels
   EU Arabidopsis seguencing project;
Supmifra (AFP-1000) to the FMPL/Contant/CTRT databases.
  PROSITE; PSS0297; ANK_REP_PESION; 1.
ANK repeat; Hypothetical protein; Repeat.
SEQUENCE 669 AA; 75339 MW; 676ACC5795H85H4 CRC64;
                          Eypothetical protein; Complete proteome.
SEQUENCE 531 AA: SROR3 MW; 25R3DC3DG0B4165R CRC64;
  01-0CT-2000 (TrEMBLrel. 15, Created)
01 OCT 2000 (TrEMBLrel. 15, Last sequence update)
   PRT; 669 AA.
   705 AA.
   2; Mismatches
  2; Mismatches
  PRT;
   MEDLINE-98162728; PubMed:9501997;
  DNÁ RES. 4:401-414(1997).
FMBL, AL162972; CAB86012.1; -.
EMBL, AH008271; BAB08974.1; -.
EMBL; AP000984; BAB66041.1; -
   Conservative
  InterPro; IPR002110; ANK.
  Conservative
   PRELIMINARY;
  FRELIMINARY;
   Query Match
Best Local Similarity
'... 6; Conserva
  Query Match
Best Local Similarity
Matches 6; Conserv
  102 NIFSTPLLA 110
   SEQUENCE FROM N.A.
  SEQUENCE FROM N.A.
   SEQUENCE FROM N.A.
  ||:|||:|
| 112 NLYETPLL ||19
  1 NLFETPILA 9
  eurosids II, Bra:
NCBL_TaxID=3702;
   STRAIN-COLUMBIA;
   1 NLFETPIL 8
  CLONE: MUK11).
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interPro; IPR000205; NAD_binding.
  SECUENCE
   Q9RAH3;
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  Q9RAH2
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   NOSB
  PESHIT
  PESULT
  075814
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  PETRIN 1937V)
MEDITRE-9899597: PubMed-98-47-60;
MEDITRE-9899597: PubMed-98-47-60;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Cold. S.V., Eigluncht R., Tas S., Hentry J.E. 111, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davises R., Devin R., Feltwell T., Gentles S., Hamilin N., Holcoyd S., Barrety T. Tagala K., Keltwell T., Gentles S., Murghy I., Oliver S., Sepaper K., Skelton S., Squares F., Skelton J.E., Taylor K., Whitehead S., Barrell B.G.;
Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
Deciphering the blology of Mycobacterium Luberculusis from the complete genome Sequence."
   Arabidopsis thaliana (Mousereal cress).
Enkaryota, Viridiplantae, Streptophyta, Embryophyta, Trashosphyta;
Spermatophyta, Magnoliophyta, cadiostyledons, our endieds; Rusidae,
eurosids II; Brassicales, Biassicaceae, Arabidopsis.
   -!- CATALYTIC ACTIVITY: L-3-HYDROXYACYL.-COA + NAD(+) + 4-OXOACYL-COA
   Gaps
  -1- STRMELLHTAR LOMATION: MITOMHORIA, (RY SIMILARITY).
-1- SIMILARITY: RELONGS TO THE SHORT-CHAIN PERVEGGENASES/PEDUCHASES
  Forteria, Firefeates, Artimobacteria, Astimobacteradae,
Actimomy etales, Petrobacterineae, Mysabacteriascae, Mysabacteriam
  Bevan M., Terryn N., Ardiles W., Buysshaert C., Dasseville R., Por Clorek P. De Keyser A., Neyt F., Poure F., Van Den Gaele H., Villarcol P., Gislou J., Van Montagu M., Bancreft T., Nowes H. W., Budd S., Leweke K., Amayer K.F. X., Submitted (APR-2000) to the EMBL/GenBank/DDRJ databases
   0;
   80 0%; Seare %, DB D; Dength 705, 75 0%; Pred No 34;
  01-DEC-2001 (PERMETER) 04, LAST SEQUENCE OPGATE)
01-DEC-2001 (PERMETER) 19, LAST SENDOTALING OPGALE)
FEGRALES 3 HISTORYACYLOGA DEHYDROGENASE 25 8 KIA 1YPE 11 (EC 1.1.1.35) (TYPE IT HANH)
MYCHAGA OF MICLES.11
MYCHAGA OF MICLES.11
  0; Indels
   EU Arabidopsis sequencing project,
Submitted (APR-2000) to the EMBL/GenHank/DDRJ databases
EMBL; AL162972; CARRAO10 1; -
  Interpro: IPPON110; ANK.
PROSITE; PSG0297; ANK_REP_REGION; 1.
ANK_repeat; Hypotherical protein; Pepcat.
SEQUENCE 705 AA; 79491 MW; 9194481448012027 CMU54;
01-DEC-2001 (TremBirel, 19, Last annotation update)
  250 AA
  2; Mismatches
  006544;
01-JUL-1997 (TFEMBLER) 04, LASE Sequil 1701-1997 (TFEMBLER) 01-JUL-1997 (TFEMBLER) 19 LASE BRD
   PRT;
  InterPro, IPRO62198, ADH_short
   HYPOTHETICAL 79.5 KDA PROTEIN.
  Mycobacterium tuberculosis.
   FMRI; 295584; CAB09032.1;
HSSP; 070351; 1838
  6; Conservative
  PPELIMINAPY;
   Nature 393.537-544(1998)
   Tuberculist; Rv1144; -
  Query Match
Best Local Similarity
   SEQUENCE FROM N.A.
  SEQUENCE FROM N.A.
   SECUENCE FROM N.A.
   99 NLYETPLL 106
  NCBI_TaxID=1773;
   FAMILY (SDP)
  NCBI_TaxID-3707;
   1 NLFETFIL 8
  T1E3_40
   006544
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   Matches
   006544
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  Hoffmann D., Hevel J.M., Moore R.E.;
"Characterization of the nostreportalide biosynthetic gene cluster of
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  77 GB, Score 34, DB D, Length 1244; 66 78, Prej Ne. 1.74±02; five 2; Mismatches 1; Indels
   75.68, Score 34, DB 16, Longth 250, 75.09, Prod No. 32, 10.00 (ive. 2, Miscatches 0, Indias
Pram; PFUUlU6; adh_short; 1.
PROSITE; PSOAO61; ADH_SHORT; 1.
Hypothetical protein, Gxidoreductase, NAD; Mitochondrion;
  Nostoc sp. GSV224.
Bacteria, Cyanabacteria, Bestewales, Besteranoane, Nostoc.
NCBL_TaxiD=76334;
  Nostoc sp. 62V224.";
Submitted (DEC-1949) to the EMBL/GenBank/DDBJ databases. EMBL; APEGGGGE-1949) to the EMBL/GenBank/DDBJ databases. HSSP; P25715; 1MLA.
HSSP; P25715; 1MLA.
HSSP; P25715; 1MLA.
HRSP; P2571
  ...11 AA; 137545 MW, ASECE74.BEGA8A81 CRO64;
   POLY-VAL.
NAD (BY SIMILARITY).
BY SIMILARITY.
; 124AlüübAl.Rümbe "Pob4;
   itum, Producy, Actuacy, synt, 1.

Firm, Producy, Actuacy, synt, 1.

From, PRODSO, po-binding, 1.

PROSITE, PSEGOTS, ACEDOMAIN, 1.

PROSITE, PSEGOTS, MITCHLOAFFIEL, THRNOWN, 1.

PROSIDE, PSEGOTS, MITCHLOAFFIEL, THRNOWN, 1.

PROSIDE, PSEGOTS, MITCHLOAFFIEL, THRNOWN, 1.

PROSIDE, PSEGOTS, MITCHLOAFFIEL, THRNOWN, 1.
  01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-PET-2001 (TrEMBLrel. 14, Last annotation optate)
   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-160-2001 (TrEMBLrel. 19, Last annotation update)
  PRT; 245 AA.
   InterPro; IPE003880; Phosphopant_attach.
  Q75814;
01-NOV-1996 (TEBMELED] 01, Treated)
   250 AA; 25787 MW;
   Rost Lonal Similarity of 7
Matches 6, Conservative
  Conservative
   PRELIMINARY;
   35
32
186
   PRELIMINARY;
   Quory Match
Host Local Similarity
For Consciva
  Db 1210 NLFESPTIA 1218
   Possible proteome.
FomAlN 32
  SEQUENCE FROM N.A.
  188 LFDTPLLA 195
   1 NLFETPILA 9
   5.2
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5.5
5.5
   2 LFETPILA 9
  STRAIN-GSV224;
   NP_BIND
ACT_SITE
   Query Match
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92 FETPIIA 98

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investigating biology, The C
Science 282:2012-2018(1998).
  6; Conservative
   PRELIMINARY;
  PRELIMINARY;
   SMART; SM00450; RHOD; 1.
Hypothetical protein.
   Caemothabditis elegans.
  Latineally were interesting.
   01-pm-2001 (Premirel.
  01-NOV-1998 (TERMELTE)
01 NOV-1998 (ITEMELTE)
   Schizosaccharomyces.
   Query Match
Rest Local Similarity
   STRAIN-BRISTOL NZ;
   SEQUENCE FROM N A.
  SEQUENCE FROM N.A.
   STRAIN=BRISTOL N2;
   SEQUENCE FROM N.A.
   STRAIN-BRISTOL N2;
  SEQUENCE FROM N A
  NCBI_TaxID=6239;
  2 LFETPILA 9
  NCBI_TaxID=4896;
  Waterston R.;
  STRAIN=972;
  SPBCZD10.04
   044508;
   074798,
  044508
  O74798
                   10
   RESULT 11
  Matches
                   RESULT
044508
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   A Subman P., Frangeul L., Buchrieser C., Rusniok C., Amend A., A Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A., A Glaser P. Frangeul L., Buchrieser C., Rusniok C., Amend A., A Acqueror P. Horrine P. Romann F., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O., A Gontier L., Goebel W., Gamez-Lopez N., Hain T., Hauf J., Jackson D., A Gontier L., Goebel W., Karish A., Man W., Kunst F., Kurapkat G., A Jones L.-M., Kaerst U., Krell J., Kunh M., Kunst F., Kurapkat G., A Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H., A Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H., A Kemmel B. Rose M., Schluder T., Sinces N., Tierrez A., A Kemmel B. Rose M., Schluder T., Sinces N., Tierrez A., A Vazquez Beland J. A., Vass H., Wehland J., Cassait P.,
   Caps
  Gaps
  "Sequence analyses of the reverse transcriptuse region of HLV-i
isolates from Sydney, Australia.";
Submitted (JUL 1996) to the EMBL/Packank/IMBA databases.
  STRAIN-TR324 FROM AUSTRALIA;
Edeng N.R., Hatten L., Neitan B.A., Goget D.A., Ledaney S.F.,
McGnoon P.W.:
   Ö
  73 3%; Score 33; DR 16; Length 304;
85 7%; Pred No 64;
  73.3%; Score 33; DB 15, Length 245,
66.7%; Prod No 51;
tive 1; Mismatches 2; Indels
  0; Indels
  28756 MW: hD518A336PC3848; (78264)
  304 AA: 32225 MW; 67391416A4PR5291 CHC64;
   01-DEC-2001 (TERMRIFE) 19, Created)
01-DEC-2001 (TERMRIFE) 19, Last seguence update)
01-DEC-2001 (TERMRIFE), 19, Last annotation update)
             Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
   Bacteria, Firmicutus, fucilius/Clostridium group,
Bacillus/Staphyloroccus group; Listeria.
   304 AA.

    Mismatches

   PRT;
Human immunodeficiency virus type 1.
  STRAIN-CLIP 11252 / SERCVAR 5A;
   Science 294:849-852(2001)
EMBL, ALS96170; CAC97177.1; -.
Listilist; Lin01947; -.
  EMBL; U64171; AABO5314.1; -.
InterPro; IPROO0477; RVTSA
  RNA-directed DNA polymerase.
  6; Conservative
   6; Conservative
   PRELIMINARY;
   Pfam; PF00078; rvt.; 1.
   245
   245 ...
245 AA;
  Query Match
Best Local Similarity
   Bost Local Similarity
   SEQUENCE FROM N.A.
  Complete protecume
SEQUENCE 304 AA:
  44 NLYNTPLEA 52
  SHOUTENCE FROM N.A.
  Listeria innocua.
   1 NLFETPILA 9
   PYRD OR LIN1947.
  NCBI_TaxID=1642;
   3 FETPILA 9
   PYRD PROTEIN.
  -: --
  SECTION
   NON_TER
NON_TER
  Query Match
  092AH5;
   Q92AH5
  5
   Matches
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RESULT. **092AH5** 

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Gaps
   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
  "Genome sequence of the nematode C. elegans, a platform for investigation biology and the C. elegans Sequencing Consortium.";
  ..
O
   Wood V., Rajandream M.A., Barrell B.G., Taylor K., Harris D.,
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: TO YEAST YJL084L.
  73.3%, Score 33, DB 5, Length 572, 75.0%, Prod No. 1.2c+02, Live 2, Mismatches 0, indels
  DB 5,
26+02;
nos 0, indels
  "Direct Submission.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF030618, AMB92073.1;
InterPro; IPR001763; Phodanese_domain.
InterPro; IPR0000063; Thiored.
   01 NOV-1998 (TEMPLE). 08, Jast September update)
01-001-2000 (TrEMBLE). 15, Last annotation update)
HYPOPHETICAL 57.9 KDA PROPEIN CIDIO 04 IN CHROMOSOME II.
  Gattung S., Holmes A.;
"The sequence of C. elegans cosmid P4208.";
Submitted (PEC-1947) to the EMRL/GenBank/PDRJ databases.
   572 AA, co648 MW, SBICBEF23438474C CECC4.
   Eukaryota, Eungi, Asonmyoota, Schiersscharomyeetes;
Schiersachersmyoctales; Schiersachdaromyootacee;
  ut, Last sequence update)
19, Last annotation update)
  PRI; by8 AA.
   Schizosaccharcmyces pombe (Fission yeast).
  Phabditidae; Peloderinae; Caenorhabditis
  01-JUN-1998 (TrEMBLrel. 06, Created)
  กล Created)
PKI;
   MEDIINEEsasonsanis pubmed-sasis16;
  EYPOINETICAL 66.6 KDA PROTEIN.
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SMART, SM00487; DEXDC: 1.
  CARNEO
  Q9Y4B4;
   00N560
   Q9Y4B4
   Matches
  RESULT 14
  098660
  Q9Y4B4
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  Gaps
   Gaps
   Eukarycha: Motacca; Nomatoda; Chromodorna, Phabdilidu, Elukdilidu.;
Rhabdilidae: Pelodorinae; Caenorhabdilis.
NCBI_TaxiD=6239;
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homlnidae; Homo.
NCRI_TAXID=9606;
  Ö
  c,
   73.3%; Score 33; DB 5; Length 694; 66.7%; Pred. No. 1 50+02; Live 2; Mismatches 1; Indels
   73.3%; Score 33; DB 3, Length 658, 100.0%; Pred. No. 1.4e+02; Five 0; Mismatches 0; Indels
   "Genome sequence of the nematode C elegans. A platform for
  Strausberg R.;
Submitted (DEC 2000) to the EMBL/Workankylded databases.
EMBT: RC001474: AAM01474 l; -.
  Gardner A.E.;
Submitted (JUL-1996) to the EMRI/DenHank/UDBJ databases
                     EMBL: AL031788; CAA21162.1; ·. SPQIENCE 658 AA; 72731 MW; 49FR066BB970B4F7 CRC64;
   694 AA; 78366 MW; 984655D087A3049B CPC64;
  01-NOV-1996 (TrEMBLrel, 01, Created)
01-NOV-1996 (TrEMBLrel, 01, Last sequence update)
01-DEC-2001 (TrEMBLrel, 19, Last annotation update)
  01-JUN-2001 (TremBlrel, 17, Last sequence update)
01-DEC-2001 (TremBlrel, 19, Last annotation update)
   PPT; 1162 AA.
   HYPOTHETICAL 128.7 KDA PROTEIN (FRAGMENI).
Homo sapiens (Human).
   01-JUN-2001 (TrFMRLrol, 17, Created)
   FRT,
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TISSUE=PLACENTA, CHORIOGARCINOMA;
   MEDLINE=99069613; PubMed-9851916;
   73.44,
100.0%; Pre
   InterPro, IPPAAA10, BFAD
InterPro, IPPAAA10, Helicase_C
  LuterPro; IPK000 < 40; SNF2_N.
Pfam: PF00271; helicase_C; 1.
Pfam; PF00176: SNF2_N; 1</pre>
  investigating biology.";
Science 282:2012-2018(1998).
EMRL: 275712: CARGO043.1; -.
  Quory Warch
Best Local Similarity 100.05,
hos 6: Conservative
   Best Local Similarity 66.79
Matches 6; Conservative
   PPELIMINAPY:
   PRELIMINARY,
   Caenorhabditis elegans.
   SEQUENCE FROM N.A.
  || |:|:||
584 NLVESPVLA 592
  SEQUENCE FROM N.A.
  1 NLFETPILA 9
   K04G2.6 PROTEIN.
   423 NLFETP 428
  1 NIFFTP 6
   SEQUENCE
   Query Match
  Q9BV54;
   QGRV54
  RESULT 12
   Q9BV54
  021225
  ACCOS OCCOS SENT THE ```

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Nagase T., Ishikawa K., Suyama M., Kikano R., Miyajima N., Tanaka A., Kotana H., Momura N., Ohara O., Momura N., Ohara O., Production of the ceding sequences of unidentified human genes. XI. The complete sequences of 100 new cDNA clones from brain which code for large perceins in vitro."; Ind. Large perceins in vitro."; EMML: AB018352, RAA34529:1; -.
                                                                                                                                                                                                                              Gaps
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Marmalia: Eutheria; Bodentia: Sciurognathi: Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                           73.3%; Score 33; DB 4; Length 1162;
75.0%; Pred. No. 2.5e+02;
tive 1; Mismatches 1; Indels
SMART: SM00490; HELICC: 1.
ATP-binding: Helicase: Hypothetical protein.
NON_TER
SEQUENCE: 1162 AA, 128656 MW, 42FEIC6114B7BBD3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NON_TER 1 1 SEQUENCE 1241 AA; 137451 MW; E7B11A45F8769C40 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NeV-1999 (TEEMBLrel. 12, Created)
01 NOV-1999 (TEEMBLrel. 12, Last. sequence update)
01-DBC-2001 (TEEMBLrel. 19, Last annotation update)
EIAAA9909 ECTLIB (FEACHINF).
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01 JUN 2001 (TEDMBLIEL, 15, Last sequence update)
01-1962-2001 (TEDMBLIEL, 19, Last assectation update)
structo added (TEDMBLIEL) 19, Last assectation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 1241 AA.
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MEDLINE-99087487; PubMed-9872452;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; 1PR001410; DEAD.
InterPro; 1PR001650; Helicase_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam, PF00271, helicase_C; 1.
Pfam; PF00176; SNF2_N; 1.
SMART; SM00487; DEXDC: 1.
SMART; SM00490; HELICC: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000330; SNF2_N.
                                                                                                                                      Query Match
Bost Local Similarity 75.00
Local 6, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Censerrative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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Best Local Similarity
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296 NMFERPIL 303
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217 NMFERPIL 224
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                                                                                                                                                                                                                                                                             1 NLFETPIL 8
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NCB1\_Tax1D: 10090;

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                                                                                                                                                                                                                                           Consider the Marker Mills Tissue-11-Day Embryo;
Consider the Marker Mills Tissue-11-Day Embryo;
Consider the Marker Mills Mills Merster Mills Mills Merster Mills Merster Mills Merster Mills Merster Mills Merster Medition of a novel Sub-11-se family member protein as a consequent of a novel Sub-11-se family member protein as a consequence of a novel Sub-11-se Mills Mills Mills Mills Mills Merster Mills Mil
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Search completed: September 5, 2002, 15:31:03 Job time: 468 sec

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Copyright (a) 1993 - 2000 Founturyon Ltd
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OM protein - protein search, using sw model

September 5, 2002, 15,27.34 / Search time 58.86 Seconds (without alignments) 3.735 Million cell updates/sec Pun on:

115-04-144-804-311 Ferfect sour ritle:

1 NLFETPVEA 9 Sequence:

Gapop 10 0 , Gaprat 0 5 BLOSUM62 Scoring table:

231528 segs, 24425594 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: Հոնոնոնումո

Listing first 45 summaries Maximum Match 100% Post-pro⊶ssing: Minimum Mateh 0≗

Issued\_Patents\_AA:\* Database :

/rgf2\_6/ptodata/2/inayfa\_rown.pop.\*
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Pred. No. is the number of results predicted by chance to have a SCOTE greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

# SUMMARIES

Description	Sequence 10. Arel			c	1 : 4	٠	σ.	September 12, April		α	C.	344	T,	Sequence 3, Aprl:	E.	11	12	ci	ci	Sequence 2, Appli	Se partice 22, Appl	e i	Sequence ', April	Sequence 5, Appli	Ġ	<i>[</i>	Sequence 6, Appli
ID	ES-08-162-402B 10	-6.37	16.2	- 1	1261	98-08 152-4028-6	75-08-142-402R-9	75 08 162-402R 12	13-58-150 4028-56	115-118-584-0118A-8	715 09-187-859-40		CS 68-971-158 1	rrs-08-971-158-3	437 054A-12	US 08-984-618-11	9 061-961-68 85	3 Ty3 6y9-80-Su	0.5-0.4-20.6.490-2	FCT-US96:11445 2	US+08+322+32	113 ON 2001-152A-2	US-((Ŕ-4]2-272 º	US-09-026-039-5	US-08-904 263A-6	US-08-858-207A 417	9 V065-588-80 S0
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Sector 46, 28.2, Longth 160; Pred. No. 0.038;

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Querr Match Bost Local Similarity

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# ALIGNMENTS

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TITLE OF INVENTION: 46 KDALTON HUMAN MILK FAT
TITLE OF INVENTION CLOWEL (BMPC) ANTIOCH, FRADMENTS & FUELON FROTEIN
NUMBER OF INVENTION CLOWERS 1.
CORFESSIONALINGE ANDERSS.
                                                                                                                                                                                                                                                                                                                                     ALPRESSEE: Frett, Schrouder a Popiawaki
STREET: 444 South Flower St., 19th Floor
CITY: Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PAR 38215
                              Sequence Lo, Application 98/08/05492B Patent No. 5972337
                                                                              APPLICANT: CERTANT, ROBERTO L. APPLICANT: PETERSON, JEPRY A. AFFLICANT: LARCCCA, DAVID J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30,430
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IBM Compatible
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SHQUENCE CHAPACTEPISTICS:
LENGTH: 160 amino acids
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MEDIUM TYPE: Diskett
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                                                                   GENERAL INFORMATION:
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POLYEPPITDE WITH 46
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FACTORS V AND VIII LIGHH-FAHAIN HOMOLOGHES,
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NUCLECTIDE ENCODING THE POLYPEPITDE, ANTI-
POLYPEPITDE AN
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         D. Mishartches
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 943-1931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          118/07/607,5380
                                                                                                                                                                                                                                                                                                                                                                         Ceriani Dr., Poberto L
                                                                                                                                                                                                                                                                                                                                                                                                             Jerry A.
                                                                                                                                                                                                                                                                         Sequence 3, Application US/07607538C Patent No. 5455031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/08162402B Patent No. 5972337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USE THEREOF
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REGISTRATION NUMBER: 30,930
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                                                                                                                                                                                                                                                                                                                                                                                                         Peterson Dr., Jer
Larocca, David J.
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INFORMATION FOR SEQ ID NO: 3:
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mer FFAX: (510) 943-1189
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         9. Sansanvation
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FRAGMENT TYPE:
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                                                                                                      GENERAL INFORMATION:
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DIFFERENTIALION ANTIGEN BINDING SPECIFITY AND CLOTTING FACTORS V AND VII LIGHT-CHAIN HOMOTOGIES, FUSION PROTEIN, POLYMPLEPTIER AND POLYBED NUCLEOTILE ENCODING THE POLYPEPTIDE, ANTI-
APPLICANT: LETERSON, TEREY A
APPLICANT: LEADOCCA, DAVID J.
TITLE OF INVENTION: GLOBULE (HMFG) ANTIGEN, FRAMENTS & FUSION PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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POLYPEPTIDE ANTIBODIES, KITS AND METHODS OF
USE THEREOF
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100.0%; Pred. No. 0.053;
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                                                                                                                                                                                                                                                                                                                            SOFTWARE: Fast SEQ for Windows Version 2.0
CUMPENT APPLICATION DATA:
APPLICATION NUMBER: US/08/162,402B
                                                                                                                            ADDRESSEE: Pretty, Schroeder & Poplawski
STREET: 444 South Flower St., 19th Floor
CITY: Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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_U3-DEC-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 2, Application US/07607538C
; Patent No. 5455031
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                                                                                                                                                                                                                                                                                              IBM Compatible
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                                                                                                                                                                                                                                                                                                                 DOS
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TELEFAX: 213-489-4210
                                                                                                                                                                                                                                                                            Diskette
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                                                                                                        CORRESPONDENCE ADDRESS:
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STATE: Californ's
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                                                                                     NUMBER OF SEQUENCES:
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TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: unb
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TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM:
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APPLICANT: LAROCCA, DAVID J.
TITLE OP INVONTION: 46 KFALTON HIMMAN MILK FAT
TITLE OP INVONTION: GLOBULE (HMPG) ANTIGEN, PRAGMENTS & FUSION PROTEIN
                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                               Coery Match 100.0%, Score 46, DB 2, Longtl 218; Best Local Similarity 100.0%; Pred. No. 0.053; Matches 9; Conservative 0; Mismatches 0; Indels
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AFFLICATION HOMBER: 05/08/167,4028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Pretty, Schroeder & Poplawski
STREET: 444 South Flower St., 19th Floor
CITY: Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence E. Application 95,09162402E
Patent No. 5972337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amzel, Viviana
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                                                         INFORMATION FOR SEC ID No: 2:
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IBM Compatible
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TELEPHONE: 213-622-7700
                                                                                                 218 amino acids
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                                                                           SEQUENCE CHARACTERISTICS:
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                     TELEFAX: 213 489-4210
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                                                                                                                                                                     MOLECULE TYPE: peptide US 08-162-4028-2
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PRIOR APPLICATION DATA:
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Rust Lucal Similarity
Matches 9, Conserv
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                                                                                                                                 STPANDEDNESS:
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                                                                                                                                                       TOPOLOGY:
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APPLICANT: PETERSON, JERRY A.
APPLICANT: LAFOCCA, DAVID J.
TITLE OF INVENTION: GLOBULE (HMFG) ANTIGEN, FRAGMENTS & FUSION PROTEIN
NUMBER OF SEQUENCES: 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 46; DB 1; Length 218; 100.0%; Prod No 0.053; tive 0; Mismatches 0; Indels
                                                                                       SOFTWARE: Patentin Pelease #1.0, Version #1.25 CURRENT APPLICATION DATA:
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444 South Flower St., 19th Floor
                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
                                                                                                                                                                                                                         RECISTRATION NUMBER: 30,930
REPERENCE/POTET NUMBER: PERSONAL TELECOMMUNICATION INPORMATION:
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FILING DATE: 03-DEC-1993
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TELECOMMUNICATION INFORMATION -
                                                                                                                                                                                                                                                                                   (510) 943-1931
(510) 943-1189
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IBM Compatible
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                                                                                                                                                                                                                                                                                                                                                                               218 amino acids
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MOLECULE TYPE: profein
FRAGMENT TYPE:
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               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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CLASSIFICATION: 435
                                                                                                                               APPLICATION NUMBER.
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                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: sin
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APPLICANT: PETERSON, JERRY A.
APPLICANT: ASOCCA, DAVID J.
TITLE OF INVENTION: 46 KDALION HUMAN MILK FAI
TITLE OF INVENTION: GLORULE (HMFG) ANTIGEN, FPAGMENTS 6 FUSTON PROTEIN
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APPLICANT: CERIANI, ROBERTO L.

APPLICANT: PETERSON, JERRY A.

APPLICANT: LAROCCA, DAVID J.

TITLE OF INVENTION: GLORULE (HMFG) ANTIGEN, FPAGMENTS & FUSTON PROTEIN
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SOFTWARE: Fast.SEO for Windows Versian 2 0
CURRENT APPLICATION DATA:
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444 South Flower St , 19th Floor
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CLASSIFICATION:
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; Patent No. 5972337
                                                                                                                     Sequence 8, Application US/08162402B
Patent No. 5972337
GENERAL INFORMATION:
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TELEPHONE: 213-622-7700
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Rest Local Similarity 160.00
Ens 9: Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 213-489-4210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SS unknown
unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                 Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: peptide US-08-162-402B 8
                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 2 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PEGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                             STREET. 444 ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM:
                                 194 NLFETPVEA 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            272 NLFETPVEA 280
1 NLFETPVEA 9
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                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amze
                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                            90071
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                    US-08-162-402B-8
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APPLICANT: CEPTANT, POREPTO L.
APPLICANT: PEFFERSON, JEPRY A
APPLICANT: LAMOCCA, DAVID J.
TITLE OF INVENTION: GLORULE (HMFS) ANTICEN, FRAGMENTS & FUSION PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 37, DB 2, Length 159,
Fred. No. 2.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   l, Indels
                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: 18,208,116,402B FILING DATE: 03,002-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
NUMBER OF SEQUENCES: 29
CORPRESCES: ADDRESS: ADDRESS: ADDRESSE: Pretty, Schroeder & Poplawski
STREET. 444 South Flower St., 19th Floor
CITY: Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Pretty, Schroeder & Poplawski
444 South Flower St., 19th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1, Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: P66 38215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JMBEK: US/UN/162,402B
03-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 26, Application US/00152402B
; Patent No. 5972337
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                              30,930
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION POP SEQ ID NO: 12: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80.4%;
77.8%;
                                                                                                                                                                                   IRM Compatible
                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Diskette
IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFRONE: 213-622-7700
TELEFAX: 213-489-4210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 159 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 77.8°
Matches 7, Conservative
                                                                                                                                                                                                           DOS
                                                                                                                                                                      Diskette
                                                                                                                                                                                                                                                                                                                                                                                              Amzel, Viviana
                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READARLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 444 cc. STREET: Los Angeles
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FILLING DATE: 03-DEC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
                                                                                                                                                                                                       OPERATING SYSTEM:
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OPERATING SYSTEM:
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                                                                                                                USA
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                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                             90071
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                                                                                            CA
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US-08-162-402B-26
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                                                                                                                COUNTRY:
                                                                                                                                                                                     COMPUTER
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Gaps

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APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
TITLE OF INVENTION: CADHERIN. MEDIATED FUNCTIONS
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IIILE OF INVENTION. Polypeptides and Their Uses
                                                                                                                                                                                69.5%, Score 3., DB 4, Length 306;
66.7%, Fred. No. 51,
tive 2, Mismatches 1, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 67.4%; Score 31; DB 4; Length 108; Best Local Similarity 75.0%, Pred. No. 25; Matches 5; Conservative ; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE, SmithKline Reecham Corporation STREET: 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CUPPENT APPLICATION NUMBER: US/04/187,859A CURRENT FILING DATE: 1998-11-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 344, Application US/08936165A Fatent No. 6348582 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                    , Sequence 40, Application US/U918/859A
, Patent No. 6358920
, GENEFAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Nicholas, Richard APPLICANT: Pratt, Julie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Reichard, Richard AFFLICANT: Rosenberg, Martin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AFFLICANT. Lonetto, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Black, Michael APPLICANT: Burnham, Martin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Blaschuk, Orest W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  payid
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                           306 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Hodgson, John APPLICANT: Knowles, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 4052
SOFTWARE: Patentin Ver 2 0
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                                                                                                                                                                                                                          6; Conservative
    SEQUENCE CHARACTERISTICS:
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STATE: PA
                                                                               ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-584-008A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 53
COPPESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Mus musculus
US-09-187-859-40
                                            TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                  Query Match
Best Local Similarity
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205 NLFDTTVDA 213
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                                                                                                                                                                                                                                                                1 NLFETPVEA 9
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73 LYEIPVEA 80
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                                                                                                                                                                                                                                                                                                                                                                                 US 09 187 859-40
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                           LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEO ID NO 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                        78 3%; Score 36; DR 2; Length 14; 75.0%; Pred. No. 0.24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0, Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: JACOBSON, PRICE, HOLMAN & STERN
The Jenifer Eqilding, 400 Seventh St
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.JAN-1996
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06-JUL-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Varghese, Joseph N.
APPLICANT: Gartett, Thomas P.J.
APPLICANT: Fincher, Geoffrey B.
APPLICANT: Hoj, Peter B.
APPLICANT: Chen, Lin
TITLE OF INVENTION: BETA-GLUCANAS
NUMBER OF SEQUENCES: B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 8, Application US/08584008A
; Patent No. 6277615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: AU PL9821
FHLNG DATE: 07-JUL-1993
PRIOR APPLICATION DATA: APPLICATION NUMBER: F-T/AH-4.4
                                                                                    Incom.
Viviana
Teo. 30,930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Holman, J.C.
PEGISTPATION NUMBEP: 22,769
                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 213-622-7700
TELEFAX: 213-489-4210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE TRANSKET NUMBER 44
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-638-6666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                            REFERENCE, LOCKET NUMBER:
                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                              LENGIH: 14 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Conservative
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                        unknown
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide
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                                                                                                                     REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                     unknown
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                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
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                                                                                                    Amzel,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20004
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Gaps

us-09-744-804-38.rai

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RESULT 14
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APPLICANT: Bandman, Olga
APPLICANT: Boldi, Surya K
TITLE OF INVENTION: HUMAN MITOCHONDFIAL CHAPERONE PROTEIN
NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67 48, Sector 31, DR 4, Longth 162,
62 58, Prod No 39,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Indels
                                                         OPERATING SYSTEM: DOS
SOFTWARE: FastSop for Windows Version 2.0
SURRENT APPLICATION DATE:
APPLICATION NUMBER 183/1874-0.1165A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
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RECISTRATION NUMBER: 36,749
REFERENCE,FOCKET NUMBER: PF-0245-1 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE 650.875.0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Incyte Pharmaceuticals, inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/971,158
FILING DATE: Herewith
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                                                                                                                                                                                       APPLICATION NUMBER: bujuz7,032
FILING DATE: 24-SEP-1996
ATTORNEY/AGENT INFORMATION:
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FILING DATE: March 26, 1997
ATTORNEY/AGENT INFORMATION:
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Patent No. 6010879
                                                                                                                                                                                                                                                                    38,891
                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
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                                                                                                                      CLASSIFICATION 536
GOR APPLICATION
                                     IBM Compatible
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IBM Compatible
                                                                                                                                                                                                                                                                                                                         TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,
REFERENCE/ixa*KET NUMBER*
                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 162 amino acids
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Rest Local Similarity 62 55
Test Local Similarity 62 55
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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PRIOR APPLICATION DATA:
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MEDIUM TYPE: Diskett
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                                                       OPERATING SYSTEM:
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| 117 NFFDTPAE 124
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                                       COMPUTER:
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APPLICANT: Goli, Surya K.
TITLE OF INVENTION GUMAN MITOMICHERIAL CHAFFRONF PROTEIN
KUMBER OF SPRUENCES. 5
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                                                                                                                                                                                                                               Score 31, DB 3, Longth 217;
Pred No 55;
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SOFTWARE: FastSEG for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: IIS/08/971,158
                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: lucyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PF-0245-1 CIP
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; Sequence 3, Application US/08971158
; Patent No. 6010879
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NAME: Billings, Lucy J.
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TELECOMMUNICATION INFORMATION-
TELEPHONE: 650-855-0555
TELEPHONE: 650-845-4166
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85.74
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                                INFORMATION FOR SEQ ID NO: 1:
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 08/94, FILING DATE: March 26, 19 ATTORNEY/AGENT INFORMATION:
                                                                  217 amino acids
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Hest Local Similarity Rocco.
6. Conservative
                                                 SEQUENCE CHARACTERISTICS:
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TELEFAX: 650-845-4166
                                                                                                  single
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US-08-971-158-3
                                                                                                                                                COLNNOTOB
                                                                              TYPE: amino acid
                                                                                                                linear
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STRANDEDNESS: sir
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Rest Loral Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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CLUNE: 1844121
US-08-971-158-1
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                                                                                                                TOPOLOGY: line IMMEDIATE SOURCE:
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178 LFHTPVE 184
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                                                                  LENGTH;
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GenCore version 4.5
Copyright (c) Pass - 2000 Compuges Ltd.
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OM protein - protein search, using sw model

(without alignments) 6.310 Million cell apdates/sec September 5, 3302, 15,26-30 , Search time if K 4 / Seconds Pute ce.

US-Û9-744-804-38 46 1 NIFETPVEA 9 Title: Perfect score· Sequence

BLOSUM62 Gapop 10 0 , Gapext O 5 Scoting table:

747574 seqs, 111073796 residues Searched.

Total number of hits satisfying chosen parameters.

Maximum DB seq length: 200000000 Minimum DB seq length: 0

Maximum Match 1008 Post-provessing: Minimum Match 0%

A\_Geneseq\_032802:\* 1: /SIDS1/grgdata/l Database :

Listing first 45 summaries

SIDSI/gradata/hold-grass-grassegrassegrammit,/AN1983.181.\*
SIDSI/gradata/hold-grassegrassegr-empt/AA1984.DAT;
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SIDSI/gradata/hold-genesegraenesegr-empt/AA1981.DAT;
SIDSI/gradata/hold-genesegraenese /SIDSI/gegdata/held-geneseq/geneseqp---mbl/AA1990 DAT-\* /STBS1/goddata/hold-geneseq/geneseqr-embl/AA1992.DAT:\*/SIDS1/gogdata/hold-geneseq/geneseqr-embl/AA1992.DAT:\* /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1993.DAT:\*/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1994.DAT:\* /STEST/gradata/huld-gradseq/geneseup-emb1/AA1980.1A1.\*/STEST/gradata/holid-geneseq/geneseup-emb1/AA1981.EA1.\*/SIDST/gedata/holid-geneseq/geneseqp-emb1/AA1982.EA1:\* 

/SIDSI/gogdata/hold-genesel/genesegfrend)/AAzhim (ATEA/SIDSI/gogdata/hold-genesel/genesegfrend) /AAzhim (ATEA) Pred No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/SIDS1/jeydata/hold-geneseq/geneseqp-embl/AA1996.DAT:\* /SIDS1/gcgdata/hold-geneseg/genesegp-embl/AA1998\_DAT·\* /SIDS1/gcgdata/hold-geneseq/genesegp-embl/AA1999\_DAT \*

/SIDSI/gogdata/hold-geneseq/genesegp\_embl/AA1995

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### SUMMARIES

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Result		Query				
ON .	41.78	Match	- Match Tength DB	五	IC	bescription
-	46	106 û		Ξ;		Lactadheric (BA-46
CI	46	100.0		-	AAE77253	HMFG 46 kDa antige
m	46	löö.u		q Ţ	AAK77.54	HMFC 46 KDa antige
4	46	100.0		15	AAR77252	HMFG 46 kDa antige
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9	38	83 V		C1 C1	AAREJE94	ABC1 protein exter
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8	38	4 78		71 74	AAHU2144	Himan ARC1 mutant
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11	38	82.6	2130	C1	AAU02190	Human ABC1 mutant

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13	38	82.6	2201	ç.;	AAY79380	Human	ATP binding
1.4	ž	a L	10.11	ŝi	AAE1 021	Human	ATP binding
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16	38	C1	2259	21	AAB38107	Human	ABC1 FHA-3 m
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97	38	3. 7. 2.	2251	17	AAB38105	Human	ABC1 cholest
Ξ,	Ť	is a	[477	7,	AARERIOG	Human	ARCI cholest
C1	တ	9.29	2261	21	AAB38110	Human	ABC1 cholest
e e	3.8	82.6	2261	21	AAE38111	Human	ABC1 cholest.
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r)	38	82.6	2261	21	AAB38113	Human	ABC1 cholest
95	3,5	30 1,1	1377	21	AAB38114	Human	ABC1 cholest
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Ô۶	Σ,		1977	ĵ:	AAP1 4000	Human	ATP binding
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33	3.5	r	(977	7	AAH02176	нимаг	APril Homo
	38	82.6	2261	C	AAU02177	Human	ABC1 mutant
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36	38	82.6	2261	C1	AAU02182	Human	ABC1 mutant
ار در	38	8.1.6	1777	71	AAU02183	Human	ABC1 mutant
30 (1	38	8.1.6	1377	74	AAUUZlae	Human	ABC1 mutant
39	38		2261	급	AAU02188	Human	ABC1 metant
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- T	38	82.6	2261	<u>(1)</u>	AAB71749	нашал	ABC1 protein
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۲.	Ξ. .~	2	19::	(1) (1)	AAB31365	An.inc	acid sequenc

# ALIGNMENTS

Lartadherin (BA-44) peptide fragment (tumour associated antigen). AAYRZR4 standard; poptide; 9 AA. (first catry) 19 JUN 2000 AAY82843; AAY82843 KESULT 

teratocarcinoma derived growth factor; PSA; PSMA; PAP; CRIPIO-1. Tuneor assectiated antigen peptide; IAA, causer, carcinoma; treatment; prevention; ours, anti-timent vaccine; metastases; breast, brader, prestate, janetees; evary, thyroid; colon; stomach; carcinoma; MHC Class I; HLA A2; human; Mistocompatibility Complex; uroplakin; prestate specific antigen; prestate specific antigen; prestate specific membrane antigen; prestate acid phosphatase; mucin; lactadherin;

Homo sapiens.

Woz00006723-A1.

10 FEB 2300.

99WO-1L00417. 29-JUL-1999; 98IL-0125608. 30-JUL-1998;

(YEDA ) YEDA EES & DEV 30 LTD. (HIOT) RIO-TECHNOLOGY GEN CORP.

Bar haim E, Faz A, Fridkin M; Eisenbach L, Carmon L, Tirosh B, Fitzer-attas C;

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used in assays to determine the presence of a cancerous tumour of
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27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tumour associated antique peptides (TAA) may be used for the treatment, prevention and cure of cancer or cancer metastases. The cancer metastases. The cancer metastases The cancer may be breast, bladder, prostate, particles, ovary, thytoid, colon, stomach, head or neck cancer or a carcinoma. The tumour associated antiques are presentable to the immune system by HLA-A2 molecules and are generally between 8 to 10 amino acids in length. The e tumour associated acid antigens are described in records AAY82805-YR28820 are derived from Uroplakin 24. Uroplakin 14. Uroplakin 14. Uroplakin 17. Those described in records AAY82805 are derived from prostate specific antigen (PSA). Those described in records AAY82805 are derived from prostate acid phospholase (PAP). Those described in records AAY82805 are derived from accounts AAY82805 are derived from accounts AAY82805 are derived from prostate acid phospholase (PAP). Those described in records AAY82807 are derived from lactadherin (BA-46). Those described in records AAY82807 are derived from and those described in records AAY82807 are derived from mactadherin and those described in records AAY82807 are derived from mactadherin and those described in records AAY82807 are derived from general are derived from Seconds AAY82807 are derived from accounts AAY82807 are derived from general are derived from Seconds AAY82807 are derived seconds AAY82807 are derived seconds AAY82807 are deri
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0
                                                                                                                                                                                   Tumor associated antigen peptides, especially derived from uroplakin,
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epithelium; tumor, breast cancer, monoclonal antibody; MAb.
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                                                                                                                                                                                                                                                        useful as vaccines to prevent or cure cancers including breast, bladder, prestate, practices, every, thyrold, evolutional stomach \tau
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 17; Page löö; il⁴pp∙ English
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Processory
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HMFG, human milk fat globule, astiges, immusegen; vaceine, virucide; epithelium, tumor; breast cancer; monoclonal antibody; MAb.
                                                         A Fortial classificate MANGEL (AAGG183) for the 45 kbs HMIC antigen, a major component of the apical surface of the normal breast epithelial cell, was obtained by POP of CDNA from a lactating breast CDNA library. The C-terminal region of the encoded protein showed 43% identity to corresp. regions of human Factor-V and 38%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A partial cEMA close EA45-1 (AAQ31195) for the 45 kFs HME3 unligen, a major component of the apical surface of the normal breast epithelial cell, was obtained by PCR of cDNA from a lactating
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                                                                                                                                                                                                                                                         0;
epithelial origin, and in a vaccine against neoplastic tumours
                                                                                                                                                                                                                         Sector 46, 198-16; Longth 217;
Pred No. 0.19;
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/label=_N-glycosylation_site
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/label N-glycosylation_site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HMFG 46 kDa antigen partial sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 7; Page 38-40; 68pp; English.
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                              Claim 7; Page 41; 68pp; English.
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Matches 9; Conservative
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                                                                                                                                                                          217 AA;
                                                                                                                                                                                                                                                                                                         1 NLFETPVEA 9
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31-MAY-2000.
  AAY94453;
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                                                                                                                    Pept.ide
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                                                                                                                                                                                                                                        HMFG; human milk fat globule; antigen, immunoqen, vaccine; virucide; epithelium; tumor; breast cancer; monoclonal antibody; MAb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A complete CDNA septence for the 46 KDa HNFG antiqen, a major component of the apical surface of the normal breast epithellal cell, was obtained by PCR and RACE methods. CDNA clones can be used to proper: MANS for use in immunotherapy, immunotherapathology, prognosis, imaging and therapy. Recombinant antigen can
                                                                                                                                                                                                                                                                                                                                                                                                                                          46 kD apparent molecular weight human milk fat globule antigen used in assays to determine the presence of a cancerous tumous of epithelial origin, and in a vaccine against neoplastic tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             prognosis, diagnosis, imaging and therapy. Recombinant antigen of be expressed in prokaryotic or (9)posylated) in eskaryotic or18.
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                                               100.0%; Score 46; DB 16; Length 218; 1c0.0%; Pred N. 0.19; Cive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                            Larocca DJ, Peterson JA;
                                                                                                                                                                                                                                                                                                                                                                        (CANG-) CANCER PPS FUND CONTRA COSTA.
                                                                                                                                                          AAR77252 standard, Frutein, 387 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY94453 standard; Protein; 387 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 6; Page 46.47, 68pp, English
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                                                       Best Local Similarity 100 Matches 9; Conservative
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breast cDNA library.
                                                                                                                                                                                                                     HMFG 46 kDa antigen.
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Best Local Similarity
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                     Sequence 218 AA;
                                                                                                  1 NEFETPVEA 9
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                                                                                                                                                                                                                                                                                                                                                                                            Ceriani RL,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chimeric isolated (human) lactadherin polypeptide that functions as an adaptor of cross priming to eliminate pathogenic antiqens, e.g. in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lactadherin protein was found in exosomes produced by dendritic cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= Integrin_binding_site
                                                                                                                                                                                                                                                                                                                                                 /label= Secretion_signal
                                                                                                                                                                                                                                                                                                                                                                        24..387
/label= Lactadherin
46..48
                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 4, Puge 12; 20pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98EP 0402925.
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                                                                                                                       Human, lastadherin, MGF-F8,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
11-SEP-2000 (first entry)
                                                              Human lactadherin protein.
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                                                                                                                                                           exosome; dendritic cell.
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Best Local Similarity
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                                                                                                                                                                                                                          Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Binding Site
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RESULT
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                                                                                                                                                                                                                                                                 The invention relates to a new method for inhibiting cholest-rol uptake in the gut that comprises administration of an inhibitor of an ARCI protein. The method is useful for: lowering levels of LDL (low density lip-qrivity) shalester of by teducing the activity of ABVI protein in the intestinal cells and the absorbance of the ARVI protein in the information that absorbance of the ARVI protein in the individual by inhibiting the activity of the protein; identifying drugs that can bown choiseterol and LDL levels comprises assaying the drug to test if it can bind to an ABVI protein; testing LDL cholesterol lowering agents; and for modulation of ABVI phological activity Sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABC1, antilipemie, cholesterol, inhibitor, low density lipoprotein; LDE.
        ARCT: antiliperie: choiesterol; inhibitor; low density lipoprotein; LbL
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                                                                                                                                                                                                                New method for inhibiting cholesterol uptake in the gat comprises administration of an inhibitor of an ABC1 protein \dot{z}
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                                                                                                                                                               Cook M, Gray-Keller MP, Hayden MR, Pimstone S;
                                                                                                                                                                                                                                                                                                                                                                                                              82.5%; Secre 38; DB 22; Leggth 26; illarity 87.5%; Pred, No. 0.82; Conservative 1, Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                    0, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB62691 standard; Protein; 1089 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human ABC1 protein partial fragment
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                                                                                                                                          (WISC ) WISCONSIN ALUMNI RES FOUND
                                                                                                                                                                                                                                               Disclosure; Page 9, 41pp; English.
                                                                                                              99US-0162803.
                                                                                                                       NO-JUN-2000; 2000US-0215564.
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                                                                                         01-NOV-2000; 2000W0-HS30109
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                                                                                                                                                                                             WPI; 2001-335779,75
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                                                                                                                                                                         Brooks Wilson A,
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|4 nlfespve 21
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                              Homo sapiens
                                                                                                             01 -NOV - 1999;
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The invention relates to a new method for inhibiting chalestered sprake in the gut that comprises administration of an inhibitor of an ABC1 problem. The method is useful for: lowering levels of IDL (low density lipoprotein) cholesterol by reducing the activity of ABC1 protein in the intestinal cells and the abundance of the ABC1 protein in the individual by inhibiting the activity of the protein, identifying drugs that can lower serum cholesterol and IDL before, comprises assaying the drug to test if it can bind to an ABC1 protein, resting IDL cholesterol lowering agents, and for modulation of ABC1 biological activity. The present sequences tepresents a homen ABC1 protein partial fragment.

Note: Pages containing part of the present sequence secuns to be missing from the specification; the protein secuns to contain at least 2261 amino acid residues as found by translating the corresponding DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human, ABCl gene; atheroscietosis, reverse transport, cholesterol; cardiovascular; neurological, Tangier disease, LCAT deficiency; mutant; lecithin-cholesterol acetyltransferase; malaria, diabetes; mutein.
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Duverger N, Jaye M, Scarfoss CH, Remaley A, Brewer HB;
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                                                                                                                                                                                           New method for inhibiting cholesterol uptake in the gut comprises administration of an inhibitor of an ABCl protein \,
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Pinstone S;
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   Hayden MF,
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Pred. No.
Gray-Keller MP,
                                                                                                                                                                                                                                                                                        Disclosure; Page 37-; 41pp; English.
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87 58.
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es 7, Conservative
                                                                                            2001 335779/35.
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                                  Brooks-Wilson A;
                                                                                                                              PSDB; AAF83826
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Lemoine C.
Dean M.
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atherosclerosis, malaria and diabetes
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                            Claim 46, Page 287 293; 368pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU02187 standard; Protein: 1525 AA.
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                                                                                                                                                                                                                                                                                  Query Match
Bost Local Similarity 87.55
Fost Local 7, Conservative
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                                                                                                                                                                                                                                                     Sequence 1144 AA;
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AAU02187
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 The sequence represents the amino acid sequence of human ABCI mutant polypeptide #8. The polypeptide and nucleic acid sequence, primers and probes derived from the ARCI sequence, and vertors are useful for the prevention of atherosciences; in a subject attected by a dystunction in the reverse transport of chalesterol. The polypeptide encoded by the ABCI gene is useful for screening for an active instead of the reverse resulting from dysfunction in the reverse transport of a disease resulting from dysfunction in the reverse transport of cholesterol. The upoleic acids and polypeptides are also useful for treating and preventing cardiovascular and neurological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human, ABCI gene, atheroscherosis, reverse transport; cholesterol;
cardiovas.ular, neurological, Tanglet discase, 1947 deficiency; mutant,
lecithin-cholesterol acetyltransferase, malaria, diabetes; mutein.
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Duverger N, Jaye M, Searfoss GH, Romaley A, Brewer HB;
                                                                                                                                                                                                                                                                                                                                                                                                                  Saps
                                                                                                                                                                                                                                                                                  pathologies, and other diseases e.g. Tangier disease, lecithin-cholesterol (LCAI) deficiency, malaria and diabetes.
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                                                             New human ABC1 nucleic acids and polypeptides for treating
                                                                                                           Claim 46; Page 281-287; 368pp; English.
                                                                              atherostlerusis, majaria and diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU02185 standard; Protein; 1144 AA.
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01-MAR-2000; 2000US-0186260.
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les 7; Conservativo
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              WPI; 2001-316327,33.
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                               N-PSDB; AAS06132
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Lemoine C,
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the reverse transport of cholesterol. The polypeptide encoded by the ABC1 determined for several for an active induction. Ltd. the privention of treatment of adsease resulting from dysfunction in the reverse transport of cholesterol. The number edids and polypeptides are also
                   polypephide #9. The polypephide and nucleic acid sequence, primers and probes derived from the ABCI sequence, and vectors are useful for the prevention of atherosclerosis, in a subject affected by a dysfunction in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; ABCl gene; atheroselerosis; reverse transport; cholesterol; cardiovascular; nearclogical; Tangior disease;, LCAT deficiency; mutant; lecithin-cholesterol acetyltransferase; maiaria; diabetes; nutein.
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Jaye M. Searfoss GH, Remaley A, Brewer HB;
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The sequence represents the amino acid sequence of human ABC1 mutant
                                                                                                                                                                useful for trouting and preventing cardicularmilar and neurological pathologics, and other diseases e.g. Tangler disease, lecithin-cholesterol (LCAI) deficiency, malaria and diabetes.
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                                                                                                                                                                                                                                                                                                        82.6%; Score 38; DB 22; Length 1144;
87.5%; Pred. No. 45;
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                                                            the reverse transport of cholesterol. The polypeptide encoded by the ABC1 gene is useful for screening for an active ingredient for the prevention or treatment of a disease resulting from dysfunction in the reverse transport of cholesterol. The incleic acids and polypeptides are also useful for treating and preventing cardiovascular and neurological
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probes derived from the ARTI sequence, and vectors are useful for the prevention of atherosclerosis, in a subject affected by a dysfunction in
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cardiovascular, neurological, Tangier disease;, LCAT deficiency, mutant,
lecithin cholesteroi acetyltransferase; malaria, diabetes, mutein.
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Duverger N, Taye M, Searfess GH, Pemaley A, Prewer HB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ö;
                                                                                                                                                                                                                                      pathologies, and other diseases e.g. Tangier disease, lecithin-
cholesterol (17A1) deficiency, mainta and diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 22; Length 1525,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ů; indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 atheroselerosis, malaria and diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU02190 standard; Protein; 2130 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human ABC1 mutant polypeptide #14.
                                                                                                                                                                                                                                                                                                                                                                                                                                         87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2000; 2000US-0185260.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-ОСТ-2005; 25000WO БР] Эййк
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12 SPP 2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (AVET ) AVENTIS PHARMA SA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference 2112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-316327/33.
                                                                                                                                                                                                                                                                                                                                     1525 AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Hest Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 NLFETPVE 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Denefle P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lemoine C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAU02190;
                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human ABC1 cholesterol fransportor, chromosome 9931;
ATF binding cussette, #DL deficiency Afserder, Eigh density lipspretein;
Tangier disease, TD; familial HDL deficiency; FHA; polymorphism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X-linked adrenoleukodystrophy; cancer; gene therapy; genetic diagnosis;
prognosis, prophylaxis, drug screening, transpenic animal; mutant;
transport of cholestorn). The north-ic acids and polypoptides are also useful for treating and preventing cardiovascular and neurological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cardiovascular disease, coronary aftery disease, coronary realemosis; cerebrovascular disease; peripheral vascular disease; Alzheimer's disease; Niemann-Pick disease; Huntington's disease;
                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Now ABC1 polypoptide is useful for treating diseases associated with ABC1 biological activity, e.g. Alzheimer's disease, Huntington's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human ARC1 cholesterel transporter PHA-1 mutant protein (R2144STOP).
                                                                                                                                                                                             0;
                                        pathologies, and other diseases e.g. Tangier disease, lecithin-
cholesterol (LCAT) deficiency, malaria and diabetes.
                                                                                                                                                       State 3P, DR 22, Langth 2130;
Pred, No. 88;
                                                                                                                                                                                             1ndels
                                                                                                                                                                                             0,
                                                                                                                                                                                               1, Mismatches
                                                                                                                                                                                                                                                                                                                                                                        AAB38108 standard; Fretein; 2143 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hayden MR, Wils∪n AR, Pinstone SN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Examples; Page -; 229pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HYRR-) HNIV BRITISH COLUMBIA
                                                                                                                                                       82 (1)
87.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (XENO-) XENON BIORESEARCH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            990S-0138048.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-JAN-2001 (first entry)
                                                                                                                                                                                               7, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      disease and cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPT: 2000-587528755
                                                                                                2130 AA:
                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                          808 nitespve 815
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                                                                                                                                                                                                                                   1 NLFETPVE 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-SEP-2000
                                                                                                    Seguence
                                                                                                                                                                                                                                                                                                                                                                                                             AAB38108;
                                                                                                                                                         Eures y Materit
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                                                                                                                                                                                               Matches
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are distinguishable in that TD is an autosomal iccessive disorder, while PHA is inherited as an autosomal dominant trait. Tow levels of HDL ("good choesterol") in the blond correlate with a high lish of cardiovascular disease, particularly 'nentry disease, but also cerebrovascular disease, coronary restencies, and peripheral vascular disease. Conversely, a high level of HDL has protective effects against cardiovascular disease.
                                                                                                                                                                                                                                                                                                                                                             cerebrovascular disease, coronary testenosis or peripheral vascular disease. They may also be used in the treatment of diseases associated with ABC1 biological activity, such as Alrhelmer's disease, Nichann-Fick disease, Huntington's disease, X-linked adrenol-wkodystrophy and cannot Fick the throation specifically excludes pendins with the ward animo acid sequences of general Acression No 'AADHOUN', and XYSVA, and the public acid with the exact sequence as GenBank Acression No ADD1376 1 The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                present sequence represents a mutant human ABC1 choisesterol transporter associated with an altered cholesterol level and therefore an altered
                                                                                                                                              transgents cells and non-homan animits compristing bumon ARC1 morboic acids, and mothods of your therapy for the treatment or prevention of cardiovascular disease comprising the administration of an expression vector exceding ABC1 or an active fragment thereof. The invention also
                                                                                                                                                                                                                                stimulate ABC1 expression and methods of screening for such compounds which stimulate ABC1 expression and methods of screening for such compounds. It further relates to methods for determining whether a patient has an increased risk for cardiovascular disease due to polymorphisms in the ABC1 gone. Haman ABC1 proteins and nucleotides can be used to treat or prevent cardiovascular disease, especially consular uttery disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Note: The present sequence is not shown in the specification, but is derived from the native human ABC1 shown on pages 152\cdot157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   interleukin-1 beta, transporter, inflammation; septir shook; freductiod atthicks: Tangler disease, hypothiglycetidemia, splenomegaly; attheresteris; lipid disease, dyslipidemia, psoriasis, lupus etythematosus; diagnosis; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82 f8, Saara 29, PR 21, Length 2143,
87.5%; Pred. No. 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABCAl; ABCl; ATF binding cassette, human, cholesterol,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human ATP binding cassette ABCA1 (ABC1) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 88;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY79380 standard; Frotein, 2201 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             risk of cardiovascular disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99WO-EP06991,
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Best Local Similarity 87.55
and 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2143 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      808 nlfespve 815
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Human, ATP binding cassette transporter 1, ABC1, coronary heart disease,
                                                                                                                                                         AbcAl (ABCl), the human homologue of mouse ABCAl (94% identity). The sequence was deduced from ABCAL cDNA (see AAS94/54), identified in a differential servering of luman measowers for cholesteric seasitive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          dermatological, atherosclerosis; cardiovascuiat, infiammatory disease, psoriasis, lipid disorder, antibacterial, septic shock, gene therapy, immunosuppressive, lupus erythematosus; rheumatoid arthritis.
                                                                                                                                                                                                                                                                             splenomegaly. ABCAL is also a transporter for interleukin-1 beta, making the gene a candidate for treatment of infiammatory diseases such as the manacola arthritis and sective shock. The invention also provides other coolesterol sensitive AMC genes (see AAZ94775-63) that can be used for diagnostic and therapeutic applications, and for biochemical or cell-based assays to screen for pharmonically artive remaining assays to screen for pharmonically artive remaining assays to screen for pharmonically artive remaining assays are the treatment of such as psoriasis and lupus crythematosus.
                                    Adenosine triphosphate binding proteins useful for identifying agents for treating atheroscierosis and other infimumatory disorders ^{\circ}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                    The present asspecie is that of human AFP binding cassette protein
                                                                                                                                                                                                                     genes, the ABCAL gene maps to chromosome Systral, orstegulated ARCAL is the gene longs involved in the His definitions syndrome Tangier disease, associated with hypertriallyceridemia and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82.6%; Score 38; DB 21; Length 2201;
87.5%; Pred, No. 91;
17ve 1; Mismatches 0; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Encoded by AAC"
                                                                                             Claim 6, Page 94 105, 154pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pest Local Similarity 87.5
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2201 AA;
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N-PSEB; AAS94734
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The invention relates to four symmem polymorphisms in the gene considing decreased Apost mediated efflux of choiseterol. The polymorphisms in ARP1 directly affects setliar lipid boundstack. The polymorphisms in the atherogenetic processes the ARC1 polymorphisms are useful for diagnosing and treating lipid disorders, cardiovascular diseases coronary heart disease, atheroseletosis) and inflammatory diseases (psociasis, jupus erythematosus). The identification of ABC1 as a transporter for interleakin-libeta (IL-libeta) identification of ABC1 as a candidate for interleakin-libeta (IL-libeta) identification peneral acadidate for interleakin-libeta (IL-libeta) identifies this gene as a candidate for interleakin-libeta (IL-libeta) identifies this spene as a candidate for interleakin-libeta (IL-libeta) identifies this spene as a candidate for interleakin-libeta (IL-libeta) identifies this peneral architician and septic shock the present sequence is basen ABC1 protein
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                 New adenosine triphosphate binding cassette transporter: T gene polymorphisms, useful for diagnosing and treating lipid disorders, cardiovascular diseases and inflammatory diseases.
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                                                                                                 Claim 8, Laye 23 29, 48pp, Edlish.
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N-PSDB; AAI70314.
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may affect its function. The 2 most common polymorphisms are both associated with a decreased in vitro ApoA-1 mediated cfflux of Tanger the last and the second from moneous last are significantly increased in a population of men having low high density lipoprofein-cholesterol acceptablished coronary bent disease (CHP) relative to CHP relative to CHP relative to the displacts. The use of the provided ABCI polymorphisms for the displacts and transment of lipid diseases, and displacts are relatively diseases, and inflammatory diseases (e.g. psoriasis) lupus exploning by antisease of the provided BBCI transcripts or proving by antisease or the control of ABCI transcripts or proving by antisease or the control of ABCI transcripts or proving by antisease or the control of ABCI transcripts or proving by antisease or the control of ABCI transcripts or proving the control of ABCI transcripts or proving the control of ABCI transcripts or proving the control of ABCI transcripts or the control of ABCI transcripts and control of ABCI transcripts or the control of ABCI transcripts and control o
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Search completed. September 5, 2002, 15:26:31 Job time: 371 sec

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Copyright (c) 1993 - 2000 Compuger Ltd.

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September 5, 2002, 15:28:51; Search time 69:78 Seconds (without alignments) 12:393 Million cell updates/sec

US-09-744-804-38 1 NLFETFVEA 9 Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283138 seqs, 96089334 residues Searched: Total number of hits satisfying chosen parameters:

Maximum DB seq length: 200000000 Minimum DB seq length: 0

Post-processing: Minimum Match 0%

Listing first 45 summaries Maximum Match 100%

pirl:\*
pirz:\*
pir3:\* PIR\_71:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

		*			SUMMARIES	
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m	3.7	80.4	381	Cŧ	AC2631	تد
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근 전	9.69	571	<b>C1</b>	101511	hypothetical profe
ci e	69.69	744	C1	557061	
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32	63.6	826	~	F89630	protein F59F5.7 [i
្ត	69.6	1363	C 4	158375	Prote.s-tyrosine k

A47285

milk fat globale protein homan (fragment)

C)Species: Homo sapiens (man) C)Species: H-Dec 1993 #sequence\_revision 31-Dec 1993 #1-04\_change 28 May-1999 C; Accession: A47285

Altarosca, D., Feterson, J.A., Urrea, E., Kaniyoshi, J., Bistrain, A.M., Gerlani, R.L. Cancer Res. 51, 4994-4998, 1991
Arither A.M.r. 45,000 human milk lat. globale protein that is highly expressed in huma Arketernore number. A47285; MUID:91:71351
Arketession: A47285
Arstalus: proliminary

Ayolecule type: mRNA AyResiducs: 1-218 <LAR> AyCross references. 0B.856151, R19:q235396; PIDN:AAB19771.1; PID.q225397 Cysuperfamily: milk tat globule protein; discoidin 1 amino-terminal homology; EGF hom 1,1 56/bomain; discoidin 1 amino terminal homology; (tragment) <DNL> F;60-218/Domain; discoidin 1 amino terminal homology; CNL>

C; Gaps 100.0%; Score 46; DB 2; Length 218; 100.0%; Pred. No. 0.048; u: Indels 0; Mismatches 9; Conservative Query Match Best Local Similarity Matches

25 NLFETPVEA 33 : NEFFETEVEN 9

RESULT

Dinin, CS Apr 1935 \*sequence mouse) Glacession: A54774 Eluciani, M.E., Denimit P. C.

Luciand, M.P. Denizit, F.: Carary, E.: Mattel, M.G.: Chimini, G. Octomics 2), 150-159, 1994

A.Title, Closing of two morel ACC transporters mapping on human chromosome 9, A.Fitle, Closing of two morel ACC transporters mapping on human chromosome 9, A. Accession, A54774

A. Accession, A54774

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A. Molecule type: mRAN

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A. Molecule type: mRAN

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E. 1880, 1893/Region: nucleotide-binding molif A (P-loop)

82.6%, Score 38; DB D; Longth 2201;

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C;Species: Bos primigenius taurus (cattle)
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A Residues 1987-394 ** FINA
C Superfamily: milk fat globule protein, discoldin Tamino terminal homotogy; EGF hom
C Superfamily: milk fat globule protein, discoldin Tamino terminal homotogy; EGF hom
C Keywords: blocked amino end; disalfide bond, glyoprotein, milk
E)1-B8/Domain: signal sequence #status predicted sSiG>
E)10-12/Product: PAS-6/7 protein #status experimental **AATS-
F)24-59/Domain: EGF homotogy **EG2>
E)66-105/Domain: EGF homotogy **EG2>
                                          glycoprotein antigen MCP57/53, mammary gland - borine (fragment)
N.Altenade names, 9/Focpfockin somponent 16/major fattglubule membann protein,MEG-E-
C.Species: Bos primigenius taurus (attle)
C.Species: Bos primigenius taurus (attle)
C.Species: Pe-Ort-1998 #seguence_revision 14-Mar-1997 #fext_change 07-Aug-1998
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A president set of 85 and 140-165,174-216,221-232,248-277;285-293,309-337,739-420-425-
A) Freshins Hopkys Acts 1122, 203-211, 1992
B Hischim, Hispkys Acts 1122, 203-211, 1992
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C,Septerfamily, milk fat globule protein, discoldin 1 amino-forminal homology, BGF hom
C,Reywords: glycoprotein
P,1-32,Pommin: BGP homology (fragmont) <BGl>
                                                                                                                                                                                                                                  C)Accession: S65138, G48394
R;Acki, N.; Kishi, M.; Taniquchi, Y.; Adachi, T.; Nakamura, R.; Matsuda, T.
Biochim. Biochims. Acta 1245, 385-381, 1995
A;Ttile—Molecular closing of glycopertein antigens MGP57/53 recognized by monoclonal A;keference number: S65138; MH16:96125736
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A.TILLE: The major fat-globule membrane proteins, bovine components 15/16 and guinea-
11-11ke and the major fat-globule membrane proteins, bovine components 15/16 and guinea-
11-11ke and the member A48394, MHH: 93250576.
A.Reference number: A48394.
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F:82-139/Ecumain: discoidin I amino terminal homology -FM1>
F:243-401/Domain: discoidin I amino terminal homology -EH2>
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A.Molecule type, protein
A.Pesidues, 207 220 -MAT-
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A; Residues: 1-427 <HVA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   conserved hypothetical protein Atu3446 [imported] - Agrobacterium tumefaciens (strain C5
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A;Reference number: A97359; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A)Authors: You, H., Tao, Y.; Biddle, P., dung, M., Krespan, W., Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A)Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58. A)Reference number, AB2577, PMID.11743193
A)Acression: AC2633
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C:Dater II-Jan-2002 #Sequence_revision II Jan-2002 #test_change II-Jan-2002
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G.Comment, This engine catalyses anspecific polyaden/lation.
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C.Late. 11-Jan-1909 #sequence_register 17-Jan 1999 #text_etuge 22 Oct 1999
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A;Map position: 3
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36 Nirespaes 44
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A/Ille. Complete genome sequence of a multiple drug resistant Salmonella enterioa serow
A/R/forence comber ARASO2, FMID.11677658
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A;Proid_was lifer:PAF.
A;Proid_was lifer:PAF.
C;Genetios:
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       P.265-427/Frain, disseldin i aminoriennest heading, #status predicted P.24 35,29-42,49 sk 60-77,21-44,96 105/Fish Fib. Londs, #status predicted P.27/Bitaling site: carbobydrate (Sct.) (covalent) #status experimental P.34/Binding site: carbobydrate (Act.) (covalent) #status experimental P.55,227,Binding site: carbobydrate (Act.) (covalent) #status experimental P.55,227,Binding site: carbobydrate (Act.) (covalent) #status experimental P.109-765,252,252,254,053,170,427,638,17104, P.303, #status experimental
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100 08; Pred No. 21;
tive 0; Mismatches 0; Indels
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Best Local Similarity 100 us
Best Local 7; Conservative
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Trans 6, Conservative
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C:Species: Campylobacter jejuni
C.Date, (1-Mar-1000 #sequence_revision (1-Mar-1000 #text_cbange 31-Mar-2000)
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A;Accession: E81282
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Appress references: EMELSAITX2798, FILMERAECTOS I, ESFIGECTARGERE, SHEESRATIRE IS
A)Experimental source: strain 972h( ); cosmid C222
                                                                                                                                                                                                                                                                                      Ajonoss-references: BMBL 235604; PIDN:CAA84676 1; GSPDR-GNOGO21; CESP-2K1958.1
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submitted to the EMRL Data Library, November 1999
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C.bute. 15.0ct.1393 #sequence_revision 15.0ct.1999 #text_change 04 Mar 2000
C.Accession: T27674
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66.7%; Pred. No. 67;
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                                                                                             submitted to the EMBL Data Library, August 1994
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C.Species. Schizosacctaromyces pombe
?[oute, Gerlun-wöre #septemen_revision Gerlun
                                                                                                                                                                                                                                                                                                                        A;Experimental source, cione 7K1058
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ues 6, Conservative
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A;Introns: 53/1; 78/1; 106/3
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A;Accession: T50155
                                                                                                                            A;Reference number: 220403
A;Accession: T27674
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A; Fesidies: 1 744 -WIL:
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A,Molecule type, DNA
A,PesiJues: 1 269 PAF
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Affile: Molecular relating and characterization of E47, a novel boar sperm-associated on A; Reference number: 217325; MUID:98206817
A; Accession: T11743
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C.Superfamily: bloc homology
F.61-159/Domain: bloc homology
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                                                                                                                                                                                                                                                                                                                                                                                 Riklenk, H.F., Clayton, R.A., Tomb, J.F., While, O., Nelson, K.E., Ketchum, K.A.; Bodson, Prischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.P. Glodek, A.; Phen, I. Gentheck F. Gentymer, T.E., Weichan, T.F., Metechli, L. Nature 390, 864-370, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AlAuthors: Ulterback, T.; Cotton, M.D.; Spriggs, T.; Artlach, P.; Kaine, B.P.; Sykes, S. Smith, H.O.; Noese, C.R.; Venter, J.C.
Affilie: The complete genome sequence of the hyperthermorphilie, sulfate reducing archaem
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C.Dato: 05-lear-1997 #sequence_revision (6-lear-1997 #1ext_-d.arge 21 lul_2usu
C.Acression: 069267
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C:Species: Sus screfa domestica (domestic pig)
C:Dator 16-in}-1999 #scquence_revision 16-in|-1999 #text_cbasge 21-Jul-2000
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C;Species: Caenorhabditis elegans
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A;Molecule type: mRNA
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Gaps

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A:Cross-references: GB:AL149078; GB:AL111168; NID:q6968723; FILM:CAB73803.1; FID:q696881
A:Experimental source: serotype O2, strain NCTC 11168
C:Genetics:
A:Gene: C:1376
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.; Gaps 0 Query Match 71.7%; Score 33; DB 2; Length 269; Best Loral Similarity 75.0%; Pred. No. 34; Matches 6; Conservative 1; Mismatches 1; indels 1 NLFETPVE 8 ||| ||||: 80 NLFNTPVK 87 Š

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105224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100% Maximum Match 100% Listing first 45 summaries

SwissProt\_40.\* Database .

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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## ALIGNMENTS

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   the European Ricinformatics Institute There are no restrictions on its mass by non-profit institutions as loss as its souther is in no way modified and this statement is not renoved. Usage by and for connection entities requires a license agreement (See http://www.isb-sib.ch/announce/
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-1 SIMILARITY: CONTAINS 1 ESP-LIKE PAMAIN

-1 SIMILARITY: CONTAINS 2 ES/A TYPP C PAMAINS
              -!- FUNCTION: MAY HE INVOLVED IN PHOSPHOLIPID BINDING, BINDS SPECIFICALLY TO ROTAVIEUS AND INHIBITS ITS PEPLICATION.
-!- FUNCTION: MEDIN IS THE MAIN CONSTITUENT OF AGRIC MEDIAL AMYLOID.
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MEDIA: OVEREXPRESSED IN SEVERAL CARCINOMAS.
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DNA Cell Biol, 16:861-869(1997).
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PROSTE: PS00022; PCF_1: 1.
PROSTE: PS01186: BCB_2: 1.
PROSTE: PS01285; PA58C_1: 2.
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                                                                                                                                                                                                                                                                             MEDLINE-23345099; FubMed 19884128; Santamarina-Fejo S., Peterson K.M., Knappor C.L., Qin Y., Santamarina-Fejo S., Peterson K.M., Cheng J.-P., Osorio J., Pemana L.A., Cheng J.-P., Osorio J., Radenschild C.C., Prades C., Chimini G., Riackmon E.E., Francois T.L., Duverger N., Rohin E.M., Rosier M., Donetle P., Fredrickson D.S., Brewer H.B. Jr., "Complete genomic sequence of the human ARCAL quae: analysis of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (hBC1): evidence for sterol-dependent regulation in macrophages."; Blochem. Blochys. Res. Commun. 257.29-33(1999).
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                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria; Primates, Catarrhini; Hominidae; Homo.
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"A new topological model of functional buran ABCAl siqual peptide
clearage and glycosylation of a large extracellular domain.";
Submitted (EEB-2061) to the EMPL, Octaback, Time Jatubases.
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Chimini G., Kaminski W.E., Schmitz G.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human and mouse Alb binding cassette A promoter.";
Prio Natl Acad Sci H S A 97:7987-7492(2000).
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MEDLINE-99194549; Pubmed-19092505;
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MEDLINE-99364413; Pubmed-10431238;
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ABCA1 OR ABC1 OR CERP.
                                           Homo sapiens (Human).
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"Age and residual cholesterol efflux affect HDL cholesterol levels and
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MEDISTURE-21157003; PubMod-11257561;
Brousseau M.E., Rodziach M., Schaefer E.J., Goldkamp A.L., Kielar D.,
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Bronss-au M.E., Schaefer E., Thurston L.M., Filisteraid M.C.,

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MEDLINE=20390653; PubMed=10938021;
Mang J., Buitett J R., Near S., Yening K., Zinman B., Haniey A. L.G.,
Connelly P.W., Harris S.B., Hegele R.J.;
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Arteriosoler Thromb. Vaso. Riol. 20-1983-1989(2000)
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                                                                                                                                           VARIANTS TD SER-590; SEP-935 AND VAL-937, AND VARIANTS ALA-399 AND
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Bertolini S., Pisciotta L., Seri M., Cusano R., Cantafora A.,
Calabresi L., Farmo-schini G., Parazzootta F., Calabda S.,
"A point mutation in ABC1 gene in a patient with severe premature coronary heart disease and mild clinical phenotype of Tangier
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MFCIENE-20540402, PubMod 11088-627.
Gloo S. M., Kastelein J.J.P., van Dam M., Marcil M., Pocmp K., Zwatts K. Y., Pollins I. M., Rocharts P., Tamashan N., Stulc T., Suda T., Caska P., Roucher R., Pondan C., DeScuich C., Brocks-Wijson A., McHaisen H.O.F., Frehlich I., Genest J. Tr.
"Mutations in ABC1 in Tangier disease and familiai high-density
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Bloomfield Rubins H., Collins D., Robins S.J., Wilson P.W.F.,
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J. Slin Invest, 166-126(-1278(2000)
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                                  lipoptoteim deficiency.",
Nat. Gepet - 22:336-345(1999)
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VARIANTS 15 ASM 1289 AND TEFFICES, AND VARIANT LYS 219.
MEDLINE LIGEOGRS, Probled 1179-965.
MEDLINE LIGEOGRS, Probled 1179-965.
MENANGER, MANNEY E., KOGS T., Hus H., Agets M., Kawabata S., Mawatari K., Imamura T., Eto T., Kawamura M., Teramoto T., Sasaki J., "Novel mutations in ABCAI gene in Japanese patients with Tangier corogary heart disease."
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MEDIANE 2164591, PobMed 11785958; Mishida V. Hishne F. Tsukamerto E. Nagado M. Ekegami C. Ecomp E., Ishnata M. Sarane H., Chang C., Isajii E., Matsuyama A., Giama T., Matsuyama E., Ishnama M., Sakai M., Hiroka H., Hattori H., Wellington C., Yoshida Y., Misugi S., Hayden M.R., Egashira T., Yamashita S., Matsuzawa Y.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Expression and functional analyses of notel mutations of AIF-binding eassette transporter 1 in japanese patients with high-density lipoprotein deficiency.",
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-t- ginvition: Pamp-heppendent and Suffeonythrea-Sensitive anion
Transporter key Gatekefelk influencing intracellular Ceolesterol
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IS A PECUSSIVE FISOREM: TAMEALIERIZED BY ABSENCE OF HIGH GENSITY
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FF-OCT-2001 (Rel. 40, Last sequence update)
Ol-MAP-2002 (Pel. 41, Last association update)
FF-binding cassette, Sub family A, member 1 (ATF binding cassette Lidusgouter 1) (ATP-binding cassette ABCAL OR ABCI).
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Mammalia: Eufheria; Modentia; Scinnegnathi; Moridae; Murimae; Mus.
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Molbulzen H.O.P., Poomp K., Jukema J.W., van Wijland M., van Dan
Hudson T.J., Brooks Wilson A., Genest J. Jr., Kastelein J.J.P.,
Hayden M.R.;
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Best Local Similarity 87.5%, Fred. No. 10,
Matches 7; Conservative 1; Mismatches 0, Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                              MET-883; ASP-1172; LYS-1587 AND CYS-1731.
MEDLINE-211283/9; PubMed-11238261;
                                                                                                                                                                                                                                                                                                                Blochim, Blophys, Acta 1537:71-78(2001).
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                                                                                                                Qin Y , Cavelier L., Phiu S , Fubin E , Cheng J.-F ;
"Human and mouse ABCAl comparative sequencing and fransgenesis studies identify pertential regulatory sequences."
Submitted (UIL-2000) to the EMRL/GenRank/DDRT databases
                                                                                                                                                               - PENNCITON: CAMP-GEFENDENT AND SULFONTLINEA-SENSITIVE AND TRANSPORTER KEY GATEKEELER INFIDIENCING INFAGELLULAR OFF-LESTER-OF-TRANSPORT (BY SIMILARITY).

- PISSUE SPECIFICITY: WIDELY EXPRESSED IN ADULT TISSUES. HIGHEST LEVELS ARE FOUND IN PREGNANT UTERIC WITH TWO HOMOLOGOUS HALVES, EACH CONTAINN AN HYDROHGHER MEMBERS AND TERM FOR SULFERNING AN HYDROHGHER MEMBERS.
                                                                                                                                                                                                                                                         ATP BINDING CASSETTE (ABC) DOMAIN. SIMILARITY: RELANSE TO THE ARC PENNING TO THE ARC TEANSPORTER FAMILY: ABCA SUBFAMILY.
                        Inciani M F . Femigrat F , Savary S , Matter M _{\rm eff} , chimin it ; "Cloning of two novel APC transporters mapping on human chromosomes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL)
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N-LINKED GLUNG. .
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N-LINKED GLUNAC
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MGD: MGL:99607; Abcal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    IPPO03439; ABC_transportr.
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STRAIN-DWA/2; FISSUE MACCOPETGO;
MEDLINE-94375008; Pubmed-8098782;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro, IPR001687, ATF_GTF_A
InterPro; IPR003838, DUE214.
InterPro; IPR000897; SRP54.
Pfam; PP000055, ABC_tran; 2.
Pfam; PF000055, ABC_tran; 2.
                                                               Genomics 21:150-159(1994)
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MEDITINE 4325,075, FULME-4-8485470, Mather I H., Ranghart L P., Lane W S.; The major far-globule membrane proteins, boying components 15,/16 and guinea-pig 85. a murine qlycoprotein containing epidermal growth factor-like and factor V/VIII-like sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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STRAIN-HOLSTEIN, TISSUE-Mammary gland;
MEDLINE-97008954; Pubmed-8856064;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ψ95114; υ27959; P79344;

ni-Nav-1947 (Pel 35, Created)

ni-Nav-1947 (Pel 35, Created)

16-in-Nav-1947 (Pel 36, Last sequence update)

16-in-1-20il (Pel 40, Last annotation update)

Lactadherin precursor (MILK fat globule-EGF factor 8) (MFG-E8)

(MGF97/53) (FAS-6/PAS-7) glycoptotein) (MFGM) (Sperm surface protein

SP47) (BP47) (Components 15/16).
N-IINKED (GLCNAC. ...) (POTENTIAL).
N-IINKED (GLCNAC. ...) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Melecular chants of glycynchin antigens MTP5753 receptived by monoclonal antibodies raised against bovine milk fat globule membrane.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bos taurus (Bovine).
Eukaryota, Mctasca, Chordata, Craniata, Vertebrata, Euteleosiomi,
Mamumalia, Eutheria, Cetaitiodactyla, Ruminantia, Pecora, Bovoidea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ċ
                                                                                                                                                                                                                                                                                                                                                                                                     Hyarregaard J., Andersen M.H., Beiglund L., Rasmussen J.T.,
                                                                                                                                                                                                                                                                                                                         MW; FARELBLIFDIDGSF9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , Kishi M., Taniguchi Y., Adachi T., Nakamura P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (NOV-1447) to the EMEL/GenBank/DDB. databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      427 AA.
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MEDLINE-96125736; PubMed=8541316;
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1567 1568
2024 2024
2261 AA: 254011 M
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87.58;
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Best Local Similarity
Matches 7, Conserv
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MFGM_BOVIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HYRPID) (IN PAS-6
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FUNCTION: PROBABLY ASSOCIATES WITH PHOSPHOLIPINS ON THE SURFACE OF
                              -i- ALTERNALIVE PRODUCTS: 2 ISOPERMS; A LOWS FORM (SHOWN HERE) AND A SCHORT FORM ARE PRODUCED BY ALTERNALIVE SPLICING. THE SHOPT FORM LACKS 53 AMINO ACLIS WITHIN THE ESSE TYPE C ) COMMIN.
-i- TISSUE SPECIFICITY AND SPERMY-OFFAN.
-i- FIRSTE SPECIFICITY AND SPERMY-OFFAN.
-i- FIRSTE SPECIFICITY THE ADDISORDER SHOWN SHOWN.
-i- STATE 2 COUNTRIES OF SECTION TERMINALS.
-i- SIMILARITY: CONTAINS 2 ESF-LIKE DOMAINS.
        MAMMARY EPITHELIAL CELLS AND MILK FAT GLOBULES. ZONA PELLUCIDA-
BINDING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                            P5/8 TYPE C 1.
P5/8 TYPE C 2.
CELL ATTACHMENT SITE (POTENTIAL).
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O-LINKED (FUC. ) (IN PAS-7)
N-LINKED (GLCNAC. . ) (HYRPID)
AND PAS-7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MISSING (IN SHORT ISOFORM).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-LINKED (GLONAC
PAS-6).
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                                                                                                                                                                                                                                                                                                                                                                                                                         FGF-LIKE 1
FGF-LIKE 2
                                                                                                                                                                                                                                                                 Interpro; IPP0000561; FGF-like
Interpro; IPP000421; FA58_C.
Pfam: PF00008; BGF; 2.
SART: SM00181; BGF; 2.
SMART: SM00181; EGF; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47413 MW;
                                                                                                                                                                                                                                                                                                                                   PP-SITE, FS00012; ESE_1; 2.
PPOSITE; PS01186; PSP_2; 2.
PF-SITE; PS01286; FASR_1; 2.
PPOSITE; PS01286; FASR_2; 2.
                                                                                                                                                                                                                                                                                                                                                                             Signal, Glycoprotein, Milk, Alternative splicing.
                                                                                                                                                                                                                                EMBL, S80643 AAR3FR94.2,
EMRL, Y11719, CAA72406.1; -
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427 AA;
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Query Match
Best Local Similarity 75.0%; Prod No. 4.7;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0.
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this SWISS-FROM early is copyright. It is produced through a callaboration between the SWISS Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no testrictions on its use by now point institutions as long as its content is it so way modified and this statement is not removed. Tsage by and for commercial cuttiles requirement is not removed. Tsage by and for commercial or send an exalt to licensells sib. Only 1.//www islead to by ancested.
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                                                                                                                   15-JUL-1998 (Rel. 36, Last sequence update)
30-MAY-2000 (Pol. 39, Last annotation update)
Lactadherin (Milk fat globule-ESF lactor 8) (MFG-E8) (MFGM) (Sperm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BY SIMILAPITY.
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N. LINKED (GLORO...) (POTENTIAL).
H INFER (GLONC...) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                         Eukaryota, Netazoa, Chordata, Craniata, Vertebrata, Euteleostomi.
Admilia, Eutheria, Petarti-darijia, Seina, Sidae, Sus.
NCBL_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F5/8 TYPE C 1.
F5/8 TYPE C 2.
CELL ATTACHMENT SITE (FOTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73.93, Score 34, FB 1, Tength 409, 75.08; Prof. No. 12, tive 1, Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BUCCOTAFBOOLSGLIA CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -t-similarity: contains 2 fge-fike fomains.
-t-similarity: contains 2 f5/8 type of domains
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            409 AA
MFGM_PIG STANDARD; P
P79385,
nl-nnV-1947 (Rel. 35, Created)
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                                                                                                                                                                                                                                          surface protein SP47) (PP47).
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372
409 AA;
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                                                                                                                                                                                                                                                                                                                             Sus scrota (P1g).
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                     SPERENCE OF COURT OF 
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                                                                                                                                                                                                                                                                                                                                                                                                 -i- FUNCTION: INVOLVED, IN MAN, IN THE DEGRADATION OF SEVERAL AMINO ACIDS, ODD-CHAIN FAITY ACIDS AND CHOLESTERGE, VIA PROPTONYL-COA TO THE TRICARBOXYLIC ACID CYCLE, MON HAS DIFFERENT FUNCTIONS IN OTHER SPECIES (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saps
                                                                                                                                                                                                                                  Nemateda, Chromodorea, Phibalitida, Phabditeldea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mitochondrion; Transit peptide; Isomerase; Vitamin B12; Cobalt.
TRANSIT 1 7 MITOCHONINION (POTEWILLD.).
CHAIN 2 7 FROBALE METHILMALONYL-COA.
DOMAIN 616 694 COBALAMIN-BINDING (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Barteria, Erotéobarteria; alpha subdivision; Rhodobarter group;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -1- STRUNIT- HOMODIMER (RY SIMILÀPITY)
-1- SURC'ELLULAR LOCATION- Mitochondrial matrix (Ry similarity).
-1- SIMILARITY: BELONGS TO THE METHYLMALONYL-COA MUTASE FAMILY.
                                                                                                      01-NOV-1997 (Ref. 35, Last sequence update)
16-OCT-2001 (Ref. 40, Last annotation updato)
Probable methylmalonyl-GaA motaso, mitochondrial precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73.9%; Score 34; DB 1; Length 744; 75.0%; Prod No 22,
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                                                                                                                                                                                                                                                                                                                                                                               Submitted (AUG-1944) to the EMRL/Georgank/PDRJ dataloases
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16 05T 2301 (Rel. 45, Last annotation opdate)
Beta-lactamase precursor (EC 3.5.2.6) (Penicillinase).
Rhodobacter capsulatus (Phodopsondomonas capsulata).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COBALT (POTENTIAL).
7 487101EAG30PF206 0PC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- COFACTOR: ADENOSYLCOBALAMIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               293 AA.
                                           744 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam: PF02310; R12 binding: 1
Ptam; PF01642; MM_COA_matase; 1.
PROSITE; PS00544; METWALONYL_COA_MUTASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2) Mismaiches
                                                                                                                                                                                                                                  Eukary ta, Metara, Nematoda, Chromadoros
Rhabditidae, Peloderinae, Caenorhabditis
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                                           PRT;
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InterPro; IPR003312; B12-binding.
InterPro; IPR001679; MM_ncA_mitase
                                                                                  01-NOV-1997 (Rel. 35, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JAN-1990 (Rel. 13, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMRI: 235604; CAA84676 1; -
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                                           STANDARD;
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                                                                                                                                                                                                          Caenorhabditis elegans.
                                                                                                                                                                   (EC 5.4.99.2) (MCM).
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                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN BRISTOF N2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ||:||:||
| 641 LFOTPLEA 648
                                                                                                                                                                                                                                                                           NCB1_Tax1D-6239;
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618
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P14171;
                                           MUTA_CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                                                                                                                                           ZK1058 ]
                     MUTA_CAREL
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This SWISS PROT entry is recytlight. It is preduced through a collaboration between the Swiss Institute of Richformatics and the EMBL outstation the European Floinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial contribes requires a liberage districtions.
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                                                                                                          MEDLINE=89350855; PubMed-2788410; Familiar P.P.; Familiar P.P.; Familiar S. Gibson T., Anther P.P.; The photetrophic bacterian Shod-pseudomonas rapsulata sp108 encodes in indigenous cass A betain Shod-pseudomonas."; Rinchem. 1. 260 803-812(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                               FUNCTION: HYDROLYSES BETA-LACTAMS ANTIBLOTICS. RATES OF HYDROLYSIS FELATIVE TO RENAVITHING 11.1N - 1000 AMERICALIN - 27, CARRENICILIN - 26, CHONACTIAIN - 0, CEPHALORIDINE - 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Olinovings (Rel. 35, Created)
Olinovings (Rel. 35, Last sequence update)
16-077-2001 (Rel. 40, Tast annotation update)
Hypothetical 51.3 kba protein T1963 5 in chromesome 111 precursor.
                                                                                                                                                                                                                                                                                                                                                                                       -:- SUBCELLULAE LOCATION: Periplasmic.
-:- SIMILARITY: RELONGS TO THE CLASS-A BETA-LACTAMASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71 79; Score 33; PR 1; Longth 293; 77 88; Prod No. 14;
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-!- SIMILAMITY: SOME, TO THE REL/PFIP/LEP/LEP/EMILY.
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SHRSTPATE (RY SIMILAPITY).
FHHZSHREGSR917F] CPC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hydrolase, Antibiotic resistance, Feriplasmic, Signal. SIGNAL 1\, 27\, POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RETA-LACTAMASE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FROSTIE, PSOUT45; BETA_LACTAMASE_A; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001466; Beta_lactam.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PFüül44; beta-lactamase; l.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TAM TATTLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PPINTS; PPONTIR; BLACTAMASEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMPL; X15791; CAA33795.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 77 Ri
Les 7, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27
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240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           238
294 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; P00810; 1TEM.
                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25 SLAETPVEA 33
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NCBI_TaxID=1061;
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                                                                                                                                                                                                                                                                                                                                                                amino acid
                                                                                   STRAIN-SP108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YSV5_CAEEL,
Q10011;
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BINFING
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                               use by non-profit institutions as burg as its content is in no way modified and this statement is not removed. Usage by and for commercial contilies requires a library agreement (See Litp.//www.ish sib.chyannounce; or send an email to libraselisb sib.ch).
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   the European Bioinformatics institute. There are no restrictions on its
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gabs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE 97961201, PubMed-8905231;
Kanoko T., Sato S., Kotani H., Tanaka A., Asamiru E., Nakamura Y.,
Miyojima N., Hirosawa M., Sogjura M., Sasameto S., Kimoria T.,
Hosouchi T., Matsuno A., Myraki A., Nakaraki N., Naruo K., Okumura
Shimpo S., Takeuchi C., Wada T., Watanako A., Yanada M., Yasuda M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'Sequence analysis of the genome of the unicellular eyanobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kamei A., Ikeuchi M.;
"A nozoi gato, spEC, encodes active Ser/The protein kinase in the
motile eyanobarterium Syrechocystis Sp. per 6803 ";
Submitted (JUL-2000) to the EMBL/Genbank/Drmi databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: BELONGS TO THE SER/THP FAMILY OF PROTEIN KINASES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHAIN 18 464 HYPOTHEFICAL PROTEIN T19C3.5. SEQUENCE 464 AA; 51939 MW; 3029CFD/2F65E67F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71.7%; Score 33, DB 1, Length 464
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16-00T-2001 (Fc). 40, Last sequence applie)
16-00T-2001 (Rc). 40, Last annotation applie)
Probable series/threonine-profein kinase C (EC 2.7.1.-).
SPKC OR SLR0599.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cyanobacteria: Chromomains; Symphocystis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Prod. No. 22;
Nive 0, Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00400; LBP_BPI_CETP; FALSE_NEG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL
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InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002298; Ser_thr_pkinase.
                                                                                                                                                                                        EMBL; U24412; AAC46506 1; WOTHDEP: TPPGG1 5; FN625A5; FN625A5; Interpro; TPPGG1124; IRP_RPL_CETP. Pfam, FFC2846; IRP_RPL_CETP. 1. SPAM: SR00328; BPI1; 1. SMART; SM00328; BPI1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synechocystis sp. (strain PCC 6803).
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SiGNAL
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Best Local Similarity 1997.
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SEQUENCE FFOM N A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 NLFETP 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fabata S
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                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Edkaryota McLabour Chordata, Chandata, Vettebrata; Eutelbeustomi;
Actinopterygii, Kosprerygii, Telesatei, Enterestei, Nestelbeustei;
Aranleometpha, Bararanthopterygii; Gadifermes, Gadodei, Gadidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Johansen S., Bakke I., \fi The complete mitochondrial DNA sequence of Atlantic cod (Gadus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1- CATALYTI' ATTIVITY: NAPH + ubiquinone = NAP(+) + ubiquinol.
                                                                                                                                                                                                                                                                                                                                            0
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PPLNS PERINS NARPHONASES.
Oxidered actives NAD, Objector Mitachendrian; Transmembrane.
SPORTER F. Fiz A., Frank M., AARASPEPFIPHAISE CPC64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mel. Mar. Piel. Ristochnel. 5:203 (14(1996).
                                                                                         Transferase, Serinc/threonine protein Ainase, AIP binding;
Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71.7%; Score 33, DB 1, Length 612;
85.7%; Pred No. 30;
                                                                                                                                                                                                                                                                                                 71.7%; Score 33; DB 1; Length 535;
                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                             533CD9FC0E3D23D8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 25, Last Sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
NADH-ubiquinone oxidoreductase chain 5 (EC 1.6.5.3).
                                                                                                                                                          ATP (BY SIMILARITY). ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                         Fred. Mc. 26;
                                                                                                                                    PROTEIN KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         612 AA.
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                                                                                                                                                                                                        SIMILARITY
                   PROSTIE: PSSOGII: PROGENERNASELDOM; I. PPOSTIP: PSOGIO7; PPOSTIP: LINOSIE; PSOGIO8; PROLEIN_NIMASE_ST; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to licenseaish-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; iPหลีผู้จิจิโต้; NADHub_oxdrdctse5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001750; Oxidored_q1.
Interpro; iPP001516; Oxidored_q1_N.
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STRAIN=NORWEGIAN COASTAL 1;
MEDLINE=96414995; PubMed=8817926;
                                                                                                                                                                                                            3.
                                                                                                                               12 277 FER
18 26 ATT
18 26 ATT
112 143 ATT
535 AA; 56141 MW; 3
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                                                                                                                                                                                                                                                                                                                       Bost Local Similarity 100.0
Matches 6; Conservative
Piam; PFOOO69; pkinase; l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                   396 NLFETP 401
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BINDING
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     REPRESENTATION OF THE PROPERTY                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PPOT only is requisible It is produced through a reilaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Recipiesteries in the intervent are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not lenoved. Usage by and for conference of such these requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-0CT-1989 (Rel. 12, 1981 representation update)
15-JUL-1998 (Rel. 36, Last annotation update)
Lichenase II precursor (EC 3.2.1.72) (Endo beta-1,3·1,4 glucanase II)
((1->3,1->4)-beta-glucanase isoenzyme EII) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                       Palm P., Schleper C., Grampp B., Yeats S., McWilliam P., Reiter W.-D.
Zillig W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          o; Caps
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Bukarysta, Viridipluntae: Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnollophyta, Liliopsida, Poales; Poaceae, Pooldeae,
                                                                                                                                                                                                                                                                Sulfolobus virus-like particle SSVI
Viruses, dsDNA miroses, to ENA stage, Euseliavizidae, Fuscilavirus.
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Wettenhall R E H., Morrer J F R., Brandt A., Thomsen K R.;
Prinary at ructure of the (1-3,1-4)-beta-p-glucan 4-glucchydrolase
from barley aleurone.;
Proc. Nail Asad. Sei H S A RR:2081 2085(1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69.6%; Score 32; DB 1; Length 291; es.ex, Fred No. 20;
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Woodward J.E., Magan F.J., Fincher G.B.,
"Amino acid sequence homology in two 1,3;1,4 beta-glucan
                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Complete nucleotide sequence of the virus SSVI of the archaebacterium Sulfolders shibatae.", Virology 185 242 250(194)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29] AA; 31669 MW; 84D231AB748DBF2A CRC64;
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                                                                                                                                                                                       01-FER-1991 (Ref. 17, East sequence update)
01-AUN-1992 (Pol. 23, East monoration :pdate)
Hypotherical 31.7 kDa protein (OPF A 291)
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                                                                                                                                                                 01-FEB-1991 (Pel. 17, Created)
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                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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Matches 5. Consor
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479 NLFKTPV 485
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P12257;
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                                                                                                                                                                                                                  "Three-dimensional structures of two plant beta-qlucan endohydrolases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- CATALYTIC ACTIVITY: Hydrolysis of 1.4-beta-D-glycosidic linkages in beta-D-glucans containing 1.3 and 1.4 bonds.
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                                                                                                                                                                                                                                                                                                                                                                                                                          "Crystal structure of barley 1.3-1,4-beta-glucanase at 2 0.A resolution and comparison with Bacillus 1,3 1,4 beta-glucanase."; J. Riol. Chem. 273.3138-3446(1998).
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                                                                                                                         MEDLINE 94195828, PubMed 8146192,
Varghese I.N., Garrett T.P.T., Colman P.M., Chon L., Hom) P.B.,
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endobydrolases from germinating barley (Hordeum vulgare).";
FERS Lett. 138:198-200(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -1 - FUNCTION FUNCTION IN PLANT CELL WALL HYPROLYSIS PUPING
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7018C2A6PPS22E17 CPC64;
                                                                                                                                                                                                                                                  with distinct substrate specificities.";
Proc. Natl. Acad. Sci. U.S.A. 91:2785:2789(1994)
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(1-AUG-1990 (Pel. 15, Created)
01-ANR-2002 (Rel. 41, Last acquence update)
01-MAR-2002 (Pel. 41, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                 X-PAY CPYSTALLOGPAPHY (2.0 ANGSTPOMS).
MELLINE SELSIL7, Fabmad SatateG.
Mueller J.J., Thomsen K.K., Heinemann U.;
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Pfim, PF00332; Glyss-hydro_17; 1.
PROSITE: PS00587; GLYCOSVI_HYDROI_F17; 1.
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YopM oP Yop48 oP YPCD1_260 oP Y0059
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A25455; A25455.
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                                                                                                                                                                                                                                                                                                                              Hu P., Elliott J., McCready P., Skowronski E., Garnes J.,
Febbyski A., Brubaker E.F., Garda E.,
"Structural organization of Virulence associated piasmids of Yersinia
                                                                                                                                                                                                                         PNA sequencing and analysis of the low Ca2+ response plasmid pCD1 of
                                                     MEDLINE-89336900, pubmod=2670888;
Leung K.Y., Straley S.C.;
The yordh gather of Persiste pestis encodes a released protein baving
homology with the bunna platelet sarface protein opts alpha ";
J. Bacteriol. 171.4623-4432(1989).
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Gulog Gemblado, Frgest, Lessine Filt report, Antigon, Plasmid,
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-1- SIMILARITY: TO S.FLEXNERT TPAH 7.8
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LRR 6.
LRR 7.
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EMBL; AF074612; AACKAGN6 j. -
EMBL; AF053946; AACK2SR0 j. -.
EMBL; AL117189; CAR54903 lj. -.
PIR; A33950; A33950.
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InterPro; IPP063592; LRP_-ut
Pfam; PF00560; LRR; 6.
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NCBI_TaxID=632;
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SECURRED FROM H.A., AND SEQUENCE OF 31 39; 123 138 AND 708-718.
SECURPED S., Sequence C., Firsper M., Paye V., Tekotte H., Weise C., Emig S., Sequence A., Hurt B.C.,
Tange S., Sequence C., Hurt B.C.,
Tange C., Secure C., Michael C., Michael C., Secure C., Michael C., Secure C., Secur
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Sacoharomyootules, Sacoharomyootuseae, Sacoharomyoes.
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                                                                                                                                                                                                                                             69 68; Score 32; DB 1; Length 409; 77 88; Prod No. 32; Live 0; Mishatches 2; Lidels
LRR 11.
LRR 12.
MISSING (IN REF. 1).
ELL4000071A59951 CEC64;
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01-NVV-1998 (Bcl. 32, Last sequence update)
36 MAX 2596 (Bcl. 39, Last uncetation update)
Nucleoperin NHPRS (Nuclear pore protein NHPRS)
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Biol cell Zim17-934(1996).
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MERTINE GAGITARGE, EDEMMARREGAR,
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EMBL: X90955; CAA62481.1; -
EMBL: Z49542; CAA89569.1; -
FMRL: 136344; AA88744 1; -
SGD: S0003803; NUP85.
Nuclear protein; Transport.
                                                                                                                        46205 MM.
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P46673;
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CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no wa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-1994 (Ref. 29, Last Sequence update)
01-MAR-2002 (Ref. 41, Last annotation update)
Vascular endothelial growth factor receptor 3 precursor (EC 2.7.1.112)
FLI4 OR FLI 4.
                                                                                                 Gaps
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PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE: PS00200; RECEPTOK_TYR_KIN_111; 1.
PROSITE: PS002011; PROTEIN_KINASE_DOM; 1.
Transferase; Tyrosine protein kinase, Phosphorylation; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertobrata; Eutoleostomi;
Mammalia; Eutheria; Rodentia; Sciuroquathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Onrogene 8:2291-2208(1993)
-!- FUNCTION: RECEPTOR FOR VERP-1 HAS A TYPOSINE-PROTEIN KINASE
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                                                               69.6%; Score 32; DB 1; Length 744;
66.7%; Pred. No. 59;
                                                                                                 l; Indels
71 F -> E (IN REF. 1).
84897 MW. 400A4AD30B57A023 CEC64.
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                                                                                                 2: Mismatches
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InterPro; IPR000719; Euk_pkinase.
InterPro; IPR003006; Ig_MHC.
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InterPro; IPR003600; Iq_like.
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Pfam; PF00069; pkinase; 2.
SMART; SM00410; IG_like; 3.
SMART; SM00408; IGC2; 2.
                                                                                                 6; Conservative
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F35917;
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PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
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                                                       VASCULAR ENDOTHELIAL GROWTH FACTOR
Receptor: Transmembrane; Signal; (mmunoglobulin domain; Repost;
                                                                                                                                                       1G-LIKE C2-TYPE DOMAIN 1.
1G-LIKE C2-TYPE DOMAIN 2.
1G-LIKE C2-TYPE DOMAIN 3.
1G-LIKE C2-TYPE DOMAIN 4.
1G-LIKE C2-TYPE DOMAIN 6.
1G-LIKE C2-TYPE DOMAIN 6.
1G-LIKE C2-TYPE DOMAIN 6.
1G-LIKE C2-TYPE DOMAIN 6.
PROTEIN KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FIBF8A2BDEF99BE9 CRC64;
                                                                                               EXTRACELLULAR (POTENTIAL).
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ATP (BY SIMILARITY).
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POTENTIAL.
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query Match 69.69; Score 32; DB 1; Length 1363; Best Local Similatity 66.79; Pred. No. 1.18+02; Matches E; Conservative 2; Mismatches 1; Indels 0; daps

Oy 1 NLFETPVEA 9 :|| || || || || Db 614 HLFATPLEA 622 Search completed: September 5, 2002, 15 31:42 Job time: 477 sec

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Page 1

us-09-744-804-38.rspt

OM protein - protein search, using sw model

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US-09-744-804-38 46 Title. Perfect score:

RiosnM42 Gapop 10 0 , dapext 0.5 1 NLFETPVEA 9 Scoring table: Sequence:

562222 seqs, 172994929 residues Searched: Total number of hits satistying chosen parameters:

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Listing first 45 summaries Post-processing: Minimum Match 08 Maximum Match 100%

sp\_unclassified \*
sp\_rvirus:\*
sp\_bacteriap:\* sp\_invertebrate:\*
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sp\_bacteria:\*
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sp\_human:\* sp\_organelle:\* sp\_phage:\* sp\_rodent:\* sp\_plant:\* sp\_virus:\* SPTREMBL\_19:\* sp\_mhc:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the test sector distribution.

sp\_archeap:\*

#### SUMMARIES

	ID Description	098T/3	036t85 homo	F1-00-1	- 0982t3	f-4	184560	010295 Sthizmsandh			Oscynta arabidinal	030097 orchaeodlob	0941M0 brassica o	Q9AV92	Ofute0 schizosacch	Q983T3 Thizohium	100 mt 2
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porry Maint. Bost Local Similarity 100.0%; Pred. No. 0.11; Matches 9; Conservative 0; Mismatches 0; Indels

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### ALIGNMENTS

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					Homo sapiens (Human). Eukaryota: Metazoa: Chordata: Cramiata: Vertebrata: Eutoleostomi:	E																					
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-	9 Q9BTLS 04BTL4+	01-JUN-2001	01-JUN-2001 01-DEC-2001	SIMILAP TO MILK FAT GLORULE-EGF FACTOR R PROTEIN	Homo sapiens (Human) Eukaryota; Metazoa;	Mammalia, Euther NCBI TaxID=9606.	1 - 1	SEQUENCE FROM N.A.	TISSUE=MELANOMA.;	Strausberg R.;	1	<ul><li>-!- SIMILARITY: CONTAINS 1 F5/8 TYPE C DOMAIN.</li></ul>	EMBL: BC003610; AAH03610.1;	HSSP; PO8709; 1BF9.	InterPro: 1PR000561;	InterPro;	InterPro; IPR000421; FA58_	PRINTS: PROCOCO: EGFBLOOD.	SMART; SMU0181; EGF; 1	HAFT	SMAR		FROS TES	PR(351 LE)	PROSE TEX	KGF-11Ke	
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"Human and Mouse ARCAL Comparative Sequencing and Transgenesis Studies
Revealing Novel Requiatory Sequences";
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Mammalia; Butherla, Primates, Catarrhini, Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tanaka A.P., Abe-Dobmae S., Arakawa R., Sadanami K., Kidera A., Kioka N., Amachi T., Yokoyama S., Ueda K.; A new topological model of functional bomen ABPAI-Signal poptible cleavage and glycosylation of a large extracelular domain."; Submitted (FEB-2001) to the EMBL/GenBank/Dukt databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Embaryoka, Matazoa, Oberbata, Oraniata, Vertebrata, Extereostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82.68, Septe 28, 58.4; Length 2261; 87.5%; Fred. No. 48; 6; indels tive 1; Mismatches 6; indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82.6%, Score 38, DB 4, Length 2261, 87.5%; Pred. No. 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2261 AA; 254298 MW; 248080403888041AF 3M064;
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                                                                                                                                                                                               01-DEC-2001 (TrEMBLES: 19, Created)
01-DEC-2001 (TrEMBLES: 19, Last sequence update)
01-DEC-2001 (TrEMBLES: 19, Last annotation update)
ATP-BINDING CASSETTE 1 SUB-FAMILY A MEMBER 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1, Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-21251004; PubMed-11352567;
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EMBL, AF287262; AAK4352k 1; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                       PRELIMINAPY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Overy Match Best Local Similarity T_{\rm L} = 0.000 \, {\rm L}_{\rm L} \, {\rm Consert9}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
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es 7, Conserv
                                            194 NLFETPVEA 202
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1 NLFETPVEA 9
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Best Local C:
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Faceko T., Nakamuta Y., Sato S., Asamizu E., Kato T., Sasamoto S., Natanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsumo A., Mochipuki Y., Nakayama S., Nakazaki N., Shimpo S., Suqimoto M., Takegebi C., Yamada M., Tabata S., Singimoto M., Takegebi C., Yamada M., Tabata S., Singimoto M., Takegebi C., Yamada M., Tabata S., Fingi S., Suqimoto M., Tabata S., Funka Jasa S., Sandimoto M., Funka Pes. 7.331.338(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Molecular clearing and characterisation of 147, a seven bear sperms associated zona perlucida binding protein homologus to a family of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chardata, Craniata; Vertebrata, Erbebrata
                                                                                                                                                                                                  Rhizobium loti (Mesorhizobium loti).
Racteria; Protocharteria, alpha subdimision, Phirobiacoae group;
Phyllobacteriaceae; Mesorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PETITINE SWIDSKIZ, FURMAG SGAFZAD.
Ensslin M., Vogel T., Calvete J.J., Thole H.H., Schmidtke J.,
Matsuda T., Toepfer-Petersen E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 37: DB 16: Longth 393;
Prod No 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryola, Melazoa, Chordata, Itaniata, Vertebrata, Elleh
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       393 AA; 43166 MW; 427F5CC3BBF59B6B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thesis (1996), University of Handover, Handover, FPG.
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                                                                                                                   Last annotation update)
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                                                                                        Last sequence update)
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393 AA.
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PROSITE; PSGGGS; No_MTASE; UNKNOWN_I.
                                                             Created)
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     PPT:
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                                                                                                                                                                                                                                                                                                                                                                       STRAIN-MAFF303099;
MEDIINE 21082930, BURMAS 11214968,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mammalian sevretory proteins.";
Riol Peprod 58-1057-1064(1998).
EMBL: Y11718; CAA72405.1; -.
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PROSITE; PS01286; FA58C_2; 1.
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77.8%;
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Homo sapiens (Human).
     PRELIMINARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Rest Local Similarity
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|173 NLYETPPEA 181
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                                                                                                                                                MLR8507 PROTEIN.
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STRAIN-972H-;
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RAG DE LEE LEE COME DE LEE COM
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Obnacker M., Minivielle Schastia L., Keller W.,
"The Schinschardmerse pumber plat gener convoles a poly(A) polymetaser
and can functionally replace its Saccharomyces cerevisiae homologue.";
Nucleic Acids Res. 24:2585-2591(1996).
                                                                                                                              7. T
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Eukaryotu, Fungi, Asomycota, Policomycotina, Eurotiomycetes,
Eurotiales, Trichocomaceae, Emericella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 76.1%, Score 35, DB 3, Length 192, Best Loral Similarity 75.0%, prod No 32, Matches 6, Conservative 1: Mismatches 1, Indels
                                                    78.39, Sector 36, DR 4; Longth, 78, 75.08; Pred, No. 3.3;
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Eukarjota, Fungi, Aschmynda, Schinosaccharomycetes;
Schizosaccharomycetales; Schinosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last Sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 392 AA.
                                                                                                                          2) Mishatches
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Probom, PF001374, Filossomal_L3; 1.
PROSITE: PS00474, RIBGSOMAL_L3; UNKNOWN_L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMRI, AE198447, AAF15500.1; -.
InterPro; IPE000597; Ribesomal_L3.
Pfam, PF00297, Filessandl_L3.
                                                                                                                          Petront Sat 1869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60S PIROSOMAL PROTRIN L3
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                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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                                                                                Local Similarity
Hes f, Potenty
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                     28 NLFDTPLE 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=5072;
                                                                                                                                                                                         1 NLFETPVE 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-FGSC4;
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                                                           Olory Matoh
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             09UV31;
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                                                                                           Best Loca
Matches
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Bacteria, Protechasteria, epsilon sublivisien, Helioebacter group;
Helioobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ·.
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Submitted (SEP-1998) to the EMEL/SenBank/DöBJ databases.
-!- SIMILARITY: TO YEAST YIL084L.
EMBL, ALUGITSB; ACALIEC.1; -.
76.1%; Score 35; DB 3; Length 566; 66.7%; Pred. No. 47; 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76.1%; Score 35; DB 3; Length 658; 87.5%; Pred. No. 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 18, Last sequence update)
01-OCT-2006 (TrEMBLrel. 15, Last annotation update)
HYPOTHERICAL 57 9 KTA PROTEIN CZDIO 04 IN CHROMOSOME II.
STBCCDIO.04.
SCHICOSACCHROMYCES FORDE (Fission yeast).
Eukaryota, Puroj, Assomyceta, Schicosaccharomycetes; schicosaccharomycetes;
                                                                                                                                                                         PFOSITE; PS00430; TONB_DEPENDENT_REC_1; UNKNOWN_1.
SEQUENCE 500 AA; 04108 MW; EBEUE4105AAED5D5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              658 AA; 72/31 MW; 40EBU06BB970B4F7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (i.NAY-1969 (TrEMFLED), 10, Created)
(i.MAY-1999 (TrEMFLED) 10, Last sequence update)
(i.JUN-ZUQU (TrEMFLED) 14, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         658 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 56;
O; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PPT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FRT;
                                                                                                                                  InterPro; IPR001201; PAP_25A_core.
InterPro; IPR000531; TonR_boxC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDITAE-98453456; PupMed=9780260;
                                                                                                           InterPro, TPR002934; NTP_transf.
                                                                     . VAUR. . . VV.
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Best Local Similarity 87.5.
From 7; Conservative
                                                                                                                                                                                                                                                                                       Query Match 76.1
Best Local Similarity 66.7
Matches 6, Caservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PPFL.IMINAFY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schizosaccharomyces.
NCBl_TaxlD=4896;
                                                                 EMRI, ALGASTE, AA HSSP, P25500; 1F5A.
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                                                                                                                                                                                                                                                                                                                                                                                                      36 NLFESPAES 44
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                                                                                                                                                                                                                                                                                                                                                                               1 NLFETPVEA 9
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Dioxygenase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q941M0;
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  AC DIT
                                                                                                                                                             c:
                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana (Mouse-ear cress).
Editory La. Viri High-Indua: Strepteddyta Embrycedytu, Trachecedytu;
Spermatophyta; Magnoliophytu, eudicotyledoms, core endicots; Rosidae;
curosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                             Sabs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       o, Gaps
            Puriyama M.;
"Full-Length Sequence analysis of the varA gene from cytotoxic and
"Full-Length Sequence fylori";
J. Intect. Dis 178-191 1348(1948)
EMBL; AF049619; AAD04260 1,
lto Y., Aruma T., Ito S., Suto B., Miyaji H., Yamaraki Y., Kohli Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Purnelle B., Boutry M., Goffeau A., Mewes H W , Rudd S , Lemeke K.
Mayer K.F.X., Quetier F., Salanoubat M ;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                              c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JAN-1998 (TreMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-077-2091 (TrEMBLrel. 18, Last annotatios update)
01-077-7801 (TrEMBLRel. 18, Last annotatios update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73.9%; Score 34; DB 10; Length 177; 77.8%; Prod No. 22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
                                                                                                                                 73.9%; Score 34; DB 2; Length 79; 75.0%; Pred R+ 9 l,
                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EU Arabidopsis sequencing project,
Submitted (APR-2080) to the EMBE/Asenbank/Object databases
EMBE, ALGS0300, CAR4312.1; -.
EXPENDENTED Protein.
SEQUENTEL 177 AA. 2020W NW. MADEOWRYAAGESED SEAT,
                                                                                          SEQUENCE 79 AA: 9102 MW; 5337EH21676A9A0E CRC64
                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                PRT; 177 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         261 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     O; Mismatches
                                                                                                                                                             2; Mismatches
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                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=98049343; PubMcd-9389475;
                                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL 20 3 KDA PROTFIN
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Best Lacal Similarity 77 on
T; Conservative
                                                                                                                                                             6; Conservative
                                                                                                                                                                                                                                                                                PRELIMINARY;
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                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N A
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                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID-3702;
                                                                                                                                                                                                               60 LYETPLEA 67
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                                                                                                                                                                                      2 LFETPVEA 9
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                                                                                                                                    Query Match
                                                                             NON_TER
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                                                                                                                                                           Matches
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Mark outlineds, Fusidans
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Rionk H.F., Clayton P.A., Tomb '-E., White O., Notson V.E., Peterbum K.A., Dodson P.I., Cwinn M. Hickey P.E., Deterson J.D., Pichardson D.E., Cranam D.E., Stribon G. Gill S., Fleischmann P.E., Guarkenbush T., Lee N. H., Suiton G. Gill S., Erishensen E.E., Dougherty R.A., McKenney K., Adams M.D., Lottus B., Peterson S., Peich G.I., Markill K., Radger J.H., Glodek A., Shou Overbeek R., Gorague T.D., Weidman J.F., McDonald L., Otterback T., Catton M.D., Spriggs T., Artisch F., Krinc R.P., Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fujil G., Garland S.A., Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Viridiplantae, Streptophyta, Embryaphyta, Tracheophyta,
Spermalophyta, Magneliophyta, endie tyledens, este endiests, Essida
eurosids II; Brassicales, Brassicaceae, Brassica.
                                                                                                                                                                                                                                                                                                                                                                          "The examplete geneine sequence of the hyperthermophilis, sulphater reducing archaeon Archaeoglobus fulgidus.";
Nature 390:s64-370(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein; Transferase; Methyltiansferase, Ubiquinone;
Complete proteome.
SEQUENCE 101 AA; 30156 MW; ElFMABARLICKSFEB CRIG4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. In G., Quiros C.F., "Cloning of two major genes involved in aliphatic glucosinolate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73 9%; Scorp 34; DR 10; Length 439;
87.5%; Pred. No. 59;
Live 0; Mishatches 1, Hodels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73.9%; Score 34; EB 17; Length 261; 75 0%; Pred. No. 33; 0; Indels Live 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      synthesis in Brassica öleracea.", Submitted (JUL-2001) to the FMRL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         439 AA; 48313 MW; B7062014AR923F3E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-2001 (TrEMBLrel. 19, Created)
01 DEC 2001 (TrEMBLrel. 19, Last. sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ul-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR004033; ubiE_COU5_methyltransf.
Pfam; PF01209; Ubie_methyltran; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PPT: 439 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2-oxogarrakale-bependent broxygenase
Brassica oleradea (Gauliflower),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001601; Meth-transf.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AEUÜlUY6; AABY1083.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000051; SAM_bind.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AY044425; AAK95851.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Hest Local Similarity 75 A%
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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Best Local Similarity
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|64 LFELPVEA 71
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                              Oryza sativa (Rice).
Bakazy da Vihidiplattos, Streptophytu; Embrycehyta, irasheophyta,
Sportatophyta: Majon Dighyta; Eillopsida; Foales, Poacese,
Ehrhartoidese, Oryseae; Orysa.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73.9%; Score 34; DB 3; Length 762; 66.7%; Pred. No. 1.1e+02; attive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=972;
Hamiin N., Churcher C M , McDougall R.C , Pajandream M.A.
Barrell B.G.
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                                                                                                                                                              "Organ sativa kinase like protein.":
Submitted (ARR-2001) to the BMBL/GenBank/PDRT databases
EMBL; AB060276; RAR41SPS-1; .
Pfan, PF00439; know-obserin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2010 (TrEMBLrel. 16, Last annotation update)
HYPOTHETICAL 87.5 KDA PPOTEIN 0222.140 IN CHPOMOSOME 1.
                                                                                                                                                                                                                                      PRINTS, PRO0503; BROWODOMAIN,
SMART; SM00297; BROWO, 1
PROSTIE; PSSG014; BROWOWWMAIN_2; i
SEQUENCE 714 AA; 78710 MW; 4F22074281199484 CPC44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schilosaccharomyces pombe (Fission yeast).
Eukarysta, Puggl. Astampeta, Schilosaccharomycetes;
Schilosaccharomycetales; Schilosaccharomycetaceae;
   18, Last angotation update)
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01-0CT-2001 (TrEMBLrel. 18, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       762 AA.
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                                                                                                                                   STRAIN-CV. AKITAKOMACHI; TISSUE-LEAF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein; Transmembrane.
TRANSMEM 683 703 POTENTIR
SEQUENCE 762 AA; 87510 MW; 3ADDA.
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EMBL; AL132798; CAB60706.1; -.
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Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                Local Similarity 55.6
ses 5, Conservative
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01-OCT-2001 (TrEMBLIF) KINASE-LIKE PROTETN.
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                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                             1 MUPETFVEA 9
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                                                                                       NCBI_TaxID=4530;
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Matches
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MEDITINE-21080303; PubMod-11214968; Karcher T., Sasamoto S., Kanteko T., Nakhmura Y., Sato S., Asmuta E., Kato T., Sasamoto S., Matanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyekawa C., Kebara M., Matsumeto M., Matsumeto M., Matsumeto A., Masyama S., Nakaraki N., Shimpo S., Sugimeto M., Tabata S., Nakaraki N., Shimpo S., Sugimeto M., Tabata S., Omplete genome studene of the nitrogen-fixing symbiotic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                           O; Caps
                                                 Rhibobiam Joti (Mosorbitobium Joti).
Bacteria: Fritesbacteria: arghi sandivision, Shirobiaceae group:
Phyllobacteriaceae, Mosorbitobium.
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Pred. No. 9.9;
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                                                                                                                                                                                                                                                                                                                                                                   54 AA; 5414 MW; C807E2EC4758C859 CRC64;
01-07T-2001 (TrFMPL.ro) 18, Last annotation update) MSR8189 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           3, Mismatches
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DNA Poss 7:831-338(2000).
EXBL APOSSI, FARS 1797.1;
Complete proteome.
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Best Local Similarity 56.77
Tea 6) Conservative
                                                                                                                                                         STRAIN=MAFF 103099;
                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                      NCBI_TaxID=381;
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Copyright (c) 1983 - 2000 Ampagen Ltd
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OM protein - protein search, using sw model

5, 2002, 15:26:31; Search time 158.43 Seconds (without alignments) 6 310 Million rell updates/sec September Run on:

US - (เน้ - 744 - พ.เส - ฮน 54 1 GLOHWVPEL 9 Perfort score: Segnence.

Gapep 10 0 , Gapext 0 5 Fig. S. WES Scoring table:

747574 seqs, 111073796 residues Searched

Potal number of hits satisfying chosen parameters

Minimum DB seq length: 6 Maximum DB seq length: 2000000000

Listing first 45 summaries 100% Post processing: Minimum Match 3% Maximum Match

Database

/SIDSI/gcgdata/hold-geneseq/geneseqp-embi/AA1949.DAT.\*/SIDSI/gcgdata/hold-geneseq/geneseqp-embi/AA1949.DAT:\* /SIDSL/goddata/hold-geneseq/geneseqP-embL/AA1990.bAi;\*/SIPSL/gogdata/hold-geneseq/geneseqP-embL/AA1991 PAT \*/SIDSL/goddata/hold-geneseq/geneseqP-embL/AA1992.DAT;\* /SIDS1/gradata/hold-geneseg/genesegp-embl/AAl994 DAT+\* /SIDSI/gcgdata/hold-geneseg/genesegp-rantl/AA2001 DAT:\* /SIDS1/grgdata/hold-geneseg/genesegp-embl/AA1994 DAT:\* /S1081/gogdata/hold\_geneseg/genesegp-embl/AA1999.FAI.\* /Sibsl/gradata/hold-geneseg/gensesegp-rentel/AAzegun.bAt \* /SIDSI/qcgdata/hold-geneseq/geneseap-embl/AA1997 PAT \* /SIDS1/grgdata/hold-geneseg/genesegp-embl/AA1998.DAT:\* /STISE (Apoldana Zeolda serresengarieresenga enda), AAL (80) (1875), Apoldana Zeolda arresengarieresenga enda, AAL (80) (1801), STISE (Apoldana Zeolda arresengaçõesesenga enda, AAL (80) (1801), STISE (Apoldana Zeolda arresenga enda arresenga enda ZAAL (90) (1801), ZEIDE (Apoldana Zeolda arresenga enda ZAAL (90) (1801), AZEIDE (Apolda ar Zeolda arresenga enda ZAAL (90) (1801), AZEIDE (Apolda ar Zeolda ar /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/AA1985.DAT:\*/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/AA1985.DAT:\*/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/AA1987\_DAT:\* A\_Geneseq\_032802:\* 1: /SHS//9294414/b 2: /SIPS!/gcgl444/b 3: /SIDS!/gcglat4/a 110... 112... 112... 113... 113... 113...

Fred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by smallysis of the total score distribution.

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		bescription	Lactadherin (BA-46	EMEG 46 kDa antigo	Ruman lactadherin	Human colon cancer	Banan secreted pre-	Feptide SEO ID No:	Mouse lactadherin	1.5 MET 10 MET 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Protein #6199 enco	Human brain expres	Storage Subd Seman
		11:	AAY82844	AAP77252	AAY94453	AAG75021	AAE01423	AAW98891	AAY94454	ABB39426	ABB24200	AAMC0107	AAM72718
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Bar haim E, Fas A, Fridkin M;

Elsenbach L, Carmon L, Thosh B, Fitzer attas C,

Peptide #6135 enco	Peptide #EMME endo	Preseptila melanog	Human lung tumour-	Escherichia coli m	E. coli PTEM beta-	PTFW with bota-glo	E. coli TEM-1 beta	натар петегата	Human OPPX 0PF1298	CAP protein [ra2.	Human SHC protein	Human secreted pro	Human secreted pro	Human musculoskele	Human hacmatologic		Novel human diagno	Human normal bladd	Propingibacterium	Human basematishagic	0	Nevel human diagno			U	Alphalalpha2 regio		ine leukoc	Swine leukodyte an	- 1		Swim numosyte an	Swine leakedyte an
AAM19701	AAM32949	ABRES241	AAE13839	AAW4 H 615	AAY 08234	AAY49892	AAE05324	AARBHARE	AAR41 524	AApsaajé	AAP99784	AAB51434	AAB51442	APPRU33/5	AAMSUSUB	AAM81129	ABG13244	AAX 605 70	AAU40589	AAMRÚUSS	AAU39525	ABG27674	AAM80742	AAM80755	AAM81208	AAW10505	AAW10508	AAR69597	AAE69598	AAFecusiya	AARGUST	AAMMEN	AARedada
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#### ALIGNMENTS

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Lartadherin (BA-45) peptide fragment (tumour associated antigen).
                                                                                                                                     Furnation associated antiqui peptide, IAA) cancer, careinoma, treatment, prevention, care, anti tument raceine, netastases, breast, blosti, prestating principles, easily, thy il, esting stomach, careinoma, McColass I, HLA A2; human, Major Histocompatibility Complex; uicplakin; prestate specific antigen, prostate specific membrane antigen; prestate acid phesoplatase, meetin, lactables in embrane antigen; teratecareinoma derived growth factor; PSA; PSMA; PAP; CRIPTO-1.
                         AAYR?844 Standard, peptide, 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                     (YEDA ) YEDA RES & DEV CO LTD. (HIQF-) HIQ-IBCHNOLOGY GEN CORP.
                                                                                                                                                                                                                                                                                                                                                             09WF-11.00417.
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                                                                                   (first entry)
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                                                                                                                                                                                                                                                                           Homo sapiens
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                                                      AAYHZH44;
             AAY 8 2844
RESULT
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AAY94453;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          associated antigens are presentable to the immune system by HLA-A2 molecules and are generally between 8 to 10 amino acids in length. The amino acids located at positions 2 and 9 of the tumnour associated antigens are the anchor residual which participate in the binding to MHC class I molecules, more specifically HLA-A2. More tumnur associated associated and only us are described in TRNESEY recents ANYBERBE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            prostate specific membrane antigen (PSMA). Those described in receids YY82836 AMY82839 are derived from prostate acid phosphotase (PAP). Those described in records AMY82840 Y82846 are derived trom lar-tacherin (BA-46). Those described in records AMY82847-Y82884 are derived from Mucin and those described in records AMY8281-Y82884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Those tumour associated antigens described in records AAY82805-Y82824
                                                                                                                                                                                                         Tumor associated antigen peptides, especially derived from uroplakin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tumour associated antigen peptides (TAA) may be used for the treatment, prevention and error of rapher or cannor metastases. The case of the breat, bladder, products, punctions, the breat, thirdid colon, stomach, head or neck cancer or a carcinoma. The tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   are derived from Teratocarcinoma derived growth factor (CRIPTO-1).
                                                                                                                                                                                                                                                                                                                  bladder, prostate, pancreas, ovary, thyroid, colon and stomach -
                                                                                                                                                                                                                                                                     useful as vaccines to prevent or cure cancers including breast,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ö
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N PSDB: AAQ91198.
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Lactadherin protein was found in exosomes produced by dendritic cells. The protein is involved in the phagocytosis of particulate antiques by dendritic cells. Exosomes produced by dendritic aclis appead to tumour antiques induce potent inhumer responses. Lactadherin or variants of it may be used in the mediation of an immune response. Variants of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chimeric isolated (human) lactadherin polypeptide that functions as an adaptor of cross-priming to eliminate pathogenic antiqens, e.g. in
                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                            component of the apical surface of the normal breast epithelial cell, was obtained by PCK and RATE methods. CDNA clones can be used to prepare MAbs for use in immunotherapy, immunohistopathology, prognosis, diagnosis, diagnosis, diagnosis, diagnosis, used to prospect or (glycosylated) in cakaryotic cells.
               used in assays to determine the presence of a cancerous tumour of
epithelial origin, and in a vaccine against neoplastic tumours
46 kD apparent molecular weight human milk fat globule antigen
                                                                                                          A complete cDNA sequence for the 46 kDa HMFG antiqen, a major
                                                                                                                                                                                                                                                                                              100.0%; Score 54; DB 16; Length 387; 100.0%; Pred. No. 0.17; Live 0, Mismatches 0, Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; lactadherin; MGF-E8; anti-tumour; immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46.48
/label- Integrin_binding_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
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/label- Lactadherin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Onalitiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY94453 ctandard; Protein; 387 AA.
                                                                       Claim 6; Page 46-47; 68pp; English.
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                                                                                                                                                                                                                                                                                                                                       Conservative
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Zlabel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              exosome, dendritic cell.
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                                                                                                                                                                                                                                                                                                                  Rest Local Similarity
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                                                                                                                                                                                                                                             Sequence 387 AA;
                                                                                                                                                                                                                                                                                                                                                                                             97 glqhwvpel 105
                                                                                                                                                                                                                                                                                                                                                                         1 GLQHWVPEL 9
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AAH32943 to AAH77195 and AAG73514 to AAG77788 represent human colon cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antiques. The colon cancer antiques have myseastive as colon cancer antiques. The colon cancer antiques have myseastive as colon cancer antiques. The colon cancer antiques the myseastive in the prevention, of diagnosis and treatment of discase associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's sense that a freet the activity of P by expression in a patient's or F supplement the patient's of P by expression of D by inspection the may be used to produce the colon concert associated is, by inspecting the colon concert associated is, and P can be used in the presenting the colon of the expression of the expression of the presenting the colon colon canditreatment of colonectal carcinomes and cancers. AAH37794 to AAH37204
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lactadherin may be used for inhibition and/or stimulation of the cross-prining of antigers and stimulation of the phagographs is of antigens by dendritic cells. Compositions derived from lactadherin can also be used to monitor an immune response, more specifically a CTL (Sytokalis 7 implacyte) response and also to produce tills specific for a selected antigen. The present sequence is the human lactadherin protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Caps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; colon cancer, colon cancer antigen; diagnosis; detection;
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                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 54; DB 21; Length 387; 100.0%; Pred No. 0.17;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                387 AA;
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                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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N.B. Pages 666 to 682 and page 7053 of the sequence listing water

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Parkinson's Insease, Somitie Theorem, Shinophushin, the disorder psoriasis, sepsis, diabetes, atherosclerosis, cardiovascular disorder, inframmation, meurological disorder, Allabeimer's disease, from additive, angiognes, disease, trond additive, angiognes, disease, trond additive, pregnancy-related disorder, endocrine disorder, intection, wound healing, cell culture, chemotaxis, vulnerary, binding partner identification;
                                                                                                                                                                                                                                                                                                                                                                                                                              Human, secreted protein, proliferative disorder, cancer, tumour, asthma, fortal abnormality, developmental abnormality, bacminging in disorder, limmune system disorder, AIDS, autoimmune disease, rheumatoid arthritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid encoding one of 21 human secreted proteins for diagnosing, proceeding, treating or administrating andical conditions, such as autohomnupe disease and cancer, and used as a lood additive or
                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Znote "Corresponds to any of the naturally occuring Leamino acids"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Corresponds to any of the naturally occuring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note- "Corresponds to any of the naturally occuring
missing at time of publication, meaning no sequences are present for \rm Spg 12 Mevilo27 to 1952, 7921 and 7922.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Znote "Corresponds to any of the naturally occuring
                                                                                                                                        :.
                                                                                                    74.1%; Score 40; DB 22; Length 217: 75.0%; Pred. No. 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Baker KP;
                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fiscella M.
                                                                                                                                                                                                                                                                                                                                                                                               Human secreted protein variant, SEQ ID NO:147.
                                                                                                                                       1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 476-477; 490pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Euken aM, komataoniis GA, Wei P,
                                                                                                                                                                                                                                                                                            AAE01423 standard, Protein; 252 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  L-amino acids"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .-amino acids"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HUMA ) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   990S-0164835.
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                                                                                                                                                                                                                                                                                                                                                               18 JUL 2001 (first entry)
                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JUL 2090, 298003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WELL 2001 909779,32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mise-difference 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc difference 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mise difference 240
                                                                                                      Query Match
Best Local Similarity
                                                    217 AA:
                                                                                                                                                                                                         193 [dbwlpr] 200
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                                                                                                                                                                         2 LQHWVPEL 9
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27 JUL 2030, 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       qene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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                                                                                                                                          : ک
                                                       Sequence
                                                                                                                                                                                                                                                                                                                              AAE01423;
                                                                                                                                          Matches
                                                                                                                                                                                                                                                            RESULT
AAE01423
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                                                                                  The secreted proteins and their genes are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Fathological conditions can be diagnosed by determining the amount of the new protein in a Sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 21 penes, based on the tissues in which they are most highly expressed, and include
                                                                                                                                                                                                                                             disorders, cancer, tumours, foetal and developmental abnormalities, haematopoietic disorders, diseases of the immune system, ALDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation, allergies,
                AAD05220-AAD05282 represent cDNAs corresponding to 21 human secreted protein genes, and AAE01352 AAE01413 represent the proteins they encode. AAE01415-AAE01433 represent human secreted protein fragments or variants.
                                                                                                                                                                                                                                                                                                        cognitive disorders (e.g., Alzheimer's disease, Parkinson's disease), cognitive disorders, schizophrenia, asthma, skin disorders (e.g., pour ais), seepsis, diabetes, atheroscheroshs, cardiovascular disorders, andioquenic disorders, kidney disorders, gastrointestinal disorders, prequancy-related disorders, endocrine disorders, and infections. The proteins can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunbarn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to requenerate tissues, to identify their cognate ligands or binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   partners, and in chemotaxis, and can be used as a food additive or preservative to modify storage properties. Antibodies specific for a provious of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in diagnostic immunoassays e.g.,
                                                                                                                                                                                                                        developing products for the diagnosis or treatment of proliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Del-1, developmentally-requiated endothelial ceil locus 1, cancer, discoldin 1; tactor VIII like domain; epidermal growth factor; EGF; diabetic retinopathy; rheumatoid arthritis; endometricsis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1945 imenorasing or curpose linked inconsendent assay (ELISA). The present sequence represents a human secreted protein variant referred to in the disclosure of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72.2%; Score 39; 188 22; Length 252;
85.7%; Pred. No. 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                O; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW98891 standard; peptide; 320 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96US-0659235.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-MAY-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Guery Match
Hest Local Similarity 85.7.
The 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UYVA-) UNIV VANDERBILT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (PROG-) PROGENITOR INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 glphwvp 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GLOHWVP 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   anglogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-JUN-1996;
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07-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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Shodgrass HR, Zupancio TT;

Queriermons T.

Hoqan B,

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The present invention describes developmentally-requiated endothelial cell locus 1 (bel-1). The protein has epidormal growth factor (BGF) like domains and discoidin 1/factor VIII-like domains. The bel-1 proteins
                                                                                                                                                                                                                                                                                                                             integrin, and is an apoptosis inducer. The prosent sequence represents a sequence given in the sequence listing but not mentioned further within the specification.
                                                                                                                                                                           have an inhibitory effect on angiogenesis (blood wessel growth), this activity may be useful clinically to prevent necroscolarisation of tissues such as tumour nodules and prevention of metastases. The anti-
                                                                                                                                                                                                                            anglequaic activity of Del-1 may be used to treat abnormal conditions that result from angloquesis, including another, dishbitic retinopally, theumatoid arthritis and endometriosis, Since Del-1 promotes anglogenesis it can be used to treat cardiac ischaemia, thrombotic
                                                                                                                                                                                                                                                                                              stroke, wound healing and peripheral vascular disease, Del-1 is also useful to: promoting bone formation. Del-1 binds to alpha V beta 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 o,

    useful for treatment of cancer,

                                                              diabetic retinopathy, rheumatoid arthritis and endometriosis
                                                                                                                                                                                                                                                                                                                                                                                                                                              72.28, acore 39, 08.20, tanjth 320;
77.88; Pred. No. 59; 2, indels
tive 0. Mismatches 2, indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; lactadherin; MGF-E8; anti-tumour; immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label- Integrin_binding_site
                                                                                             Disclosure; Column 61-62; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label Secretion_signal
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Zlabel Lactadherin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY94454 standard; Protein; 426 AA.
                                             Del-1 polypeptide sequences
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Best Local Similarity 77.ev
The 7, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse lactadherin protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 exosome; dendritic cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference 93..111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87..89
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            WFI; 1999-189720/16.
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                                                                                                                                                                                                                                                                                                                                                                                               320 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28 glgrwqpel 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GLOHWVPEL 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein
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ABB24200;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ζ
                                                                                                                                                                                                            Lactadherin protein was found in exosomes produced by dendritic cells. The protein is Involved in the phagocytosis of particulate antigens by dendritic cells. Exosomes produced by dendritic cells exposed to tumour antigens induce potent immune responses. Lactadherin or variants of it may be used in the mediation of an immune tesponse. Variants of lactadherin may be used to inhibition and/or stimulation of the resonance of antigens by dendritic cells. Compositions derived from lactadherin can also be used to monitor an immune response, more specifically a CIL cytoloxic T-lymphocyte) response and also to produce CILs specific for a selected antigen. The present sequence is the mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human, foetal liver, gese expression, single exam northie wold probe
                                                    Chimetic isolated (boman) lastadherin pelypeptide that functions as adaptor of cross-priming to eliminate pathogenic antigens, e.g. in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide #6932 sprowled by human foctal liver single exon probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a single exon numbers acid probe for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 27, SEQ ID No 31871, 639pp - sequence 1181116, Treflish.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72.2%; Score 39; DB 21; Length 426; 77.8%; Pred. No. 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2, indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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                                                                                                                                                             Disclosure; Page 12; 20pp, English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         200001S - 0236 859.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Bost Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lactadherin protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   426 AA;
N-PSDB; AAA27141.
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27.SEP.2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APP39426;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABB39426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
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measuring human gene expression in a sample derived from buman heart (see NBA21535-ABA41835). The present sequence is a protein encoded by one such frish. The probes may be used for prodefithy measuring and direlating gene expression in samples derived from the human heart via microarrays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               By measuring grading, staging, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heatt and vascular system e.g. cardiovascular disease. by recession, cardiar arthythmics and conquisted human fiscase. Note: The sequence data for this parent did not form part of the printed specification, but was obtained in electronic format directly from WIPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein #6199 encoded by probe for measuring heart cell gene expression.
                liver. The single exon nucleic acid probes may be used for predicting, measuring and dispigating gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Single each carb to acid packs the analyzing processing to Arran
                                                                       nucleic acid probe of the invention.
Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from Wibo at Itp.Wipo.int/pub/pub/ished_pct_sequences.
measuring human gene expression in a sample derived from human foetal
                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to single exon nucleic acid probes for
                                                                                                                                                                                                                                                                               0,5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human, gene expression; heart; microarray; vascular system;
cardiovascular disease; hypertension; cardiar arrhythmia;
                                                                                                                                                                                                                                     70.4%; Score 38; DB 22; Length 22;
71.4%; Pred. No. 5.3;
                                                                                                                                                                                                                                                                             l, Indels

    Mismatches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Penn SC, Bannel DK, Chen W, Runk DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ARB24200 standard; Protein; 22 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-0236359.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-MAY-2000; 2000US-0189312.
26-MAY-2000; 2000US-0207456.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-0608408.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-JAN-2001; 2001WO-US00666.
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                                                                                                                                                                                                                Query Match
Hest [And] Similarity 71 40
The S. Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 congenital heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WP1: 2001 499899/53.
                                                                                                                                                                              Sequence 22 AA;
                                                                                                                                                                                                                                                                                                                                          | |||:|
| | qtqhwip 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MO200157274-A2.
                                                                                                                                                                                                                                                                                                                     1 GLOHWVP 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04 4777 2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09 AUG 2001.
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27-SEP-2000;
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AAM72718;
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                                                                                                                                                                                                                                                                                                                                                 Penn SG,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAM19701
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probes which are derived from general as single axpressed inditals brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimmer's disease, multiple scierosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of the probes of the invention.
                                                                                                                                                                                                                                finman brain expressed single exemptobe encoded protein SEQ ID No: 32212.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Single exon nucleic acid probes for analyzing gene expression in human
                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention provides a number of single exon nucleic acid
                                                                                                                                                                                                                                                     Romann britin expressed east, proceedarsel nearlysis, probes, migroarray, Alcheimer's diseast, multiple scienosis, schizophrenia,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 38; DB 22; Length 22;
Pred. No. 5.3;
1; Mismatches 1; Indels
                                                    Soure 38; DB 22; Length 22;
Pred. No. 5.3;
                                                                       1; Indels
at ttp.wipo.int/pub/published_pot_sequences.
                                                                       1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chen W. Bank DR.
                                                                                                                                                                  AAM60107 standard; Protein; 22 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70.4%;
                                                    70.48;
71.48;
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26-MAY-2000, 2000US 0207456,
30-JUN-2000, 2000US-0608408.
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                                                                                                                                                                                                                                                                                                                                                                                                                    21-5E5-7666 2000S-024887
27-SEP-2000 2000G-0236359
04-Ont-2000 2000gB-0024263
                                                                                                                                                                                                                                                                                                                                                          30-JAN-2001; 2001WO-US00667.
                                                                                                                                                                                                            05-NOV-2001 (first entry)
                                                                       5; Comservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hannel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MPI: 2001-483446/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                            Local Similarity
                      22 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22 AA;
                                                                                                                                                                                                                                                                         epilopsy: cancer
                                                                                                                                                                                                                                                                                                                 WO200157275-A2.
                                                                                           1 GLOHWVP 7
                                                                                                               2 giqhwlp 8
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                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                             04-AMG-2000;
                                                                                                                                                                                                                                                                                                                                      09-AUG-2001
                     Sequence
                                                                                                                                                                                       AAM60107;
                                                    Query Mateb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Penn SC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        brains
                                                                                                                                              RESULT 10
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probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as symphoma, lenkaemia and myelomia. The present sequence is a protein encoded by one of the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide #6135 encoded by probe for measuring cervical gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Probe; human; microarray; gene expression; cervical epithelial cell;
                                                                                                                                                                                                                              Human; bone marrow expressed exon, gene expression analysis; probe: microarray; cancer; leukaemia; lymphoma; myeloma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention provides a number of single exon nucleic acid
                                                                                                                                                                       Human bone marrow expressed probe encoded protein SEC ID NO: 33024.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human genome derived single exon nachero acid probes useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 4; SEQ ID NO. (4024, 658pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70.4%; Score 38; DB 22; Length 22;
71.4%; Pred. No. 5.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       analyzing gene expression in human bone marrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hanzel DK, Chen W, Rank DR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA.
AAM72718 standard; Protein; 22 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-0180312.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-JAN-2001; 2001WO-US00668.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-0608408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-SEP-2000, 2000US-0234687.
27 SEP 2000, 2000US 0236359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Z0000R-0024263.
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Best Lacal Similarity 71.44,
East Lacal 5, Conservative
                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-0CT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-4889000/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 qfqhwlp 8
                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MAT 2000;
JUN 2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04 - 0x, T - 2000;
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                                                                                                                   06-NOV-2001
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N PSDB, ABL12347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pharmaceutical.
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                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to human single exon nucleic acid probes (SEME) see AAII0568 AAI28459). The present seperate is a peptide consided by one such probe. The SEMPs are derived from human HeLa cells. The SEMPs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   can be used to produce a single exon microaliay, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Note. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/pub]ished_pot_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide #6986 emoded by probe for measuring placental gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                              Human genome derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70 4%; Score 3%; DB 22; Length 22; 71.4%; Pred No 5.3;
ive 1; Mismatches 1; Indeis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Probe; microarray, human; placenta, antenatal diagnosis
                                                                                                                                                                                                                                                                                                                                                                                            Claim 27; SEQ ID Nc 24527; 487pp; English.
                                                                                                                                                                                                                                                                                    Penn SG, Handel DK, Chen W, Rank DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAM32949 standard, Frotein, 22 AA.
                                                                                                                                                                                                                                                    (MOLE-) MOLDPHLAP PYNAMICS INC
                                                                                                                               04-PER-2000; 2000US-0180312.
26-MAY-1000; 2000US-02074°6.
                                                                                                                                                                          03-ATG-2000, 2000HS-06 (200)
21-SEP-2000, 2000US-0234687
27 SEP-2000, 2000HS-02 (6359)
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                                                                                                                                                                                                                         64 - 001-20gn; Jonephy 00:2428 C.
                                                                                                   30-.rAN-2001; 2001W0-US00670
                                                                                                                                                             200001S-0608408
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                                                                                                                                                                                                                                                                                                                WPI; 2001 488901/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        genetic disorder
                                         W0200157278 AD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GLQHWVP 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 gfghwlp 8
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              Home sapiens
                                                                                                                                               26-MAY-2(000)
30-JUN-2000;
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                                                                       09-Am:-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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The present invention relates to single exon nucleic acid probes (SENF, see AAI3135-AAI57546), The present sequence is a peptide encoded by one such probe. The probes are useful for for probability of properties a minrearray for predicting, measuring and displaying sere expression in semples derived from human players. The probes are useful for anti-matal diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell octlinteractions -
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analyzan) gene expression in haman placenta -
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71.4%; Pred. No. 5.3;
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                                                                                                                                                                                                                                              (MOLE-) MOLECULAP DYNAMICS INC
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04-FPR-2000, 2000US-0180312, 25-MV-2000, 2000US-020V456, 30-TIN-2000; 2000US-0568408, 004-AVG-2000; 2000US-0234687, 27-SEP-2000; 2000US-0234687, 27-SEP-2000; 2000US-0234687, 27-SEP-2000; 2000US-02359, 64-02Y-2003; 2000US-023559
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11-JUE-ZUGU; ZUUGUS-UE14150.
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Best Local Similarity 71.4.
Fest Local Similarity 71.4.
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                          The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell cell interactions in higher newlaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIGITA-ARLAGATI), expressed tNA
                                                                                                                                                               The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from Wibg at Itp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to isolated lung tumour specific proteins and their corresponding cDNA molecules. Lung tumour-specific proteins and their antique-presenting cells are useful for stimulating and/or expanding T cells specific for a tumour protein, and for inhibiting the development of cancer. The invention also relates to a composition useful for stimulating an immune response, and for treating cancer. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; lung tumour protein, immunostimulant, cytostatic; gene therapy; antisense-therapy, vaccine, immune response; lung cancer, SCC2-29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Reed SG, Lodes MJ, Mohamath R, Secrist H, Benson DR, Indilias CY;
Henderson RA, Fling SP, Algate PA, Elliot M, Mannion J, Kalos MD;
                                                                                                                                                                                                                                                                                                                      Gaps
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Disclosure, SEQ ID NC 31524, 21pp : Sequence Listing, English.
                                                                                                                                                                                                                                                                                      Length 665,
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Pred. No. 1 96+02;
Timmstches 1; Indels
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2000US-0704512
2000US-0738973.
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2000US-0640878.
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Best Local Similarity 71.4%
Fest Local Similarity 71.4%
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                                                                                                                                                (ABB57737-ABB72072)
                                                                                                                                                                                                                                    665 AA;
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33 glehwtp 39
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18-AMG-2000;
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01-NOV-2000;
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CC dagnosis, detection and treatment of lung cancer. The present sequence of dagnosis, detection and treatment of lung cancer. The present sequence XX is human lung tumour-specific protein.

XX Sequence 4019 AA:

XX LOHWYPE 8

XX Sequence 4019 AA:

XX LOHWYPE 8

XX INTEREST 6, Conservative 0, Mismatches 1, Indels 0, Gaps 0;

XX INTEREST 6, Conservative 0, Mismatches 1, Indels 0, Gaps 0;

XX INTEREST 6, Conservative 0, Mismatches 1, Indels 0, Gaps 0;

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GenCore version 4.5
Copyright (c) 1993 - 2000 - Comp
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OM protein - protein search, using sw model

Septimient 5, 2002, 15,28.5c., Search time 19,78 Seconds (without alignments) 12,393 Million cell updates/sec Run ou

65-108-747-80-3H 1 GLQHWVPEL, 9 Title. Perfect score: Sequence:

283138 seqs, 96089334 residues Gapop 10.0 , Gapext 0.5 Searched:

Scoring table.

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DP seq length: 2000000000

Listing first 45 summaries Post-processing: Minimum Match 0% Maximum Match 100%

1 Firl \* 2: pir2:\* 3: pir3:\* 4. pir4:\* PIR\_71.\* Database ·

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

# SUMMARIES

NO.	Score	Match	Length	DB	ID	Description
	1 1 1 1					
1	₹ <b>7</b> *	77 8	401	C1	565138	alvectorio antia
C3	44.0	77.8		(1	T11743	PP47 protein pig
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4	4.7	75.9		c:	S74805	DNA plantelyase S
S	41	75.9		C4	E82708	ATP dependent heli
S	40			C1	T48787	hopesthed is all produ
7	40	74.1	285	C 1	B82336	phosphatidylserine
ω	40	74 1	с. <del></del>	C I	Edve22	Similar to Flavono
6	40	74.1	480	C I	T10020	Agonthed Load protection
10	40	74.1	512	~1	G86914	probable membrane
11	40	74.1	748	(1	T30634	hypothetical prote
12	99	72.2	219		T37794	
13	33	72.2			T36025	mississission hypothesis
14	39	72 2			E83205	hypothetical prote
15	39	72.2			JC4915	ads protein precur
16	39	72.2			A36479	milk fat globule m
17	39	72.2			E83062	decayribodipyrimid
18	39	72.2			AD0771	probable PND-famil
19	39	72.2	1155		G87477	transcription repa
ja P	î	70.4	Ş		Carado	conserved hypothet
21	38	70.4		C1	H87578	transcription regu
다 다	38	70 4		C 4	A75.819	fructose bisphosph
23	38	70.4	4	C4	S68588	niocitinio acetyloh
24	3.7	68.5	155	C J	367704	hypothetical prote
C1	3,7	η. Ε. Α. Ε.	286	c:	Sr.0312	- 0
<u>ت</u> د :	3.7	6.8			G96542	hypothetical prote
C1	3,7	68.5	392		T08772	hypothetical prate
28	37	68.5	1165		C97574	mfd protein (AF300
σ. Ci	17	6.8	1165	C1	AC2795	transcription repa

transcription-repa	hypothetical prote	probable Offsee ac	364K Golgi complex	gene HLA-DQA2 prot.	H-2 class II histo	MHC Class 11 histor	IA-alpha polyprote	IA-alpha polyprote	cell surface quyes	class II histocomp	MHC class 11 histo	Mac class II histo			
AG3595	G96595	RCBY1.	JC5837	168717	HLMSA1	A47535	A5.5271	B53271	HLEUL.	179258	179357	154290	.1H0749	HLHUD7	HLHU 4C
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3.7	5	15	37	36	35	36	3	36	'\$`;	36	36	3.	36	36	Ξ,

# ALIGNMENTS

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RESULT
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Substitution antijen MSP57/53, maramary gland burth. (fragment)
NiAlternate names: glycoprotein component 16/major fat-globule membrane protein/MFG-E Cybedes: bos primidents taurus (cattle)
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1 GLOHWVPEL 9

110 GLQPWAPEL 118 ď

#### RESULT T11743

pP47 protein - pig (fragment) C.Species. Sus sciefa demostica (demostic plg) C.Date. 19 Jul 1999 #sequence\_revision 16-Jul-1999 #text\_chasge 21 Jul 2000

C.Accession: T11743 F.Ensslin, M., V.gel, T., Calvete, J.T., Thele, H.H., Schmidtke, T., Matsuda, T., Toe Flot Reprod SR, 1957-1064, 1998

A, III Let Modecalar closing and characterization of P47, a covel tear specim assectated

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C.Superfamily: ATP-dependent RNA helicase hrpB
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N;Alternate names: protein s111629
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                           C. Species: Synechocystis sp.
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A.Molecule type: DNA
A.Residaes: 1 873 <SIM>
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                                                             A; Variety: PCC 6803
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A;Fille: Characterization of 919-93-11-11-1. FAS 6,7 from momba nows of begins milk fat glob
A;Reference number: S74211; MUID:97008954
A;Accession: S74211
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Cysupertamily: undssigned EGP-related proteins; EGP homology
E76-40/Domain: EGP homology -EGF.
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AyPesiduce, 19 85,94 110,146 105,174,216,221,248,277,245 294,594 547,556,4120,427-475
Rikim, D.H.; Kauno, C.; Mizokami, Y.
Biochim, Biophys, Acta 1122, 233,211, 1992
AyFitle: Purification and characterization of major glyroporteins, PAS 6 and PAS 7, from AyFitle: Purification and characterization of major glyroporteins, PAS 6 and PAS 7, from AyFitle: Purification and characterization of major glyroporteins.
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C.Date: 04.bec-1997 #sequence_revision 12 Dec 1997 #foxt_chings 20 Fin 2000
C.Accession: 874211; 878114; 824181
E.Hvarregaard, J.; Andersen, M.H.; Berglund, L.; Rasmussen, J.T.; Petersen, T.E.
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Ajčross-references: EMRU-X91895; NID-91632778; PIDN-CAA62997-1; PID-91632779
                                                                                                                                             A)Cross-references: EMBL:Y11683, NIE.92652927, 315N.CAA72379.1, FID.92652928
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F)66-105/Dumain: BGP homology 48Gls
F)108-105/Dumain: discoldin: lamino terminal homology 10Mls
F)24-417/Pumain: discoldin: lamino terminal homology 10Mls
F)24-417/Pumain: discoldin: lamino 'erminal homology 10Mls
F)24-417/Pumain: discoldin: discolding prodicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sile
                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 77.8%; Score 42; DB 2; Length 409; Best Local Similarity 77.8%; Pred. No. 10; Matches 7; Conservative 9; Mismatches 2; Endels
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77.8%; Pred. No. 11;
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                                                             A:Status: preliminary; translated from GB/EMBL/DDBJ
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A;Reference number: 217325; MUID:98206817
A;Accession: T11743
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                                                                                                                                                                                  A; Experimental source: testis C; Function:
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                                                                                                                        A; Residues: 1 409 <ENS>
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A; Residues: 1 127 - HVA:
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                                                                                               A; Molecule type: mRNA
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A;Title: The genema sequence of the plant pathween Xylolla fastidiosa.
A;Reference number: A882515; MCD:20385717.
A;Note: for a complete list of authors see reference number A59328 below.
                                                                                                                          E.E.Berko, T., Salo, S., Kathell, H., Tonaka, A., Asamine, F., Nukhmera, Y., Miyajima, o, K., Okumura, S., Shimpo, S., Takenchi, C., Wada, T., Watanabe, A., Yamada, M., Yas. DDA, Res. 3, 109-136, 1996.
A.T.I.l.e. Sequence analysis of the geneme of the unicollibral egapobacterium symmetrys.
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A.Pross P.Foronovs EMRL.D90909, GB.ABG01319, WID.41652841; PIPN:DAA17766.1; PID:4165
A.Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
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C.Date. 18 Aug.2000 #sequence_ferision 20 Aug.2000 #text_change 17 Mec 2000
C.Accession: E82708
C.Date: 25-Apr-1997 #scquence_revision 25-Apr-1947 #foxf_chapge 20 Jun-2000
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A;Accession: S74805
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
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A;Start codon: GTG
C;Superfamily: deoxyribodipyrimidine photo-lyase
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Cybronial Asymptotic and the composition of the com
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Alanchers Hunter, J., Lerkins, J., Johnson-Herson, C., Phan, S., Khaykin, E., Kim, Alanchers Hunter, J., Lerkins, J., Liu, Z.A., Liu, Z.A., Luros, J.S., Maiti, R., Marzia Fila, M., J. H., V., Lin, X., Liu, S.A., H., H., Zakino, H., Alanchers, Salaborg, S.L., Schwartz, H., Shinn, P., Scuthwick, A.M., Sun, H., Tallo Alauthors: Salaborg, S.L., Schwartz, J.P., Shinn, P., Scuthwick, A.M., Sun, H., Tallo Alauthors, L., M., Wunter, J.C., Davis, R.W.
Altitle: Squence and analysis of chromosome I of the plant Arabidopsis.
A)Reference number: A86141: MUID:21016719
Similar to Flavonol 3-0-Glucosyltransferase [imported] - Arabidopsis thaliana G.Species. Arabidopsis thaliana (mouse ear cress)
C.Date. 02:Mai.lett Respuedent France of C.M. Mir. 10 1 **Lext_charge 31 Mai. 2001
C.Accession: F96672
R.Theologis, A.: Eker, J.T. Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon Chin, C.W.; Ching, M.K.; Cone, L.; Conway, A.P.; Conway, A.P.; Crassy, T.H.; Dewar, ansen, N.F.; Hughes, R.; Hulzar, L.
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R/Cole, S.T., Eighmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.F.; Wheeler, P.R.; R/Cole, S.T., Eighmeier, K.; Puthoy, S.; Pelfwell, T.; Fraser, A.; Hamlin, N.; Holro eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A;Authors, Euffer, S.; Seeger, K., Simon, S., Simonda, M., Skelton, J., Squares, R.;
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A)Ctoss-references: EMBL.Y14067, NIB.92300268, FIRM.GAA75138.1, FIB.92270277
C,Genetics.
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C;Species: Mycobacterium leprae
C;Date: ?n Apr 2001 *segmener_revisios :0.Apr.2001 *fext_change 29 Apr 2001
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11vc 1; Mismatches 1; Indexs
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-452 <STO>
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West Legal Stattority
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A;Status: preliminary
A;Status: preliminary
A;Molecule type: DNA
A;Pesidues: 1-2P6 <HETS
A;Pesidued: Suurce: serogroup ol; strain N16961, biotype El Tor
C;Genetics:
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C.Species Vibrio cholerae
C.Date. 18-Aug 1860 #sequence_revision on Angraniu *rext_change_c4-Aug_2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                          RiSchulte, U : Aign, V : Hoheisol, J.; Brandt, P.; Fartmann, B., Holland, F , Nyakatura, submitted to the Protein Sequence Database, April 2000
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Riffeldelberg, 3.F. Eisen, T.A.; Melsen, W.C.; Clayton, P.A.; Gwinn, M.L.; Gwisen, E.J. Fateldelberg, 3.F. Einelaeva, M.D.; Vahethevan, G.S.; Bass, S.; Qin, H.; Liagoi, I.; Seilers, I. R.R.; Makalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Tilo. DNA Seguence of bath chasesemes of the cholesta pathegen Vibric challeta.
A;Peforence number: AR2035; MHTD,20406833
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C.Daton (65-May-2000) #sequence_revision (65 May-2000) #text_change_zM-Jul-2000
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C; Superfamily: Escherichia coii phosphatidyiserine decarboxylase
C; Keywords: blocked amino end; carbon razbon lyase; carboxy-lyase
P;251.252/Cleavage site. Gly Ser (autolytic) #status predicted
F;252,/Medified site: pyruvir acid (Ser) (in mature ferm) #status predicted
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A.Recession: T48787
A.Recession: T48787
A.Molecule type: DNA
A.Posidose 1:256 -:39H-
A.Crossionses Letter number: RMR1-AINSTREE; ASH-A-ANDELLE; NCSH-14E11.550
C.Genetics:
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C:Superfamily: Neurospora crassa hypothetical protein 13E11.350
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Best Local Similarity 62.5%; Pred. No. 16;
Matches 5; Conservative 3, Mismatches 0, 7m3-18
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66.7*, Pred. No. 14;
1ve 2, Mismatches 1, Indels
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Best Local Similarity 66.7.
Fos 6: Conservative
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658 LRHWMPEL 665
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R,Seeger, K., Hailis, D., Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the RNBL Data Library, March 1999
A,Reference number: 221581
A,Accession: T36025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ristaver, C.K., Fham, X.Q.; Erwin, A.L.; Mizaguchi, S.D., Warrener, P.; Hirkey, M.J.; adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbiq, K.: L., Lory, S.; Olsen, M.V. Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A/Status: preliminary
A/Molecule type: DNA
A/Molecule type: DNA
A/Molecule type: DNA
A/Molecule type: DNA
A/Cross-references 3H AE604772, GP-AP064091, NID 99949762, FIDA AAMSGOON 1, GSPDP CR
A/Experimental source: strain PAOl
C/Gene: PA3515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A/Title. Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa
A/Reference number AR2940, MIID 20437337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A.Residues, 1:338 (SDE)
A.Cross-references. EMBL.AL035591; PIDN:CAB38142.1; GSPDB:GN00070; SCOEDB:SCC54.12c
A.Experimental source. strain A3(2)
C.Genetics.
A.Gene. SCOEDB.SCC54.12c
C;Superfamily: Bacillus subtilis conserved bypothetical protein yveJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Pseudomonas aeruginosa
C;Pate: 15:Sep-2000 #sequence_revision 15:Sep-2000 #text_change 31:Dec-2000
C;Accession: E83205
                                                                                                                                                                                                                                                                                                                   C.Species Stratempres controller
C.Dute. 03-Dec-1999 #sequence_revision 03 Dec 1999 #text_change 19-May-2000
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                                                                                                                                                                                                                                                                                      conserved hypothetical protein SCC54.12c - Streptomyces coelicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72.2%, Score 39, 08.2; Length 338; 100.0%, Pred. No. 28; 3tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 72.2%; Score 39; DB 2; Length 357; Best Local Similarity cl.5%; Fred. No. 29; Matches 5; Conservative 2; Mismatches 1; Indels
                                1300
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A,Molecule type: DNA
75.0%; Pred No. 18;
Live 1, Misautebes
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N;Alternate names: O acetyl-Gd3 ganglioside
C;Species: Kattus norvegicus (Norway rat)
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Best Local Similarity 100.00
1455 6, Conservative
                             e, Conseivative
  Best Local Similarity
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246 HWVPEL 251
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A;Reference number: #20076, MUID:96725459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A)Gross-references: EMRL-1985-3; FIDN-7AR11642.1; GSFDB.GNÖGGG; SFDB.SFAGI.EW.14c
A)Experimental source, strain 972h-, cosmid c1658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rugert, J.J., Sisler, J.R., Keonin, E.V., Darai, G., Moss, B.
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                                                                                                              A;Molecule type: DNA'
A;Rosidues: 1-512 <STO>
A;Cross-references- GR-AL450380; NTD-913092444; PIPN:CAC29555 1; GSPDB:GN00147
C;Genetics:
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Cispecies: Schinossochuromyses pombo
Cispecies: 3 Dec 1999 #sequence_revision Of Dec 1999 #text_change iB-Aug-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A)Cross references. EMBE.U60315, Nib.gi491943, FibN.AAC55160.1, FID.g1491975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein 32L Molluscum contagiosum virus 1
NATH contagn Amenia, MCO32L
C.Species: Molluscum contagiosum virus 1
C.Date: 05-New-1999 #sequence_revision 05 Nov-1999 #text_change 11-Jul 1900
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A;Reference number: 221746.
A;Accession: T37794.
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A/Introns: 12/2: 32/3: 122/1: 158/3
C/Superfamily: Neurospora crassa hypothetical protein 13E11.350
                                                                                                                                                                                                                                                                                                             74.1%; Section 40, EB 2, Longth F12, 85.7%; Pred. No. 29, arive 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74 1%; Score 40; FB 2; Length 748; 85.7%; Pred. No. 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0, Indels
A,Title, Massive grae decay in the leptosy basiliss
A;Reference number: ARGade, MULL,ELLER?42; PMID 11244002
A;Accession: G86914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Note: MC0321,
C;Superfamily: vaccinia virus hypothetical protein 49L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status, preliminary, translated from GE/EMBL/PDRT
A;Molecule type: DNA
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A:Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                            6; Conservative
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Science 273, 813-816, 1996
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Best Local Similarity
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                                                                                      A; Status: preliminary
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279 GYQHWVP 285
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

September 5, 2002, 15:31:42; Search time 33.99 Seconds (without alignments) 10.252 Million cell updates/sec Pun on-

US-09-744-804-39 54 1 GLQHWVPEL 9 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

105224 seqs, 38719550 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total group distribution.

## SUMMARIES

	**************************************	est iditiose:	Q08431 homo sapien	5 dS o	Q95114 bos taurus	013748 schizosacch		P21956 mus musculu		P48180 caenorhabdi	P19158 saccharomyc	PO4227 mus musculu	Fi4438 mus musculu			P14436 mus musculu	201	PO4226 home sapien		homo		mus m	F01308 home sapies	TACING.	T.C.M.C.	F15981 sus scrofa	Pl4434 Mus Musculu	F20037 rattus nor.	F04228 mus musculu	P01910 mus muscula	P14100 her raugus	P54750 homo sapien			
SOLIMANTES	9		MFCM_HUMAN	MEGM_FIC	MEGM_ROVIN	YDRE_SCHPO	MUSM_PAT	MFCM_MOUSE	F16P_PHOSH	ACH1_CAEEL	TPA2_YEAST	HAZO_MOUSE	HAZU_MOUSE	HA24_HIMAN	HA2F_MOTSF	HA2P_MOTISE	HA2S_MOTTSE	HA22_BITMAN	HA23_HUMAN	HA27_HUMAN	HA2C_PIG	HA2J_MOUSE	HA21_BUMAR	HA25_HUMAN	HA26_HUMAN	HA2D_FIG	HA2B_MOUSE	HA2B_RAT	HA2D_MOUSE	HA2K_MOUSE	CM1A_BOVIN	CN1A_HIJMAN	COX1_NEUCR	CN1A_MOUSE	YA4G_SCHPO
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P09495 potato viru	P1777's potato viru	053698 mycobacteri	y9hw⊀8 pseudomonas	021074 myxine glut		Q9vle3 pyrococcus	913724 homo sapien	092972 chlamydia p	P5058 homo sapien	PS6.480 mus musculu	P50584 sus scrofa
RRPO_PVX	RRPO_PVXX3	TAM_MYCTU	1C1A_PSEAE	COX1_MYXGL	COX1_SYNVU	SYE_PYRAR	GCS1_HUMAR	SYI_CHLPN	AF4A_HUMAN	AP4A_MOUSE	AP4A_PIG
		_	_	_					_		_
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66.7	66.7	64.8	64.8	64.8	64.8	64.8	5	64.8	63.0	63.0	63.0
36	36	35	35	35	35	35	50	ž	<del>*</del>	3.4	3.4

## ALIGNMENTS

MEDIA DESCRIPTION STANDARD: PRI: 487 AA.  10 DESCRIPTION STANDARD: PRI: 487 AA.  10 OF CAT 1996 (Rel. 34, CITACLEG)  10 OF CAT 1996 (Rel. 34, CITACLEG)  10 OF CAT 1996 (Rel. 34)  11 CAT 1997 (Rel. 40, Lest acquere update)  12 CAT 1997 (Rel. 40, Lest acquere update)  13 CAT 1997 (Rel. 40, Lest acquere update)  14 CAT 1997 (Rel. 40, Lest acquere update)  15 CAT 1997 (Rel. 40, Lest acquere update)  16 CAT 1997 (Rel. 40, Lest acquere update)  18 CAT 1997 (Rel. 40, Lest acquere update)  19 CAT 1997 (Rel. 40, Lest acquere update)  19 CAT 1997 (Rel. 40, Lest acquere update)  10 CAT 1997 (Rel. 40, Lest acquere update)  11 CAT 1997 (Rel. 40, Lest acquere update)  11 CAT 1997 (Rel. 40, Lest acquere update)  12 CAT 1997 (Rel. 40, Lest acquere update)  13 CAT 1997 (Rel. 40, Lest acquere update)  14 CAT 1997 (Rel. 40, Lest acquere update)  15 CAT 1997 (Rel. 40, Lest acquere update)  16 CAT 1997 (Rel. 40, Lest acquere update)  17 CAT 1997 (Rel. 40, Lest acquere update)  18 CAT 1997 (Rel. 40, Lest acquere update)  19 CAT 1997 (Rel. 40, Lest acquere update)  10 CAT 1997 (Rel. 40, Lest acquere update)  11 CAT 1997 (Rel. 40, Lest acquere update)  12 CAT 1997 (Rel. 40, Lest acquere update)  13 CAT 1997 (Rel. 40, Lest acquere update)  14 CAT 1997 (Rel. 40, Lest acquere update)  15 CAT 1997 (Rel. 40, Lest acquere update)  16 CAT 1997 (Rel. 40, Lest acquere update)  17 CAT 1997 (Rel. 40, Lest acquere update)  18 CAT 1997 (Rel. 40, Lest acquere update)  19 CAT 1997 (Rel. 40, Lest acquere update)  10 CAT 1997 (Rel. 40, Lest acquere update)  11 CAT 1997 (Rel. 40, Lest acquere update)  12 CAT 1997 (Rel. 40, Lest acquere update)  13 CAT 1997 (Rel. 40, Lest acquere update)  14 CAT 1997 (Rel. 40, Lest acquere update)  15 CAT 1997 (Rel. 40, Lest acquere update)  16 CAT 1997 (Rel. 40, Lest acquere update)  17 CAT 1997 (Rel. 40, Lest acquere update)  18 CAT 1997 (Rel. 40, Lest acquere update)  19 CAT 1997 (Rel. 40, Lest acquere update)  19 CAT 1997 (Rel. 40, Lest acquere update)  10 CAT 1997 (Rel. 40, Lest acquere update)  10 CAT 1997 (Rel. 4	MFGM_H	UMAN
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RECEINE OF 288-37, AND IDENTICATION OF MEDIN. MEGINE 19342076; PubMed-19411933; Hardayiel B. Marsland J., Sletten K., Welenmark U.T., Fichibrita G.O., Wordshelf C., Endstroen U., Weskerhark D.T., Tichibrita G.O., Nordshelf C., Endstroen U., Weskerhark D.T., Medin. an Integral Irraphet C. Endstroen U., Weskerhark P. Frec. Natl. Acad. Sci. U.S.A. 96:8669-8674(1999). [5] CHARACTERIZATION. MIDGINE 7406887, Dubmey 9260929; MIDGINE 7406887, Dubmey 9260929; Taylor M.R., Couto J.R., Scallan C.D., Cerlani R.L., Peter "Lattenferin (Formerly RA46), a membrane associated 41yro-Verny American milk and bireast cate intolnas, profiles A verne Associated In human milk and bireast cate intolnas, profiles A verne.	z	
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                                                                       -!- SUBCELLULAE LOCATION: PERIPHEPAL MEMBRANE PEGTEIN.
-!- TISSUB SPECIFICITY: MAMMARY EPITHELIAL CELL SURFACES AND AORTIC
MEDIA. OVEREXPRESSED IN SEVERAL CARCINOMAS.
-!- PTM: MEDIN HAS A RACIGED N-TERMINUS WITH MINOR SPECIES STARTING AT
AMINO ACID 264 AND 273.
DNA COLL HIOL. 16:861-869(1997).
-!- FUNCTION: MAY BE INVOLVED AND INHIBITS ITS PEDLICATION.
SPECIFICALLY TO FOTAVLEGS AND INHIBITS ITS PEDLICATION.
-!- FUNCTION: MEDIN IS THE MAIN CONSTITUENT OF ACETIC MEDIAL AMYLCID.
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- OMNY-2000 (Rel. 39, Last annotation update)
- Lactacherin (MIF fat question EGF factor 8) (MFS-F8) (MFGM) (Sperm surface protein SP47) (PP47).
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PROSTE; PS0186; EGF_2; 1.
PROSTE; PS01285; FA58C_1; 2.
PROSTE; PS01285; FA58C_2; 2.
Signal, Glycopiotein_Milk, Fegerat, EGF-like domain; Amyloid.
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-i- SIMILARITY: CONTAINS 2 F5/8 TYEE C GOMAINS.
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InterPro, IPRO00421; PA58_C.
Pfam; PF000008; BGF; 1.
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Sus serofa (Piq).
Eukaryota, Metazoa: Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria: Cetartiodaetyla; Suina; Suidae; Sus.
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EGF-LIKE 2.
ESF-TIKE 2.
ESF-TIKE C 1.
ES-8 TYPE C 2.
CELL ATTACHMENT SITE (POTENTIAL).
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N-1 INKEP (GLCNA?...
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PROSTE; PS01186; BGF_2; 2.
FROSTE; PS01285; PASR_1; 2.
FROSTE; PS01286; FASR_2; 2.
Glycoprotein, Pspear; BGF like domain.
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | Pfam; | PF00008; | RGF; | 2; | Pfam; | PF00708; | PS_FFE_5; | 2; | SMART; | SM0018; | RGF; | 2; | SMART; | SM0073; | PASRC; | 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; P00740; LEDM.
InterPro; IPR000541; PGF-11ke.
InterPro; IPR000421; PA58_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 467 E MW
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                                                                                                                                                                                                                                                                                                     TISSUE-Testis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: PROBABITY ASSOCIATES WITH PHOSPHOLIPIDS ON THE SURFACE OF MAMMARY EPITHELIAL CELLS AND MILK FAT GLOBULES, ZONA PELLUCIDA-BINDING PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mather I.H., Banghart L.R., Lane W.S.;
"The major far globule membrane proteins, bovine components 15/16 and quinearpis GP 55, are homologicus to MGF-E8, a munime glycoprotein containing epidermal growth factor like and factor V/VIII like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALTERNATIVE PRODUCTS: 2 ISOPOPMS; A LONG FORM (SHOWN HERE) AND A SHOPT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING. THE SHORT FORM LIACKS 53 AMINO ACIDS WITHIN THE ES/8 TYPE C I DOMAIN.

TISSUE SPECIFICITY: MILK AND SPERMATOZOAN.

PTM: THE 2 G-LINKED GIZCANS CONSTIST OF GAL, GLICHAG AND FUG, WITH PROBLABLY FUG AS REDUCING TERMINAL SUGAR.
                                                                                                                                              SEQUENCE FPON N A , DAPTIAL SEGGENCE, AND CARECHYDRAFE LINKAGE SITES
STPAIN-HOLSTEIN, TISSUE-Mammary gland;
MEDLINE-97008954; PubMod-8856064;
                                                                                                                                                                                                                                                                                                                                                                                                             "Miles las el alte de 1937 pe el la sel pass MGF7,53 e e giled ty
monoclonal antibodies raised against bevine milk fat globule
                                                                                                                                                                                                                                           "Characterization of glycopichein PAS 6/7 from membranes of bovine milk fat globules.";
                                                                         Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                   Bos taurus (Bewins)
Eukaryota, Metazoa: Cherdata, Craniata, Vertebrata, Euteleostomi,
                                                                                                                                                                                                     Hvarregaald J , Andersen M H , Rerglund L., Pasmussen J.T.,
                                                                                                                                                                                                                                                                                                                                                                             Kishi M., Taniguchi Y., Adachi T., Nakada R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (NOV-1997) to the EMBL/GenBank/DDBS databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 140-146; 174-187; 233-245 AND 422 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: CONTAINS 2 ESE-11KE DOMAINS.
SIMILARITY: CONTAINS 2 E5/8 TYPE C DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biochem, Mol Biol Int. 29.545-554 (1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biochim. Biophys. Acta 1245:385 391(1995).
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                                                                                                                                                                                                                                                                            Piochem 240.628-636(1996)
                                                                                                                                                                                                                                                                                                                                   TISSUE=Mammary gland;
MEDLINE=96125736; PubMed 8541316;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-93250576: PubMod-9485470:
SP47) (BP47) (Components 15/16)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro: IPPOGO421; EGF-11ke.
InterPro: IPPOGO421; FA58_C.
                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 18-427 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 19-427 FROM N.A.
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SMART; SM00231; FA58C;
                                                                                        Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P00740; 1EDM.
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                                                                                                          NCBI_TaxID-9913;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ensslin M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Milk;
                                                                                                                                                                                                                                                                                                                                                                                             Matsuda I.;
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OLINKED (FUEL ...) (IN PAS-7).
D LINKED (FUEL ...) (IN PAS-7).
AND PAS-7.
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                                                                                                                                                                                                                                                       CELL ATTACHMENT SITE (POTENTIAL).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            offers K., Harris F., Katteil B.G., Kajandream M.A., Wood V.;
Submitted (AUG-1997) to the EMBL/Genbank/DDBJ databases.
-!- SIMILARITY: TO YEAST YBR261C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 42, 188 1; Lenath 427;
Fred. No. 2.9;
0; Mismatches 2; Indele
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15-Jul-1998 (Rel. 36, Last sequence update)
15-Jul-1998 (Rel. 36, Last annotation update)
Hyperbelical 24.4 kbg protein Cl5L8.14C in chromosome 1.
SPAC16E8.14C.
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4CBBEE3A1DC4EB24 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schinosaccharomyces pombe (Fission yeast).
Edkaryota, Funji, Asromyceta: Schinosaccharomycetes;
Schinosaccharomycetales; Schinosaccharomycetaceae;
PROSTE; PS01285; FA58C_1; 2.
PROSTE; PS01286; FA58C_2; 2.
Signal Olymproduk: Milk; Seport; PCF like domain;
Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A > F (IN REF. 1).
                                                                                                                           LACTADHERIN.
EGF-LIKE 1.
EGF-LIKE 2.
F5,8 TYPE C 1.
F5,8 TYPE C 2.
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47411 MW;
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Bost Local Similarity 77.8%;
Matches 7; Conservative
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427 AA:
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|36 GEQRWAPEL 144
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                                                                                                                              STEALN-972;
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                              Sign of
                                                                                                                                                                                                                                                                            Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1947 (Mol. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
14-rand-parin precursor (Milk Fat globule-EGF Factor 8) (MFG-E8) (O-acctyl GD3 ganglioside synthase) (AGS) (MEGM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -i- TISSUE SPECIFICITY: SPLEEN, LUNG, HEART, BRAIN AND MUSCLE.
-i- SIMILARITY: CONTAINS 2 ESF-LIKE DOMAINS.
-i- SIMILARITY: CONTAINS 2 FF/R TYPP C DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=96374422; PubMod-8780713;
Ogura K., Nara K., Watanabe Y., Kohno K., Tai T., Sanai Y.;
"Cloning and expression of ePNA for 6 avetylation of GDA
72.2%; Score 39; DB 1; Leggth 219; 75.0%; Pred. No. 5; direction 1; Miscatches 1; Tudols
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Signal, Clynagestain, Ferent, PSF-like domain, Milk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F5/8 TYPE C 1.
F5/8 TYPE C 2.
BY SIMILARITY
BY SIMILARITY
BY SIMILARITY.
                                                                                                                                                            PRT; 427 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LACTADHERIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BGP-LIKE 1
EGF-LIKE 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FOTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SMOO181; EGE; 2
SMART; SMOO231; FASR; 2.
PROSITE; FSOU022; EGE_1; 2.
PROSITE; PSO1285; EGE_2; 2.
PROSITE; PSO1285; FASRC_1; 2.
PROSITE; PSO1286; FASRC_1; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ptam; PF00754; F5_F8_type_C; 2.
PRINTS; PR00010; EGFRLOOD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              interPro; IPPGGGS61; P3F-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001438; EGF_IL.
InterPro; IPR000421; PAS8_C.
Pfam: PPGGGGK; PGF; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; D84068; BAA12210.1; -.
                              10 1 Sec 744 15:
                                                                                                                                                            STANDARD;
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2267
427
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49
60
79
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               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10116;
                                                                                    110 GLONWIPE 117
                                                         1 GLOHWVPE R
                                                                                                                                                                                                                                                                                                                                                                                                                       qanqlioside.";
                                                                                                                                                                                                                                                                MFGEB OR AGS.
   Query Match
                                                                                                                                                            MFGM_RAT
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DOMAIN
DOMAIN
                                                                                                                                                                            P70490;
                              Matches
                                                                                                                                             MFGM_RAT
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tetween the Swiss Institute of Whichformalies and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by morrprofit institutions as long as its content is in no way modified and this statement is not removed Thsape by and for commercial entities requires a tremse apprehent (See Milly/Www isbraib diginal or send an email to license@isbraib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (NoV-)497) to the EMEL/Geneank/Deel databases.
-!- FUNCTION: MAY BE INVOLVED IN PHOSPHOLIFID BINDING. ZONA PELLUCIDA-
BINDING PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-Add-1991 (Rel. 19, Created)
01-Add-1991 (Rel. 19, Last sequence update)
16-oct-2081 (Rel. 44, Last annotation update)
18-oct-2081 (Rel. 1947) (Add 19-Release (STE) (MEG E8) (MEGM)
(Spein surface protein SE47) (ME47)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  - - GEVELGEMENTAL STAGE: MKNA EXFERSSION IS DETECTABLE IN MAMMARY TYSSINE FERM NORPERANT ANDARIS & MAXIMAL IN THE LACTATING GLAND. F. SIMILAKLIY: CONTAINS 2 EGF-LIKE DOMAINS. . . SIMILAKLIY: CONTAINS 2 FF, R TYPE C POWAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND SEQUENCE OF 23-35.
TISSUR=Mammary gland:
MEDINE=910.40008; PubMod=2122462;
MEDINE=910.40008; PubMod=2122462;
Stubbs 3-10. LeVatis C., Singer K.L., Bui A., Yuzuki D.,
Stinivasan U., Parry G.,
Stinivasan U., Parry G.,
Tolin Aloging of a mouse mannery epithesial cell surface protein reveals the existence of epidermal growth factor like domains linked proc. NTT-11ke sequences ",
proc. NATI Arad Sci U.S.A. 87:8417-8421(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eskatyota, Modazoa, Cherdata, Craniata, Verrebrata, Enteleostomi;
Mammalia; Estheria, Kojestia, Sciorognathi, Moridao; Murinao; Mus.
NCEL_TaxID=10090;
                                                                                                             61 N-11NKFD (GLCNAC ) (POTENTIÁL).
230 N-LINKFD (GLCNAC . ) (POTENTIAL).
280 N-LINKFD (GLCNAC . ) (POTENTIAL).
470 N-LINKED (GLCNAC . ) (POTENTIAL).
47413 MW; EA8C8631F3EE6047 CRC64;
BY SIMILARITY.
BY SIMILARITY.
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BY SIMILARITY.
CELL ATTACHMENT SITE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i- STHATELLITAR LOTATION: PERIPHERAL MEMBRANE PROTEIN.
-i- TISSUE SPECIFICITY: MAMMARY EPITHELIAL CELL SURFACES AND
                                                                                                                                                                                                                                              Query Match 72.2%; Score 39; DR 1; Length 427; Rest Local Similarity 77.8%; Pred. No. 9.9; Matches 7; Conservative 0, Mishafohes 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                       463 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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EMBL; Y11684; CAA72380.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 23-463 FFOM N A
                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
 96
107
2267
2258
427
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611
230
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                                                                                                                                                                                     427 AA;
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                                                                                                                                                                                                                                                                                                                                                            138 GLUPWGPEL 146
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                                                                                                                                                                                                                                                                                                                        1 GLQHWVPEL 9
                                     211
254
272
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87
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230
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   DISULFID
DISULFID
                                     DISULFID
                                                                            CLSULFID
                                                                                                                                    CARBOHYD
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     FT FT FT SO
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Gibson I L., Chen I -H., Tower P A., Tabita F P.;
"The form II fructose 1,6-bisphosphatase and phosphoribuiokinase
                                                                                                                                                                                                                                                                                                                                  ) (POTENTIAL)
; (M-1ENTIAL).
;) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                   .) (POTENTIAL)
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                                                                                                                                                                                                                     CELL ATTACHMENT SITE (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FFR-1996 (Rel. 33, Last sequence quality)
15-DEC-1998 (Rel. 37, Last annotation update)
Fructose-1,6-bisphesphera — II (R<sup>2</sup> 3 L<sup>3</sup> 11) (n-fructose-1,6-
bisphosphate 1-phosphohydrolase) (FBFase II).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72.2%; Score 39; DB 1; Length 463, 77.8%; Pred. No. 11;
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Y -> S (1N REF. 2).

H -> T (1N REF. 2).

I. -> S (1N REF. 2).

E -> A (1N REF. 2).

Ε -> A (1N REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rhodobacter sphaeroides (Phodopseudomonas sphaeroides).
                                                                                                                                              Repeat, EGF like Jomain, Milk.
                                                                                                                                                                                                                                                                                                BY SIMILARITY
RY SIMILARITY
BY SIMILARITY
N-1.1NKED (GIGNAC.
                                                                                                                                                                                                                                                                                                                                             N-1.1 NKELL (CILCUAL)
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N-LINKED (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                            -> P (IN PEF
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                                                                                                                                                                                               F5/8 TYPE C 1.
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                                                                                                                                                                                                                                                                  SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 11;
0; Mishatches
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                                                                                                                                                                  LACTADHERIN.
MGD, MGI-102768; Mfg-8
InterPro: IPP00045; ESP-11ke.
InterPro: IPP001438; EGF_II
InterPro: IFE00421, FA58_C.
Piam: PF000098; EGF_E.
Pfum: PF000091; EGF_E.
                                                                           SMART, SMOC181, EGF, 2.
SMART, SMOC231, EA58C, 2.
PPOSITE, PSO0022, EGF_1; 2.
PPOSITE, PSO1186, EGF_2; 2.
PPOSITE, PSO1285, FA58C_1; 2.
PPOSITE, PSO1286, FA58C_2; 2.
                                                                                                                                                                                                                                                                  BY
BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-AMG-1991 (Pel 19, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51465 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7; Conservative
                                                                                                                                                       463
463
108
303
463
                                                                                                                                                                                                                     Signal; Glycopictein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 463 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GLQHWVPEL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=1063;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      39.
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DISULFID
                                                                                                                                                                                                                                                                                                                                 CARBOHYD
CARBOHYD
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DOMAIN
DOMAIN
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DOMAIN
                                                                                                                                                       SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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between the SWISS FFG catty is cepyright. It is preduced through a collaboration between the SWISS Institute of Broinformatics and the EMEL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license alreament (See http://www.isbrsib.ci.inn.nancol...) or send an email to license@isbrsib.ch.
genes form part of a large operon in Phodobaeter sphaeroides; primary structure and insertional medgenesis analysis."; 
Hicchemistry 20:866-860(1990).
Hicchemistry 20:866-800(1990).
I CANALYTE ADILVITY: 0 fractose 1,6 bisphosphate + 8(2)0 = D- fractose 6 phosphate + phosphate.
I THE NOW FROM THE FREEL SPECTSHOOT LIST NOT ELGHT-ACTIVATED.
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Rhabditidae, Peloderinae, Caenorhabditis.
NCBL_TaxID=6239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-BRISTOL N2;
MLECLING SELECTS : Lubmod-28627624;
MLECLING M. Allicot O. Portrand S., Bertrand D.;
"Nicoting acorgichaling receptors in the nometods cancerbabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Carbohydrate metabolism, Calvin cycle, Photosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15 DEC 1998 (Rel. 37, Last annotation update)
Acetylchcling receptor like protein, alpha type chain precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ·.
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InterPro: TPR000146; In_FR_phphtase.
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PPPOPUTE; PP00149; In FR-Phphiase; I PPOSITE; PS00124; FRPASE; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mol. Biol. 258:261-269(1996).
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nos 6, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hydrolase, Carbokydi
Multigene family.
ACT_STTE 255
SEQUENCE 231 AA;
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ID ACH1_CAEEL
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  5
  SEQUENCE FROM N.A.
MEDILE-0031897; PubMed=2164637;
Tranaka K. Nakaiste M. Tamamei F. Kaziro Y., Malsumeto K., Toh-F.A.;
"IRA2, a second gene of Saccharomyces cerevisiae that encodes a
  MEDIANE-95208358; PubMed-7900427; Eumstroin E , Griffin H , Schweizer M , "Sequence of a 10.27 kb segment on the left aim of chiomosome XV from Saccharomyces cerevisiae includes part of the IRAZ gene and a
   U; Gaps
  protein with a domain homologous to mammalian rus Giidse activating
protein.";
  ACETYLOHOLINE PROFETOR LIKE PROFEIN,
   Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Fungi, Ascomycetes;
   ASSOCIATED WITH PECEPTOR ACTIVATION
  (BY SIMILARITY).
N-LINKED (GLGNAC .) (POTENTIAL).
N-LINKED (GLGNAC ) (POTENTIAL).
   PROSITE; PS002-6; NEUKOFF_LON_CHANNEL; I.
Receptor; Postsynaptic membrane; fonic channel; Glycoprotein;
  Score 38; DR 1; Longth 498;
Pred No. 17,
   1; Indeis
  EXTRACELLULAR (POTENTIAL)
   FAN JAHRAMANUFARZ OFFER
  Saccharomycetales, Saccharomycetaceae, Saccharomyces.
   CYTOPLASMIC (POTENTIAL)
  | IPA2_YPAST | STANDADD, | PPT; 3079 AA | P19158; 008239; | O08239; | O1-NOV-1990 (Rel. 16, Last sequence update) | O1-NOV-1997 (Rel. 35, Last annotation update) | O1-NOV-199
   ALPHA-TYPE CHAIN.
   Bi SIMILAKLIY.
   U; Mismatches
   TRA2 OP CLC4 OF COST OF YOLDRIW OF OURRES
   POTENTIAL.
   POTENTIAL.
  POTENTIAL.
  Interpro; IPR000188; GABAA_receptor.
Interpro; IPR001175; Neur_channel.
  Cell Riol 10:4303-4313(1990)
   Ptam, PF02931; Neur_chan_LBD, 1.
Pfam, PF02932; Neur_chan_memb, 1.
PRINTS, PP00253; NPIONOHAMNFT
  Inhibitory regulator profeso 18A2.
  КМВ., AF022973; AAC25796.1, -.
WormPep; F25G6 3; СР09639
   57164 MW;
  70 4%;
RT 74,
   SEQUENCE OF 1-2423 FROM N.A.
   EMBL; X83887; CAA58764.7,
   6; Conservative
  49B
  161
  493
   STRAIN-S288C / FY1679;
   Pransmombrane: Signal
  498 AA;
  Best Local Similarity
  133 GLVHWVP 139
   NCBL_TaxID-4932;
  50
  1 GLOHWVP 7
  DISULPID
DISULPID
  TRANSMEM
TRANSMEM
   Query Match
  TRANSMEM
   CARROHYD
   CARBOHYD
   SEQUENCE
   PRANSMEM
   SIGNAL
  DOMAIN
   DOMAIN
   CHAIN
   TRA2_YEAST
   Matches
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   qq
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   ·.
   0; Gaps
   H 2 class II histocompatibility antigen, A·g alpha chain (Fragment). Mus musculus (Mousa) amsculus (Mousa) berdata, Craniata; Vertebrata, Dutchcostomi; Mammalia; Eutheria; Rodentia; Sciurognathi, Muridae, Musinae, Mus.
  MEDLINE-92405229, PubMed 1326414, Bussereau F., Dupont C.H., Boy Marcotto E., Mallet L., Jacquet M.; Purse C231 gene from Saccharomycos ceremision which is involved in mitochondrial infortuos is identified as IRA2 an attenuator of RAS1 and PAS2 gene products.";
  Exercia M. Karsonlour. Alexandraki D.; Sequence analysis of a 3% 2 kb sequent from the left arm of yeast chromosome XV reveals eight known genes and ten new open reading frames including homologues of APC transporters, inositol phosphatuses and human expressed sequence tags.";
  CUTY GODAL 21-325-329(1902).
-!- FUNCTION: INHIBITORY REGULATOR OF THE RAS-CYCLIC AMP PATHWAY.
STIMULATES THE GTPASE ACTIVITY OF PAS PROTEINS.
   Score 37; DR 1; Longth 3079;
Pred No. 1 70+02;
2; Mismatches 2; Indels
   +> K (IN REF. 3),
651EH2A2EEB479C0 CRC64;
   20 MAR-1987 (Pol 04, Created)
20 MAR 1987 (Fol 04, Last sequence update)
01-JAN-1990 (Rel. 13, Last annotation update)
  221 AA.
   2; Mismatches
  -!- SIMILARITY: CONTAINS 1 RAS-GAP DOMAIN.
   Pfant, PFUUGIG, RASGAP; 1.
MANAPT: SMOOT23, RASGAP, T.
PROSITE: PSOOE09; RAS_GTPASE_ACTIV_1; 1.
PROSITE; PS50018; RAS_GTPASE_ACTIV_2; 1.
  POLY - ALA.
POLY - LEH
  POLY-SER.
   POLY - SER.
  FET,
   SEQUENCE OF 1982-3079 FROM N.A.
MEDLINE-97521807; Fubmed-9178509;
   3079 AA; 351631 MW;
   IDENTIFICATION OF CCS1 AS IRA2.
   EMRL; X83121; CAA58201.1; -. PMRL; X75449; CAA53202.1; -. EMBL; Z74823; CAA99093.1; -.
  InterPro: IPR001936, RasGAP.
  EMBL; M33779; AAA34710.1; -.
                           (ABST 10:1481-148/(1994).
   Rest Lecal Similarity = F.B.
Matches 5; Conservative
   SIANDARD,
   2317
   1890
   IFA2.
putative new gene.";
  PIR; S11190; PGRY12
SGP; S0005441; IPA2
   2418 GLSYWIPNL 2426
   GTPase activation.
   ΝΟΒΙ_ΙαΧΙΝ-ΙΟΌΘΟ,
  1 CLQHWVFEL 9
  520
2469
2317
   399
  HALV_MUSE
P04227;
  SEQUENCE
   Query Mat∽h
  CONFLICT
  DOMAIN
DOMAIN
DOMAIN
  Matches
   HA2Q_MOUSE
   CHARRED MANAMAKA MANAM
  AC DIT OF OCC.
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   This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS Institute of Bioinformatics and the EMBL outstation him European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as forganized by non-profit institutions as not seen to connect in the way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See Mitp.//www.ist.si.e/Auto-ner).
   Ċ
                      MEDLINE-83285339; PubMed-6305407;
Benoist G.O., Mathis D.J., Kanter M.R., Williams V.E., McDevitt B.O.;
"Regions of allelic hypervariability in the murine A alpha immune
   MEDLINE-83285339; PubMed-6309407;
Benoist C.O., Mathis D.J., Kanter M.R., Williams V.E., McDevitt H.O.;
"Regions of allelic hypervariability in the murine A alpha immune
   0; Gaps
   H-2 class II histocompatibility antiqen, A U'alpha chain (Fragment).
Mus musculus (Mouse).
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Enteleostomi:
  Mammalia: Butheria, Rodentia, Sciuroquathi, Muridae; Musimae; Mus
   .) (POTENTIAL).
   66.7%; Score 36; DB 1; Length 221; 62.5%; Fred. No. 17; ative 2; Mismatches 1; Indels
   ECOBISEAC37DB151 CRC64;
  EXTRACELLULAR ALPHA-1,
EXTRACELLULAR ALPHA-2,
CONNECTING PEPTIDE,
  CYTOFLASMIC TAIL.
   N-LINKED (GLONAC.
  01-JAN-1990 (Fel. 13, Created)
01-JAN-1990 (Bel. 13, Last Sequence update)
01-JAN-1990 (Rel. 13, Last annotation update)
   BY SIMILARITY
  PROSITE: PSE0290; IGMHC: 1.
MHC II; Transmembrane; Glycoprotein.
   IPR001003; MHC_II_alpha.
   PF00993, MHC_II_alpha; l. SM00407; IGCl; l.
   24464 MW;
   HSSP; P01910; 11AK.
InterPro; IPR063006; ig_MHC.
  EMBL; K01925; AAA39620.1; -
   Conservative
   STANDARD,
   Cell 34:169-177(1983).
   34:169-177(1983).
   Pfam; PF00047; iq; 1.
  InterPro; IPPOARA7;
   PIR; AC2218; HIMSAL.
   221 AA:
   Query Match
Best Lecal Similarity
   SEQUENCE FROM N.A.
            SEQUENCE FROM N.A.
   167 LKHWEPEI 174
  NCBI_TaxID=10090;
   171
184
210
99
110
   2 LOHWVPEL, 9
  GPNP.
   HA2U_MOUSE
ID HA2U_MOUSE
  InterPro;
   FRANSMEM
   DISULFID
   CARBOHYD
  SEQUENCE
  NON_TER
   P14438;
   DOMAIN
  DOMAIN
  DOMAIN
  SMART
   RESULT 11
   Pfam;
   Matches
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   Caps
  16-00I-2001 (Pcl. 40, Last annotation update)
HLA class II historompatibility antiqen, Dq(4) alpha chain precursor
(DQ-DRW9 alpha chain) (Fragment).
   MEDIANE 95216512 FORMED-3879467;
MONIGORIA C., MONIGORIA C., SILVER J.;
MONIGORIAGE SEQUENCE OF an HIA-DO alpha chain derived from a DRW9 cell line, according and evolutionary implications.";
Proc. Natl. Acad. Sci. U.S.A. 82:3420-3424(1985)."
   Homo Sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
   .) (HOTENTIAL).
  66.7%; Score 36; DB 1; Length 227;
62.5%; Pred. No. 18;
  1; indels
  N LINKED (GLONAC. . .) (F) PIRTEDPIRESOCRATION CROSS.
   EXTRACELLULAR ALPHA-1. EXTRACELLULAR ALPHA 2.
   CONNECTING PEPTIDE.
  CYTOPLASMIC TAIL.
   232 AA.
  04, Last sequence update)
   2) Mismatches
   BY SIMILARFIY
  or send an email to license@isb-sib.ch).
or send an email to licensedisb-sib.ch).
   PRT;
   Interpro; 1PR003597; 19_c1.
Interpro; 1PR001003; MHC_II_alpha.
  InterPro; IPR003597; 1g_cl.
interPro; IPP001003; MHC_II_alpha.
  Plant PE00047; jq. 1.
Pram, PE00093; MHC_II_alpha; 1.
cwapm: SM00407; lGcl; 1.
   Pfam; PF00047; iq; 1.
Ptam; PF00993; MHC_II_alpha; 1.
  20-MAR-1987 (Rel. 04, Created)
   25135 MW:
  InterPro; IPR003006; Iq_MHC.
  InterPro; IPR003006; 19_MHC.
   SMART; SM00407; 1Gcl; 1. PROSITE, PS00290; 1G_MHC: 1.
   EMBL; M11124; AAA59754.1; -
   EMBL; K01926; AAA39623.1; -
HSSP; P01910; 11AK.
   STANDARD;
   Conservative
   82
176
189
215
  1661;
  PIE; A02213; HIHMY,
HSSP; P01910; 11AK,
MIM; 146880; -.
   Owery Match
Rost Local Similarity
5, Conserv
   SECUENCE FROM N.A.
  173 LKHWEPET 180
  20-MAR-1987 (Rei.
  NCBI_TaxID=9606;
  2 LQHWVPEL 9
  216
  SMART; SM00407;
   HA24_HUMAN
   DOMAIN
DOMAIN
TRANSMEM
  HLA-DQAl.
  DISULFID
   SHOTHINGE
   DOMAIN
   RESULT 12
HAZ4_HUMAN
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   o,
   MEDLINE-83285339; PubMed-6309407; Renoist C G , Mathis D.1 , Kanter M F , Williams V E., McDevitt H.G.; Regions of allelic hypervariability in the marine A aigha inmune
  BLA GLASS II HISTOCOMPATERIITY ANTIGEN,
DO(4) ALBHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
  Gaps
  Bukaryota, Metazoa, Chordata, Cianiata, Vertebrata, Euteleostomi;
Mammalia, Putheria, Budentia, Sciencynathi; Moridae, Musinae, Mus
  ) (POTENTIAL).
   N-LINKED (GLCNAC, ...) (POTENTIAL).
A -P F (IN FFF 1; AAA*9774).
E -> D (IN REP 1; AAA$9754).
C*1_CRACKAA71147 (40064).
   ) (POTENTIAL)
   ;0
  Score 36, DB 1, Length 232;
Pred. No. 18;
   01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last Sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
H-2 class II histocompatibility antigen, A-F alpha chain.
   1; Indels
   EBUD4AD44FAC79D8 CKC04:
   EXTRACELLULAR ALPHA-1. EXTRACELLULAR ALPHA-2.
  CONNECTING PEPTIDE
  CONNECTING PEPTIDE
  CYTOPLASMIC TAIL.
  CYTOFLASMIC TAIL.
   N-LINKED (GLCNAC.
A -> F (IN FFF. ]
  BY SIMILARITY.
N-LINKED (GLONAC
  BY SIMILARITY.
N-IINKED (GICNAC
   66.7%, Scol.
62.5%; Pred. No. 10,
7...
2, Mishatches
MHC II; Transmembrane, Glycoprotein, Signal.
NON_TER 1 1
  PRT; 233 AA.
   Pfam; PP00047; iq; i. Ptam; PP00047; iq; i. SMART; SMO04093; MHC_II_alpha; l. SMART; SMO0407; IGCl; l. PROSITE, PS00290; IG_MHC, l. MHC_II; Transmembrane; Glycoprotein.
   EMBL, K01904; ·; NOT_ARNOTATED_CDS.
HSSP; P01910; 11AK.
   IPR003597, Iq_cl.
IPR001004, MBC_11_alpha.
  25930 MW;
   PERON MW;
  InterPro; IPR003006; Iq_MHC.
   Conservative
   STANDARD;
   88
182
  87
181
194
1194
232
232
166
81
81
81
121
84
  C4
  195
   Cell 34:169-177(1983).
   Mus musculus (Mouse).
   InterPro; IPR003597,
   222
111
172
172
233 AA;
   121
84
191
232 AA;
   Query Match
Best Local Similarity
   SEQUENCE FROM N.A.
   178 LKHWEPEL 185
   NCBI_Tax1D=10090;
   2 LQHWVPEL 9
  <u>5</u>
  5
88
182
195
218
110
   19e
  response gene.'
   HA2F_MOUSE
P14435;
   DOMAIN
TRANSMEM
  DISULFID
CAPROHYD
   CONFLICT
   TRANSMEM
   SHOUENCE
   DISULFID
  CARBOHYD
  SEQUENCE
  CARBOHYD
   DOMA I N
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  HA2F MOUSE
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0
   0;
   Gaps
   Gaps
  Landais D., Matthes H., Renoist C., Mathis D.;
"A molecular basis for the Ta 2 and Ta 19 antiquaic determinants.";
Proc. Natl Acad. Sci H. S. A. 82:2930-2934(1985).
  Eukuryota, Metassa, Chordata, Craniata, Vertebrata, Euteleostomi)
Mammalia: Eutheria: Rodentia: Sciurognathi, Muridae; Musinae; Mus
   ) (POTENTIAL).
  :
()
  \circ
66.7%; Score 36; DB 1; Length 233; 62.5%; Pred No 18;
   66.7%; Score 36; DB 1; Length 233; 62.5%; Prod No. 18;
  1; Indels
   f class II histocompatibility antigen, A·F alpha chain.
   1, Indels
  BY SIMILARITY.
N-LINKED (GLÜNAC ) (PC 918157F9EF15416A9 OPC64)
   EXTRACELLULAR ALPHA-1. EXTRACELLULAR ALPHA 2.
   CONNECTING PEPTIDE.
  CYTOPLASMIC TAIL.
   กับเล็ก-เล็ต (หมา 13. Created)
01-JAN-1990 (หมา 13, Last sequence update)
01-JAN-1990 (หมา 13, Last annotation update)
  233 AA.
   n1-JAN-1990 (Pol 13, Created)
01-JAN-1990 (Rei, 13, Last sequence update)
  2, Mismatches
  2; Mismatches
   Gly opentuin.
  FF1 ;
  HSSP; P01910; IIAK.
Inferpro; IPPGM.vms; Tq_MHC
Inferpro; IPPGM.3547; Ig_Cl.
Inferpro; IPPGM.0103; MHC_II_alpha.
  PubMed 2581258,
   Ffam; PF60047, ig, 1.
Pfam; PF00993; MHC_II_alpha; 1.
  TENER MW.
   Pram; resolutions 1601; 1.
SMART; SM00407; IGC1; 1.
PROSTE: PROA020; IG_MBC; 1.
MBC [I] Transmembrane, Gly of RR
  EMRL; M11356; AAA39621.1; -.
   Rest Land Similarity 62 5
Matches 5; Conservative
                                Rost Local Similarity 62 5
Matches 5; Conservative
  STANLIARLI
  STANDAFF
   182
195
231
  Mus musculus (Mouse).
  222
111
122
233 AA;
   SEQUENCE FROM N.A.
  MEDIINE-85190610,
  NCBI_TaxID=10090;
   179 LKHWEPEI 186
   179 LKHWEPEI 186
   2 LQHWVPEL 9
  2 LOHWVPEL 9
   HADS_MOUSE
  HA2F_MPUSE
P14436;
  Query Match
         Query Match
   TEARSMEM
  DISHLFID
  CARBOHYD
   SECTIONS
   DOMAIN
  DOMAIN
   P14437
  HA2R_MOUSE
   RESULT 15
   HAZS_MOUSE
   SEPTETET SEPTEMBER OF SEPTEMBER
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   0
   Gaps
   MEDLINE-85190610; PubMed 2581258;
Landais D., Matthes H., Henoist C., Mathis D.;
"A molecular basis for the 1a.2 and 1a.19 antiqenic determinants.";
Proc. Natl. Arad. Sri. H. S. A. 82:9938-9934(1985).
                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodenlia; Sciurognathi; Muridae; Murinae; Mus.
   BY SIMILARITY.
N EJEKED (GLCHAC. . .) (FÜLENFIAL).
6652ED01A87F3019 CRC64;
   0
  Query Match 66.7%; Score 36; DB 1; Length 233; Best Local Similarity 62.5%; Pred. M.J. 18, Matches 5; Conservative 2; Mismatches 1; Indels
                  H-2 class II histocompatibility antigen, A-S alpha chain.
  EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
CONNECTING PEPTIDE.
  CYTOPLASMIC TAIL.
01-JAN-1990 (Rel. 13, Last annotation update)
   MHC II; Transmembrane; Glycoprotein
DOMAIN 1 88 EXTRACE
  InterPro; IPR001003; MHC_II_alpha.
Pfam; PF00047; iq; ].
Pfam; PF00047; iq; ].
SMART: SM00407; IGC!: 1.
PROSITE: PS00290; IG_MHC: 1.
  25801 MW:
  InterPro; IPR003006; Iq_MHC.
InterPro; IPR003597; Iq_c1.
  EMBL; M11358; AAA39622.1; -.
   182
195
221
233
167
  222
111
122
122
233 AA;
   llak.
   SEQUENCE FROM N.A.
  NCBI_TaxID=10090;
  2 LQHWVPEI, 9
  DOMAIN
DISULFID
  TRANSMEM
  SECTIENCE
  CARBOHYD
   DOMAIN
 δ
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Search completed: September 5, 2002, 15:31:42 Job time: 477 sec

179 LKHWEPEI 186

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GenCore version 4.5 Capyiblit (c) 1993 + 2000 (compages Lid.
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OM protein - profein search, using sw model

September 5, 2002, 15:31:04 ; Search time 172.86 Seconds (without alignments) 12 67% Million cell updates/see Run on.

US-09-744-804-39 Perfect score: Title:

1 GLOHWVPEL 9 Seduemie BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

562222 seqs, 172994929 residues Sear that.

562222 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2003000000

Post-processing: Minimum Match 1008
Maximum Match 1008
Listing first 45 summaries

Database :

sp\_vertebrate:\*
sp\_un-lassified:\*
sp\_urvitus.\*
sp\_bacteriap:\*
sp\_archeap:\* SPTREMBL\_19:\*

1: Sp\_archea:\*
2: sp\_bacteria:\*
3: sp\_fungi:\*
4: Sp\_human:\*
5: Sp\_invertebrate:\*
6: Sp\_mammal:\*
7: Sp\_mhc:\*
8: Sp\_oid;\*
9: Sp\_plage:\*
10: Sp\_plage:\* sp\_plant:\* sp\_virus.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| SOUTH TES | Ouery<br>Match Leagth DB ID Description |       | 363 6 077718 | 453 16 P77967 | 521 2 00aps4 | 833 16 048509 | 256 3 OPPCY1 | 285 16 | 337 12 011317 | 452 10 09x104 | 480 3 | 74.1 512 16 Q9CDD9 09cdd9 mycobacteri | 748 12 298200 | 1005 2 243758 | 61 10 J947R5 | Constant Co. D. Co. | 200 |
|-----------|-----------------------------------------|-------|--------------|---------------|--------------|---------------|--------------|--------|---------------|---------------|-------|---------------------------------------|---------------|---------------|--------------|---------------------|-----|
| o#        | Ouery<br>Match Le                       | 100.0 | 85.2         | 75.9          | 75.9         | 75.9          | 74.1         | 74.1   | 74 1          | 74.1          | 74.1  | 74.1                                  | 74 1          | 74 1          | 72.2         |                     | /   |
|           | Scote                                   | 54    | 46           | 41            | 41           | 41            | 40           | 40     | 40            | 40            | 40    | 40                                    | 40            | 0.7           | 39           | o c                 | 33  |
|           | Result<br>No.                           |       | C4           | ec            | 4            | 5             | vc.          | 7      | œ             | 6             | 10    | 11                                    | 12            | 13            | 14           | u                   | 7   |

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| Oggwgl mus musculu<br>Ogg774 methanococc |        | <b>*</b> # |      | 29rlx9 mus musculu | O9brdC pseudomonas | 29a782 canlobacter |      | Q9xnd2 erythracaru | 0        | Ogerp85 pasteurella | Ľ.                |        |        |        |        | Q42070 arabidopsis | LT:    | SECTOR CHICAGOLILA V | 095548 sus scrofa | 093475 xenopus lae | 093476 xenopus lae | v9xnc8 halacaropsi | Q9h0g3 homo sapien | LC.      | 296m21 homo sapien |    | 034176 klebsieila |
|------------------------------------------|--------|------------|------|--------------------|--------------------|--------------------|------|--------------------|----------|---------------------|-------------------|--------|--------|--------|--------|--------------------|--------|----------------------|-------------------|--------------------|--------------------|--------------------|--------------------|----------|--------------------|----|-------------------|
| 1 040W01<br>0977V4                       | Ø92513 |            |      |                    |                    | S Q9A782           |      | CONNEC             | 6 Q9A510 | ೯ ೧೮೧೯೫೯            | n <u>0</u> 9thrts | O9W241 | 094154 | 09500  | Q9NR13 |                    |        | 020168               | 005548            | 3 093475           | Ψ.                 | SCN SC             | ٠,                 | 2 OFFERS | _                  |    | 034176            |
| 192 1                                    | 338 2  | 357 14     | _    | _                  | _                  | _                  | ~4   | 183 8              | 238 16   | 288 16              | 635, 10           | -      | 740 3  | 1335 4 | 4025 4 | 67                 | F) 174 |                      | 134 7             | 7                  | 158 1              |                    |                    | 1. 045   |                    |    | 286 2             |
| 72.2                                     | 1 1    | 42.2       | 72.2 | cr.                | 72.2               | 72.2               | 70.4 | 70.4               | 70.4     | 70.4                | 70.4              | £.57   | 70.4   | 70.1   | 70.4   | 68.5               |        |                      | 68.5              |                    | ر.<br>ع            |                    | 68.5               | r<br>x   | 68.5               |    | 68.5              |
| ტ. წ.                                    | 5.5    | di<br>C    | 39   | 39                 | 39                 | 39                 | 38   | 38                 | 38       | 38                  | 8.5               | 38     | 38     | 38     | 38     | 3.7                | 5.5    | 3.7                  | 37                | 37                 | 47                 | 3.7                | 37                 | 3.7      | 3.7                | 37 | 37                |
| 17                                       | 1      | 20         | 21   | C1                 | m<br>CI            | \$0                | 57   | 2                  | 27       | 28                  | 53                | 35     | 31     | 32     | 33     | 34                 | 5,     | 36                   | 37                | 38                 | Э,<br>Ү,           | 4 ≎                | 41                 | 4.5      | 43                 | 44 | 45                |

### ALIGNMENTS

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| rsylves) FASSULS) 5.<br>domain: Glycoprotein.<br>335 AA, 37523 MW,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     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| PS01286; FAS8C_2; 2.<br>domain: Glycoprotein.<br>335 AA, 37523 MW,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | PS01286; FA58C_2; 2.<br>domain: Glycoprotein.<br>335 AA, 37523 MW,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | PS91286; FAS8C_2; 2.<br>demain: Glycoprotein.<br>335 AA, 37523 MW,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | PS01286; FA580_2; 2.<br>domain: Glycoprotein.<br>335 AA: 37523 MW.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | PS01286; FA58C_2; 2.<br>domain; Glycoprotein.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
| PSGLI285, PASBC_1; 1.<br>PSGLI285, PASBC_2; 2.<br>demain; Glycoproficin.<br>335 AA, 37523 MW,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | PSG1285; FASRC_1; 1.<br>PSG1785; FASRC_2; 2.<br>demain: Glycoprofein.<br>335 AA, 37523 MW.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | FS01285; FA58C_1; 1.<br>PS01286; FA58C_2; 2.<br>domain: Glycoprotein.<br>335 AA, 37523 MW,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | PS01285; FA58C_1; 1.<br>PS01286; FA58C_2; 2.<br>domain: Glycoprotein.<br>335 AA. 37523 MW.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | ES01285; FA58C_1; 1.<br>PS01286; FA58C_2; 2.<br>domain; Glycoprotein.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
| FS01285; FAS8C_1; 1.<br>FS01285; FAS8C_2; 2.<br>demain; Glycoprotein.<br>335 AA, 37523 MW.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | FS01285; FAS8C_1; 1.<br>FS01285; FAS8C_2; 2.<br>demain: Glycoprotein.<br>335 AA, 37523 MW.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | FS01285; FAS8C_1; 1.<br>PS01285; PAS8C_2; 2.<br>domain; Glycoprottin.<br>335 AA, 37523 MW,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | FS01285; FAS8C_1; 1.<br>PS01286; FAS8C_2; 2.<br>demain: Glycoprotein.<br>335_AA. 37533 MW.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | FS01285; FA58C_1; 1. FS01286; FA58C_2; 2. domain; Glycoprotein.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| USGLIBS: BOF_J; 1.<br>PSGLIBS: FASBC_J; 1.<br>PSGLIBS: FASBC_J; 2.<br>demain: Glycoprotein.<br>335 AA, 37523 MW,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | USGLI85; ECF_J; 1.<br>PSGLI85; FASBC_J; 1.<br>PSGLI85; PASBC_D; 2.<br>domain; Glycoprotein.<br>335 AA, 37523 MW.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | PSGLESS: BCFLJ: 1. PSGLESS: PASSCLI: 1. PSGLESS: PASSCLI: 1. Admain: Glycoprotein. 335 AA, 37523 MW,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | ESG1286; ECF_J; 1.<br>ESG1285; EAS8C_1; 1.<br>ESG1296; EAS8C_2; 2.<br>domain: 3. A. S7503 twi                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | FSG1186; EGF_J; 1.<br>FSG1285; FA58C_J; 1.<br>FSG1286; FA58C_Z; 2.<br>domain; Glycoprotein.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
| PSG1265 20F_1) GARMAN<br>PSG1265 PASSG_1) 1.<br>PSG1265 PASSG_2) 2.<br>dondin; Glycoprotein.<br>335 AA, 37523 MW,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | FSGL186; DOF_1; UNCOLUBER FSGL185; PASSC_1; 1. PSGL185; PASSC_2; 2. domain; Glycoprotein. 335 AA, 37523 MW,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | ESSLES; SOF 1; CALLES ESSLES; PASSC_1; 1. PSS1285; PASSC_2; 2. domain; Glycoprotein. 335 AA, 37523 MW,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | ESGLES; DOFL! GALLOCK<br>ESGLES; PASGL! 1.<br>PSGLES; PASGL! 1.<br>PSGLES; PASGL! 2.<br>Admain: Glycoprotein.<br>335 AA. 37533 MM.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | ESCLERE; ECF_1; CALLON ESCLERE; EASE_1; 1. FSCLERE; FASS_1; 1. FSCLERE; FASSC_2; 2. domain; Glycoprotein.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
| PSSULZE: BDE_1, URERAM<br>PSGLZES: PGP_2; 1.<br>PSGLZES: PASSC_1; 1.<br>PSGLZES: PASSC_2; 2.<br>demain: Glycoprotein.<br>335 AA, 37523 MW,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | PSGULZ2 BDE 1 UNERWA<br>PSGLESS PASSCL1 1<br>PSGLESS PASSCL1 1<br>PSGLESS PASSCL2; 2<br>domain: Glycoprotein,<br>335 AA, 37523 MW,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | FSSULE: 50E_1, UNERWAW<br>FSSULES: PASSUL: 1.<br>FSSULES: FASSUL: 1.<br>PSSULES: FASSUL: 1.<br>Admain: Glycoprotein.<br>335 AA, 37523 MW,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | FSSC12- 505-1, URENAM FSSC12-5 1. FSSC1285; PASSC1: 1 PSSC1285; PASSC2: 2. domain: Glycoprotein. Glycoprotein. Glycoprotein. Mys. AA. 37533 MW                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | PSOUCH: BGEL, UNERAW<br>PSOLUSE: BGEL: 1.<br>PSOLUSE: PASSCL: 1.<br>PSOLUSE: PASSCL: 2.<br>Gemain: Glycoprotein.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
| FEGURES TO THE NOTE OF THE PROPERTY OF THE PRO | PSGULES DELL UNERNOM<br>FSGLISS DOFL; UNERNOM<br>FSGLISS; PASSCL; 1.<br>PSGLISS; PASSCL; 2.<br>domain; Glycoprotein.<br>335 AA, 37523 MW.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | FSCHILL TANKE, UNERWOM FSCHILL THE FSCHIBS; BOF 2: 1 1. FSCHIBS; BOS 2: 2: 2: 4000 for 1: 535 AA, 37523 MW,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | FEGULAR DE L. UNERNAM FEGULAR DE LA 1. L'SGLIRES FERBCLIS 1. PSGLIRES FERBCLIS 1. PSGLIRES FERBCLIS 1. GLYCOPTOTOTIN 315 AA. 375.33 MW.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | FSCULZ: 35-1, UNERAW<br>FSCULSE: 90F-3; 1<br>FSCULSE: FASEC1; 1<br>FSCULSE: FASEC1; 1<br>FSCULSE: SASSC2; 2<br>domain: Glycoprotein.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
| MOGEST, FACKS, 2, URERAW<br>PSSULMES, BOELST, URERAW<br>PSGLESS, FASSCL, 1,<br>PSGLESS, FASSCL, 1,<br>PSGLESS, FASSCL, 2,<br>Gundin; Glycoprotein,<br>335 AA, 37523 MW,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | MODELL FACKS, 2. PSGULMES, BASHLI, UNCHAMING USGULMES, BOELS, 1. PSGULMES, PASHCLI, 1. PSGULMES, PASHCLI, 1. PSGULMES, PASHCLI, 2. domain; Glycoprotein, 335 AA, 37523 MW,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | MODER, FARR, 2. PSGLISS, BORLL, UNERNAM FSGLISS, BORLL, 1. FSGLISS, PASRC, 1. FSGLISS, PASRC, 2. Gomain, Glycoprotein. 335 AA, 37523 MW,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | MODELL, FARK, 2, URERAW<br>FYSICLES, EDELL, URERAW<br>FYSILES, FASECLI, 1,<br>FYSILES, FASECLI, 1,<br>FYSILES, FASECLI, 2,<br>GOMENT, GLYOPPOTECTIN,<br>315, AA, 37533, MM.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | Money, FASS, 2, UNERDA PSCULL, UNERDA PSCULLE, UNERDA 1, 1 UNERDA PSCULLE, 1 UNGLES, PASSCL, 2, demain, Glycoprotein.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
| MOUGUL, SESTING, 1. MOUGUL, SESTING, 2. FYSURILL, SOEL, UNCHAUM FYSURISE, SOEL, 1. FYSULWS, PASSCL; 1. FYSULWS, PASSCL; 2. GOMINI, GLYCOPFORCEN, 335 AA, 37523 MW,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | MOGGOL, 252_11ke, 1. MOGGOL, 1. FORD, 2. FSGULZ, 2. FSGULZS, PASSC_1; 1. FSGULZS, FASSC_2; 2. domain: Glycoprotein. 335_AA, 37523_BW,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | MOUGUL, 155_11KP, 1. MOUGUL, 15682, 2. FSGULLE, 105_1, URENAW FSGULLES, 205_1, 1. FSGULRS, FASBC_1, 1. FSGULRS, FASBC_1, 2. domain, Glycoprotein, 335_AA, 37523_MW,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | MOGGOL, 252_11ke, 1. MOGGOL, 16686, 2. FSGULZ, 21. FSGLZS, FASSC_1, 1. FSGLZS, FASSC_1, 1. FSGLZS, FASSC_2, 2. domain, Glycoprotein, 315_AA, 37523 MW                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | Moudel, 252_11ke, 1. Mond31, 1665, 2. FSSucci, 202_1, URRHAW FSSuces, 202_1, 1. FSSuces, 202_2, 1. FSSuces, 203_202_2, 2. domain: Glycoprotein.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| MODEOL, EGE_like, 1. MODEOL, FASKE, 2. FYSULLES, EGE_J, UNERAW FYSULLES, EGE_J, 1. FYSULLES, FASRC_J, 1. FYSULLES, FASRC_J, 2. GOMMAIN: Glycoprotein. 335 AA, 37523 MW.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | MODEOL, EGE_like, 1. MODEOL, FARK, 2. FROUTLE, EGE_J, UNERGW FSGLESS, EGE_J, 1. FSGLESS, PASSC_J, 1. FSGLESS, PASSC_J, 2. Gendin, Glycoprotein, 335 AA, 37523 MW,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | M00001, EGE_like, 1. M00001, FASE, 2. FSGL265, EGE_J; 1. FSGL265, EGE_J; 1. FSGL265, EGE_J; 1. FSGL265, FASE_J; 1. FSGL265, EASE_J; 2. demain, Glycoprotein. 335 AA, 37523 NW,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | MODGOL, EGE_11ke, 1. MOGGOL, FASKS, 2. FSGULLE, EGE_1, UNERGW FSGULES, EGE_1, 1. FSGULES, FASEC_1, 1. FSGULES, FASEC_1, 2. AGMAINT GLYCOPTOTOTION 335 AA. 37533 MW                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | MODBOL, EGE_Like, 1. MODBOL, FASK, 2. FYSULLES EDSE_L, UNCHANK FYSULRES, EGE_J, 1. FYSULRES, PASRC_J, 1. FYSULRES, PASRC_J, 2. GOMELIN, GIVOUPTOTETH.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
| MODERT ESETIE: 1. MODERT ESETIE: 1. MODERT FORE; 2. MODERT ESETIE: 1. UNERWAR ESCULZES ESETIE: 1. UNERWAR ESCULZES FASSC_1; 1. PSOLZES FASSC_1; 1. PSOLZES FASSC_1; 2. GOMBIN: Glycoprotein. 335 AA, 37523 MW,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | MODERT ESETIE. 1. MODERT ESETIE. 1. MODERT ESETIES. 1. FESCULAS: ESETIES. 1. UNERWAR ESGLISS: PADEC. 1. FESCULAS: PADEC. 1. FESCULAS: ESSC. 2. domain: Glycoprotein. 335 AA. 37523 MW.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | MOORN, EGE_IR. MOORN, EGE_IR. MOORN, FASE_IR. FSULLES, EGE_J, UNERWW FSULLES, EGE_J, 1. FSULLES, FASE_J, 1. FSULLES, FASE_J, 1. FSULLES, FASE_Z, 2. domain, Glycoprotein. 335 AA, 37523 MW,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | MODERT ESETIE. 1. MODERT ESETIE. 1. MODERT FASS, 2. FYS. CLEER ESETIE. 1. FYS. CLEER ESETIE. 2. JOHN TO STORY THE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | MOORY, EGF. 1.<br>MOORD, EGF_11ke, 1.<br>MOORD, FARE, 2.<br>FSGULES, EGF_1, UNERWW<br>FSGLLES, EASBC_1, 1.<br>FSGLLES, FASBC_1, 1.<br>FSGLLES, FASBC_1, 2.<br>Gemain, Glycoprotein.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
| MODIBL EGE, 1. MODIBL EGELIKE, 1. MODIBL EGELIKE, 1. KNOWLLE, EGELIK, UNERNOW FESULES, EGELI, UNERNOW FESULES, EGELI, 1. FESULES, PASBCL; 1. FESULES, PASBCL; 2. domain, Glycoprofein. 335 AA, 37523 MW,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | M00181, EGF 1.  M00001, EGF 1.  FOULD ESCITA DELLINERAM FSGULZES DELLI UNERAM FSGULZES PASSC_1: 1.  FSGULZES PASSC_1: 1.  FSGULZES PASSC_2: 2.  domain: Glycoprotein. 335 AA, 37523 MW.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | M00181, EGF, 1,<br>M00201, EGF, 1,<br>M00301, EGF, 1,<br>FSUCLE, EGE, 1,<br>FSULES, EGE, 1,<br>FSULES, EASBC_1, 1,<br>FSULES, FASBC_1, 1,<br>FSULES, EASBC_1, 2,<br>Gamain, Glycoprotein,<br>335 AA, 37523 MW,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | M00181, EGF 1. M0031, EGF 1. M0031, EASS, 2. FSULLE, EGF 1. UNERUM FSULLES, EASS(1) 1. FSULLES, FASS(1) 1. FSULLES, FASS(2) 2. Gomdin, Glycoprotein. 375, AA. 375,3 MW                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | MODEL, EGF. 1. MODEL, EGF. 2. MODEL, EGF. 2. MODEL, EGF. 2. MODEL, EGF. 3. MODEL, |
| MODERL FOR 1. MODERL FOR 1. MODERL FOR 1. MODERL FORE; 2. FYSULLES DELL; UNEROW FYSULLES; EASBC_1; 1. FYSULLES; FASBC_1; 1. FYSULLES; FASBC_1; 2. GOMERL FORES FASBC_1; 2. GOMERL STRONGIN. 335 AA, 37523 MW.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | MODELL EGF. 1. UNERAW USGLES; EGF. 1. USGLES; PASSC. 1. PSGLES; PASSC. 1. PSGLES; PASSC. 1. PSGLES; PASSC. 1. PSGLES; PASSC. 1. Admidin; Glycoprotein. 335 AA, 37523 MW,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | MOOSOL ESF. 1. MOOSOL ESF. 1. MOOSOL, ESF. 1. ESGLES; BAFE. 1. FSGLES; BAFE. 1. FSGLES; BAFE. 1. FSGLES; PAFS. 1.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | MODGOL BEFFLIGHT MODGOL EGF. 1. MODGOL, EGF. 1. MODGOL, EGF. 1. FYSULLE, EGF. 1. URRAW FYSULLES, EGF. 1. FYSULLES, FASEC. 1. F                                                                                                                                                                                                           | MOOSOL ESF. 1. MOOSOL ESF. 1. MOOSOL ESF. 1. FYSOLICE SOF. 2. FYSOLICE SOF. 1. FYSOLICES ECF. 1. FYSOLICES ECF. 1. FYSOLICES ECF. 1. FYSOLICES EASBC. 1. FYSOLICES FASSC. 2. JOHN FYSOLICES EASBC. 2. JOHN FYSOLICES EASBC. 3. JOHN FYSOLICES EASBC. 3 |
| PRODOLO, PEPRICON MODISI. 1. MODISI. MODISI. 1. MODISI. MODISI. 1. MODISI. 1. GIYOOPTOTOIN. 335 AA. 37523 MW.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | PRODOLO, PEPRICON MODISI. 1. MODI | PRODOTO, BEPRIADO<br>MODIST, ESF. 1.<br>MODIST, FASE, 1.<br>FISULIZE, EDELL, UNERAW<br>FISULIZE, EDELL, 1.<br>FISULIZE, EASECL; 1.<br>FISULIZE, FASECL; 1.<br>FISULIZE, FASECL; 1.<br>SAS AA, 37523 MW,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | PRODOLO, POPRIODO<br>MODINI, ESFII.<br>MODINI, ESFIIR. 1.<br>MODINI, ESFIIR. 1.<br>PSGULES, ESFII. UNEROW<br>ESGULES, PASECL; 1.<br>FSGURES, PASECL; 1.<br>FSGURES, PASECL; 1.<br>AGMENT GIVOPOTOTORIN.<br>335 AA. 37533 MM.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | PRODOTO, POPRIODO<br>MODOTA, ESF, 1.<br>MODOTA, FARK, 2.<br>PSOULES, DOELL, UNERAW<br>FSOULES, PASSCL1, 1.<br>PSOLLES, PASSCL1, 1.<br>PSOLLES, PASSCL1, 1.<br>PSOLLES, PASSCL1, 1.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | PRODUCT PASS C. PRODUCT PRODUC |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
| PPROGUATE FASEC.   PRODUCT   PROGUE     | PRODUCT FASEC. PRODUCT FEFFICOR MODEL ESF. 1. FSGLES FASEC. 1.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | PRODUCT FASS C. PRODUCT C. PRODUCT FASS C. PRODUCT FASS T. 1. MODEOL, EGE LIKE, 1. WELKOWN C. FASS C. 1. PSOLIES; EGE L. 2. demain: Glycoprotein. 355 AA, 37523 MW,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | PPROGUATI FANGE,   PROUDTO   PREPROGE   PROUDTO   PREPROGE   PROUDTO   PROUDTO   PROUDTO   PROUDTO   PROUDTO   PROUDTO   PROUPES   PASSCAL   PROUDTO   PRO                                                                                                                                                                                                             | PPROGRAFIE FASS_C.   PROGRAM   PRO   |
| FIGURES PASSONS TO PRODUCT STREET PRODUCT STREET PASSONS PASSO | FROM   FARE      | FIGURES PASSONS TO SERVICE PRODUCTS PER PASSONS PASSON                                                                                                                                                                                                                                               | JENOUGH                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | JEMONG 450 BOK_11.<br>  PROUNTS, FASEC.<br>  PROUNTS, ESPRINGS<br>  MONGRI. ESF. 1.<br>  MONGRI. ESF. 1.<br>  ESCRILE, ESF. 2.<br>  ESGLIES, EASEC. 1.<br>  ESGLIES, EASEC. 1.<br>  ESGLIES, FASEC. 1.<br>  ESGLIES, FASEC. 1. 1.<br>  ESGLIES, FASEC. 1. 1.<br>  ESGLIES, EASEC. 1. 1.<br>  ESGLIES, EASEC. 1. 1.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
| 1   1   1   2   2   2   3   3   4   4   5   5   5   5   5   5   5   5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | : IPRU01438: BGF_II. FRANCOOTO, PASH_C. FRONCOOTO, FAREILON MOOTEL EGFTI.O. MOOTEL EGFTI.O. FRONCOOTO, FAREILON FRONCOOTO, FAREILON FRONCOOTO, FAREILON FRONCOOTO, OTO, OTO, OTO, OTO, OTO, OTO, OTO                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | ; JPKUU1438; BGF_II.<br>PFORUTAL: FASH_C.<br>PFORUTAL: EGF. I.<br>MOOTRI, EGF. I.<br>MOOTRI, EGF. I.<br>MOOTRI, EGF. I.<br>FSOULE: EGF_IK. I.<br>FSOULE: EGF_I.<br>FSOULE: EGF_I.<br>FSOULE: EGF_I.<br>FSOULE: EGF. I.<br>FSOULE: EGF. I | : JPKU01438: PGF_II. : JPKU01438: PGS_II. PF001010; PGSFII.OP MO0181: EGFFII.OP MO0181: EGFFII.OP MO0181: FGFII.OP FSULES: DSE_II.OP FSULES: PGSE_II. FSULES: P                                                                                                                                                                                                           | ; !PKUU 438; BGF_II.<br>PFORUMATI: PASH_C.<br>PFORUMATI: PASH_C.<br>MODIRI, EGF, I.<br>MODIRI, EGF, I.<br>MODIRI, EGF, I.<br>MODIRI, EGF, I.<br>FORUMATI: PASH_C.<br>FSGLIB6; BOF_J; I.<br>FSGLIB6; BOF_J; I.<br>FSGLIB6; PASH_C.<br>FSGLIB6; PASH_C.<br>GOMELIN: GLYOUPTOTEIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| Through as Estillated Personal | Through as Estilla. Through as Estilla. Through as ESF 11.  PROBOTH ESF 11.  MODEL ESF 1.  MODEL ESF | i Precoudati Estilite. i Precoudati Fasa_C. precond parenton. MODSOL, EGE_Lite. 1. MODSOL, EGE_Lite. 1. MODSOL, EGE_Lite. 1. FORCELSE: ESCH_L; 1. FORCELSE:                                                                                                                                                                                                                                                |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | PROUGUSEL SEFTINGS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
| PRO00561 BGF-11ke.  PROU01438 BGF-11.  PROU01438 BGF-11.  PRO0010 BGF-11.  MO0181 BGF-1.  MO0181 BGF-1 L.  M | IPR000561                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | ; IPR000561; EGF-11ke.; IPR0001438; EGF_11.; IPR0001438; EGF_11.; IPR000101; EGF_11.; EGF_11.; EGF_11.; EGG_11.; EGG_11.; EGG_11.; EGG_12.; EGG_12.                                                                                                                                                                                                                                               | ; IPR000561; BGF-11ke.; IPR0004488; BGF_11.; PR0001438; BGF_11. PR000101; BGFRIADD MOOSEL, ESF. 1. MOOSEL, ESF. 1. ESGLES; EGF_1, U.F.NAMOSEL, EGF_1, U.F.NAMOSEL, EGF_2, 2. ESGLES; EGF_2, 1. ESGLES; EASBC_1; 1. ESGLES; EASBC_2; 2. domain: Glycoprotein. domain: Glycoprotein. domain: Glycoprotein. domain: Glycoprotein. domain: Glycoprotein.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | ; IPR000561; BGF-11ke.; IPR001438; BGF-11.<br>; IPR001438; BGF-11.<br>PF00010; BFFFLOOP<br>MOOSE, BGF-1.<br>MOOSE, BGF-1.<br>MOOSE, BGF-1.<br>FSSULL: BGF-1, URRHAW<br>FSSULL: BGF-1, URRHAW<br>FSSULLE: BGF-1, 1.<br>FSGULE: BGF-1, 1.<br>FSGULE: BGF-1, 1.<br>FSGULE: BGF-1, 1.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| 7 TON 1287; TON  | 7.05.1285;<br>1. 1PR000561; EGF-11ke.<br>2. 1PR000471; FASH_C.<br>PR00010; EGFT1.00<br>M000181; EGFT1.00<br>M000181; EGFT1.00<br>M00011; EGFT1.01<br>FSGULES: PASH_C.<br>1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | 7.05; 1889; 1888-11ke; 1PR000561; EGF-11ke; 1PR001438; EGF_11; PR00161; EASH_C; PR00161; EGF, 1; M00161; EGF, 1; M00161; EGF, 1; M00161; EGF, 1; M00161; EGF, 1; EGG, 20E, 2; EGG, 20E, 20E, 20E, 20E, 20E, 20E, 20E, 20E                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | 7.05, 1289;<br>7. 1PR000561; EGF-11ke,<br>7. 1PR000471; FASH_C,<br>PR00010; EGFF1.00<br>M000181; EGFT1.00<br>M000181; EGFT1.01<br>M000181; EGFT1.01<br>FS01126; EGFT1.01<br>FS01126; EASH_C, 1<br>FS01126; FASH_C, 1<br>FS01126; FASH_C, 1<br>Gomdin, Glycoprotein, 3<br>JS01286; MASH_C, 1<br>JS01286; FASH_C, 1<br>Gomdin, Glycoprotein, 3<br>JS01286; MASH_C, 1<br>JS01286; FASH_C, 1<br>JS012866; FASH_C, 1<br>JS01286; FASH_C, 1<br>JS012866; FASH_C, 1<br>JS012866; FASH_C, 1<br>JS012866; FASH_C, | 707, 1287, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1787, 1 |
| ## 19709; 18F9.    IPRO00561; EGF-11ke.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | ## 19709; 18F9.  1 TPR000561; EGF-11Ke.  1 PR0001438; EGF-11Ke.  1 PR00014: FANG.C.  ## 1000181; EGF-11.  ## 10001 | 8709; 18F9.  1 PRO00561; EGF-1ike.; 1PRU01438; EGF-1it.  1 PRU0143; EGF-1ic.  MO0501; EGF, 1.  MO0501; EGF,                                                                                                                                                                                                                                                | 9709; 18F9. ; IPRO00561; EGF-11Ke.; ; IPRO00421; FA58_C. PRO0014; FA58_C. PRO0010; EGF-11. MO0181; EGF-11. MO0181; EGF-11. MO0181; EGF-11. INCOLUBERT DEFEROM FESTILIES: DEFEROM FESTILIES: PESTILIES: TESTILIES: PESTILIES:                                                                                                                                                                                                           | 9709; 18F9. ; IPRO00561; EGF-1ike.; IPRO00561; EGF-1ike.; IPRO00421; FASyLC. PRON0181; EGF, 1. MO0501; EGF, 1. MO0501; EGF, 1. MO0501; EGF, 1. ESGLES; EGF, 2. 1. ESGLES; EGF, 3. 1. ESGLES; EGF, 3. 1. ESGLES; EGF, 3. 1. ESGLES; EGF, 3. 1. EGGLES; EGF, 3. 1. ESGLES; EGF, 3. 1. ESGLES; EGF, 3. 1. EGGLES; EGF, 3. 1. EGF, 3. EGF, 3 |
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| - 3                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | - 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| 003610; AAH03610.1; -; 8709; 18F9.  1 PR000561; EGF-11; -; 1PR000561; EGF-11.  1 PR00010; EGF-11.  MODERI, FANGE, 1.  MODERI, EGF-1, UNERAW PSRULLS; EASBC_1; 1.  FSRULLS; EASBC_1; 1.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     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| HASP, BOUGAOLD, AAHOAOLD, HASP, BOUGAOLD, AAHOAOLD, InterPro; IPRO00561; EGF-like, InterPro; IPRO00561; EGF-like, InterPro; IPRO00561; EGF-like, InterPro; IPRO00681; EGF-like, InterPro; IPRO00681; EGF-like, PRINTS; PROONDIG; EGF-like, I SWAFT, SWOOGD, I SWAFT, SWOOGD, EGF-like, I SWAFT, SWOOGD, EGF-like, I SWAF       | SIMILARITY: CONTAINS 1 FS/8 TYPE C LOMAIN.  EMBL. BGU04010 AAH04010.1  HESP, P008709; 18F9.  InterPro; IPR000561; EGF-11ke.  InterPro; IPR000561; EGF-11ke.  InterPro; IPR000442; FASH_C.  PRINTS; PR000101; ERFRIAND  SWAFT, SM00001; EGF_11ke. 1.  SWAFT, SM00001; EGF_11ke. 1.  SWAFT, SM00001; EGF_11ke. 1.  SWAFT, SM00001; EGF_11ke. 1.  FESTIE: FS01126; EGF_11 I.  FESTIE: FS01126; EGF_11 I.  FESTIE: FS01126; EGF_11 I.  FESTIE: FS01126; EASHG_11 I.  FROSTIE: FS01126; EASHG_11 I.  FROSTIE: FS01126; EASHG_11 I.  FROSTIE: FS01126; EASHG_11 I.  FROSTIE: Gomain: Glycoprotein.  SEQCENCE 335 AA, 37523 MW, 20181E511878EBEDS CRC54;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | -!- SIMILARITY: CONTAINS 1 F5/8 TYPE C LÓMAIN.  BMB1; BCU04-010; A-M40-0401.;  INTERPO: IPROUD561; EGF-1ike.  SMAPT: SMOO181; EGF-1ike.  FENSILE: ISSULES: EGF-1ike.  FENSILE: ISSULES: EAFSC-1: 1.  FENSILE: EGF-1ike domain: Glycoprotein.  SEUCENCE: 335 AA, 375-23 MW, 20e84E50B7REBES                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | SIMILARITY: CONTAINS 1 F5/8 TYPE C LOMAIN.  EMBL. BGU04010, AAH04010.1,  HESP, P00709; 1BF9.  InterPro; IPR000561; EGF-11ke.  InterPro; IPR000561; EGF-11ke.  InterPro; IPR00043; EGF-11ke.  InterPro; IPR00043; EGF-11ke.  PRINTS; PR00010; EGF-11ke.  SWAFT, SW00001; EGF-11ke.  EMST, SW00001; EGF-11ke.  EMST, SW00001; EGF-11ke.  EMST, SW00001; EGF-11ke.  EMST-1; EGU126; EGF-11ke.  EMST-1; EGU126; EGF-11ke.  EMST-1; EGU126; EGF-11ke.  EMST-1; EGU126; EGG-1; 1.  PPOSTTE; EGU126; EASBC_2; 2.  EGF-11ke AGM-1; AGM-1; 1.  EMST-11ke AGM-1; AGM-1; AGM-1; 1.  EMST-11ke AGM-1;                                                                                                                                                                                                                  | -!- SIMILARITY: CONTAINS 1 F5/8 TYPE C LOMAIN.  EMBL: BCU04-010; A-MHU-0610.1;  HISSP: BCU04-010; A-MHU-0610.1;  InterPro: IPROUD561; EGF-11ke.  InterPro: IPROUD561; EGF-11ke.  InterPro: IPROUD438; BGF_11.  InterPro: IPROUD438; BGF_11.  INTERPRO: IPROUD438; BGF_11.  SMAPT: SMOO181; EGF. 1.  SMAPT: SMOO181; EGF. 1.  SMAPT: SMOO181; EGF. 1.  FENSITE: FSU1265; EGF. 2; 1.  FENSITE: FSU1265; EGF. 3; 1.  FENSITE: FSU1265; EASBC_1; 1.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
| SUBMILLEAU (FEB-ZOUT) DO UNE EMBL/GENBAUK/DEBJ GATARGSES.  EMBL; BCOUSID: AAHUSED(1): - HSSP; PORTOOS; 1BF9.  InterPro; IPROUGES; EGF-like. InterPro; IPROUGES; EGF-like. InterPro; IPROUGES; EGF-like. InterPro; IPROUGES; EGF-like. INTERPROUGES; EGF-like. SWAPT, SWOOD(1): EGF-like. SWAPT, SWOOD(1): EGF-like. FEB-LIKE, EGF-LIKE. FESTILE, ESCULZE; EGF-LIKE. FESTILE; EGF-LIKE.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | Submitted (FEEF-Zord) to the Embly definant K/DBBJ databases.  EMBL; BCOUSID: AAHUSED(1): - HSSP; PORTOGS; 18F9.  InterPro; PROUGES; ESF-like. InterPro; IPROUGES; ESF-like. InterPro; IPROUGES; ESF-like. InterPro; IPROUGES; ESF-like. InterPro; IPROUGES; ESF-like. SWAPT, SMOOD(1): ESF-like. SWAPT, SMOOD(2): ESF-like. FEES-like. FE | SUBMILLE OF THE FOOT IN THE COMMINGUIST STATEMENT OF THE COMMINGUIST STATE                                                                                                                                                                                                                                               | Submitted (FEEF-Zor) to the Emblytenbank/Pubbl databases.  EMBL; BCOUSIUS AAHUSEU1]; - TYPE C DOMAIN.  EMBL; BCOUSIUS AAHUSEU1]; -  HSSP PORTOS; 18P9.  InterPro; IPROUGES; ESF-like.  InterPro; IPROUGES; ESF-like.  InterPro; IPROUGES; ESF-like.  SMAPT, SMOOTS; ESF-LIKE.  SMAPT, SMOOTS; ESF-LIKE.  SMAPT, SMOOTS; ESF-LIKE.  SMAPT, SMOOTS; ESF-LIKE.  EMBLY: ESF-LIKE.  EMBLY                                                                                                                                                                                                           | Submitted (Editor) to the Emblytenbank/Pubbl databases.  EMBL; BCOUSELD: AAHUSELD: 1 F5/8 TYPE C FOMAIN.  EMBL; BCOUSELD: AAHUSELD: 1.  HSSP; PORTOR; BRE9.  Interpro: IPRODOSE: EGF-like.  EMAPT: SMOOTO: EGF-like. 1.  SMAPT: SMOOTO: EGF-like. 1.  SMAPT: SMOOTO: EGF-like. 1.  EMST: ESSITE: ESSITES: EGF-like. 1.  FROSTE: ESSITES: EASBC_1: 1.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| <b>11</b> (10) <b>3 3</b>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | Submitted (FEB-2001) to the EMBL/GenBank/DBBJ databases                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | Submitted (FEB-2001) to the EMBL/GenBank/DBBJ databases! SIMILARITY: CONTAINS 1 F5/8 TYPE C FOWAIN! SIMILARITY: CONTAINS 1 F5/8 TYPE C FOWAIN                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | Submitted (FEB-2001) to the EMBL/GenBank/DBBJ databases SIMILARITY: CONTAINS 1 F5/8 TYPE C FOMAIN SIMILARITY: CONTAINS 1 F5/8 TYPE C FOMAIN HSSP: P08709; 18F9 INTERPOOL 1 BF9 INTERPOOL 1 BF9 INTERPOOL 1 BF9 INTERPOOL 1 BF9 INTERPOOL 1 BF8 INTERPOOL 1                                                                                                                                                                                                                                                                                                                                                                                                     |
| Substituted (FEB-2001) to the EMBL/GenBank/DDBJ databases.  1. SIMILALITY: CONTAINS 1 F5/8 TYPE C DOMAIN.  EMBL. BCUUJOLD AAHUSEUL.1;  InterPro: IPR000561: BGF-like.  PRINTS; PRONOTO; BGF-like.  PRINTS; PRONOTO; BGF-like.  SWAFT: SWOOD(18.1 BGF. 1.  SWAFT: SWOOD(18.2 BGF. 1.  FESSIES: BGF-like. BGF-like.  EGF-like domain: Glycoprotein.  SEQUENCE: 335-AA, 37523-MW, 20e84ESDB7REBESS GRO54;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | Substitued (FEB-2001) to the EMBL/GenBank/DDBJ databases.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | Substitued (FEB-2001) to the EMBL/GenBank/DDBJ databases. 1- SIMILARITY: CONTAINS 1 F5/8 TYPE C FOMAIN. EMBL. BGU04010 AAH04010.1; InterPro: IPR000561; EGF-like. InterPro: IPR000561; EGF-like. InterPro: IPR000561; EGF-like. InterPro: IPR000661; EGF-like. InterPro: IPR000661; EGF-like. InterPro: IPR000661; EGF-like. InterPro: IPR000601; EGF-like. SWAPT, SM00181; EGF, 1. SWAPT, SM00181; EGF, 1. SWAPT, SM00181; EGF, 1. EMBLY, SM00181;                                                                                                                                                                                                                                                  | Substituted (EEB-2001) to the EMBL/GenBank/DDBJ databases.  1. SIMILARITY: CONTAINS 1 FS/8 TYPE C DOMAIN.  EMBL: BCUUGADIO! AAHU9610.1;  InterPro: IPR000561; EGF-11ike.  InterPro: IPR000561; EGF-11ike.  InterPro: IPR000421; FASH_C.  PRINTS; PROUNTO; EFFRICOD  SWAFT, SWOOGOI, EGF-11ike.  InterPro: IPR000601; EGF-11ike.  SWAFT, SWOOGOI, EGF-11ike.  SWAFT, SWOOGOI, EGF-11ike.  FESTIE: FSOULZE: EGF-11ike.  FESTIE: FSOUNLE: EGF-11ike.  FESTIE: FSOUNLE: EGF-11ike.  FESTIE: FSOUNLE: EGF-11ike.  FESTIE: FSOULZE: EGF-11ike.  FESTIE: FSOUNLE:                                                                                                                                                                                                           | Substituted (FEB-2001) to the EMBL/GenBank/DDBJ databases                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
| Stransberg A. Submilled (FEB-2001) to the EMEL/GenBank/DDBJ databases.  Submilled (FEB-2001) to the EMEL/GenBank/DDBJ databases.  EMBL BCUOADIO, AAH03610.1;  HSSP, P08709; 18P9.  InterPro; 1PR001651; EGF-11ke.  InterPro; 1PR001651; EGF-11ke.  InterPro; 1PR00143; EASH_C.  PRINTS, PRONOIG: EGF-11ke.  EMART, SM00001; EGF-11ke.  EMART, SM000001; EGF-11ke.  EMART, SM000001; EGF-11ke.  EMART, SM0000    | Stransberg A. Submilled (FEB-2001) to the EMEL/GenBank/DDBJ databases.  Submilled (FEB-2001) to the EMEL/GenBank/DDBJ databases.  EMBL: BCU04010; AAH03610.1:  HSSP: P08709; 1BF9: InterPro; 1PR001651; EGF-11ke. InterPro; 1PR001651; EGF-11ke. InterPro; 1PR001651; EGF-11ke. InterPro; 1PR001651; EGF-11ke.  PRINTS; PR00101; EGF-11ke.  EMAPT: SM00181 EGF-11ke.  EMAPT: SM00181 EGF-11ke.  EMAPT: SM00181 EGF-11ke.  FEGS.IE. PS00125; EASSC.1: 1.  FEGS.IE. PS00125; EASSC.2: 2.  FEGS.IE. PS01285; EASSC.2: 2.  EGF-11ke Jonaln: Glycoprotein.  SEQUENCE: 335 AA, 37523 MW, D0281E5DB7EEBES GROSS;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | Stransberg R. 2001) to the EMBL/GenBank/DDBJ databases. Submitted (FEB: CONTAINS I FS/B TYPE C FOMAIN.  EMBL; BCOUSDID, AAHUSSIO.1; HSSP; PORTOOS; 18F9; InterPro; 1PRO00561: EGF-like. InterPro; 1PRO00561: EGF-like. InterPro; 1PRO00661: EGF-like. InterPro; 1PRO00601: EGF-like. SWAPT, SWOOT91: EGF, 1. SWAPT, SWOOT91: EGF, 1. FESSIE; FSOUT91: EGF, 1. FESSIE; FSOUT92: EGF, 1. FESSIE; FSOUT93: EASBC_1; 1. FESSIE; FSOUT93: EASBC_1; 1. FESSIE; FSOUT95: EASBC_1; 1. FESSIE; FSOUT95: FASSC_1; 1.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | Strausberg (EE. 2001) to the EMEL/GenBank/DDBJ databases                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | Strausberg R.; Substitued (FEE-2001) to the EMBL/GenBank/DDBJ databases                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
| Substituted (FEB-2001) to the EMEL/GenBank/DDBJ databases.  Substituted (FEB-2001) to the EMEL/GenBank/DDBJ databases.  FIRE SIMILARITY: CONTAINS 1 F5/8 TYPE C LOMAIN.  HSSP; P08709; 1BF9.  InterPro: 1PR000561; BGF-11ke.  InterPro: 1PR000541; F458_C.  PRINTS; PR000181; E5F1.  FASFI, SMO0181 E5F1.  SWAPT, SMO0181 E5F1.  SWAPT, SMO0181 E5F1.  FESTIA: FSGULLE; E0ELJ: UNERAWN_1.  FESTIA: FSGULLE; E0ELJ: 1.  FROSTER: FSGULL | Substituted (FEB-2001) to the EMBL/GenBank/DDBJ databases.  Firstsberg R.; Substituted (FEB-2001) to the EMBL/GenBank/DDBJ databases.  FIRST PORTORS 1 FF/8 TYPE C FOMAIN.  HSSP; PORTORS 1 BFF. InterPro: PRO00561; BGF-1ike.  FROOFF 1 FFWGU421; FASB_C.  FROOFF 2 FFWGU421; FASB_C.  FROOFF 3 FFWGU421; FASB_C.  FROOFF 3 FFWGU421; BGF-1ike.  FROOFF 3 FFWGU421; BGF-1ike.  FROOFF 3 FFWGU421; BGF-1ike.  FROOFF 3 FFWGU421; BGF-1ike.  FROOFF 3 FFWGU421; BGF-1il.  FROOFF 3 FFWGU4 | Substituted (FEB-2001) to the EMBL/GenBank/DDBJ databases. Substituted (FEB-2001) to the EMBL/GenBank/DDBJ databases.  EMBL; BOUJOSIO; AAHOSOIO.1, - HSSP; PORTOSIO; 18F9. InterPro; 1PR000561; BGF-11ke. InterPro; 1PR000421; FASB-C; PRINTS; PROMOTO; PGFRIZON SWAPT; SMOOTOI, EGFRIZON SWAPT; SMOOTOI, EGFRIZON FEB-31; SMOOTOI, EGF-11ke, 1. SWAPT; SMOOTOI, EGF-11ke, 1. FEB-31; FSG-12; EGF-11ke, 1. FEB-31; FSG-12; EGF-11, 1. FER-31; FSG-12; EGF-12; EGF-11, 1. FER-31; FSG-12; EGF-12;                                                                                                                                                                                                                                               | Strausberg R.; Submitted (EEE-2001) to the EMBL/GenBank/DDBJ databases                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | Strausberg R.; Substituted (FEB-2001) to the EMBL/GenBank/DDBJ databases. Substituted (FEB-2001) to the EMBL/GenBank/DDBJ databases.  EMBL; BCOUSALD; AAHUSALD.1, HSSP; PORTOSI, 18F9. InterPro; 1PR000561; BGF-11ke. InterPro; 1PR000601; BGF-11ke, 1. SWAFT, SWAOTO, 1; BGF-11ke, 1. SWAFT, SWAOTO, 1; BGF-11ke, 1. FROSTE; FSG1126; BGF-2; 1. FROSTE; FSG1126; BGF-2; 1. FROSTE; FSG1126; BGF-2; 1. FROSTE; FSG1126; BASG-1; 1. FROSTE; FSG1126; BASG-1; 1. FROSTE; FSG1126; GASG-2; 2. FGF-11ke Jonain; Glycoprotein.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
| TISSUE MELLANDMA.; SUBJULTANDMA.; SUBJULLED (FEB-2001) to the EMBL/GenBank/DDBJ databases                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | TISSUE MELLANDMA.; SLEAUSBERG R.; SUBMILLED (FEB-2001) to the EMBL/GenBank/DDBJ databases. Submilled (FEB-2001) to the EMBL/GenBank/DDBJ databases                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | TISSUE MELLANDMA.; SLEAUSBERG R.; Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases: SAMIABLTY: CONTAINS 1 F5/8 TYPE C FOMAIN: SAMIABLTY: CONTAINS 1 F5/8 TYPE C FOMAIN                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | TISSUE MELLANDMA.; SLEAUSBERG R.; SUBJULLED (FEB-2001) to the EMBL/GenBank/DDBJ databases. Schalled (FEB-2001) to the EMBL/GenBank/DDBJ databases.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | TISSUE MELANDMA.; SLEAUSBERG R.; Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases: SAMILABLY: CONTAINS 1 F5/8 TYPE C FOMAIN: SAMILABLY: CONTAINS 1 F5/8 TYPE C FOMAIN: SAMILABLY: CONTAINS 1 F5/8 TYPE C FOMAIN: FAMILABLY: CONTAINS 1 F5/8 TYPE C FOMAIN                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
| TISSUB-MELANOMA.; Strausberg Arabases. Strausberg Arabases. Strausberg Arabases. Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases. Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases. EMBL BCU048010; AAH03610.1; EMBL: BCU048010; AAH03610.1; Interpro; IPR000561; BGF-11ke. Interpro; IPR000421; FAB-C. PRINTS; PR0010421; FAB-C. PRINTS; PR0010421; FAB-C. PRINTS; PR0010421; EGF-11ke. 1. SWAFT: SW00701; EGF-11ke. 1. SWAFT: SW00701; EGF-11ke. 1. SWAFT: SW00701; EGF-11ke. 1. FERSITE; FS01285; EGF-1: 1. FERSITE; FS01285; FABBC-1: 1. FERSITE; FS01285; FABBC-1: 1. FROSITE: FS01285; FABBC-1: 1.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | TISSUG-MELANOMA.; Strausberg Arabases. Strausberg Arabases. Strausberg Arabases                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | TISSUB-MELANOMA.; Strausberg R. S. Strausberg R. S. Strausberg R. S. Strausberg R. S!- SIMILARITY: CONTAINS I F5/8 TYPE C FOMAIN. EMBL; BGU048010; AAH03610.1; HSSP; DG0709; 1BF9. InterPro; IPR000561; BGF-11ke. InterPro; IPR000561; BGF-11ke. InterPro; IPR000438; BGF_11. FN PROPORTS; PROMONIO, FGFRANON SMAPT, SMONIOL, FGFRANON SWAPT, SMONIOL, FGFRANON FFRANCE, FSGLEE; FASSC_1, INFRAMM_1. FFRANCE, FSGLEE; FASSC_1, INFRAMM_1. FROSTER, FSGLEE; FASSC_2, 2. FGFSTTE; FSGLEE; FASSC_2, 2. EGFTIKE GGMMAIN: Glycoprotein. ENGSTTER STATES AN, 37523 MW, 20e84E5DB7REBESS CRC64;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | TISSUE-MELANOMA.; Strausberg Arabases. Strausberg RE.2001) to the EMBL/GenBank/DDBJ databases                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | TISSUE-MELANOMA.; Strausberg R. S. Strausberg R. J. Strausberg R. J. Strausberg R. J. Strausberg R. J. Strauturd (FEB-2001) to the EMBL/GenBank/DDBJ databasesSIMILARITY: CONTAINS I F5/8 TYPE C FOMAIN. EMBL. BCU04A010, AAH03610.1; HSSP, P08709; 1BF9. InterPro; PPR000561; BGF-11. InterPro; PPR000481; BGF-11. InterPro; PPR000481; BGF-11. InterPro; PPR000481; EGF, 1. SWAPT, SM00181; EGF, 1. SWAPT, SM00181; EGF, 1. EMBLY, SM00181; EGF, 1. FECSITE: FS01126; EGF, 2.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
| Strausberg B. 1. Strausberg B. 2. HSRP, BRO00561; BGF-11ke. InterPro: IPR000561; BGF-11ke. InterPro: IPR000561; BGF-11ke. InterPro: IPR000561; BGF-11ke. InterPro: IPR00061; BGF-11ke. InterPro: IPR00061; BGF-11ke. SWAPT, SM000601; BGF-11ke. SWAPT, SM000601; BGF-11ke. SWAPT, SM000601; BGF-11ke. SWAPT, SM000601; BGF-11ke. SWAPT, SW000601; | Strausberg B.: Interpool PR000561; BGF-11: Interpool PR000561; BGF-11: Interpool PR000561; BGF-11: Interpool PR000561; BGF-11: Interpool PR000661; BGF-11: PRINTS, PR00001; EGF-11: SWAPT SW00001; EGF-11: SWAPT SW00001; EGF-11: FESSITE, FSSULES; EGF-11: FESSITE; FSSULES; EASBC_1: FESSITE; FSSULES; EASBC_1: FESSITE; FSSULES; EASBC_1: FESSITE; FSSULES; EASBC_2: 2. EGF-11: FPOSITE; FSSULES; EASBC_2: 2. EGF-11: FPOSITE; FSSULES; EASBC_2: 3.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | Stransberg N. 1. EMBL; BCU01510; AAHU3510.1; - HSSP; P087009; 1BP9 InterPro; PR000161; ESF-like. InterPro; PR000161; ESF-like. InterPro; PR000161; ESF-like. InterPro; PR000161; ESF-like. SWAPT, SW00181; ESF, 1. SWAPT, SW00181; ESF, 1. SWAPT, SW00181; ESF, 1. EESSIE; ESGLESS; EOF J. 1. FESSIE; ESGLESS; EOF J. 1. EGST-LIKE demain: Glycoprotein. EESF-LIKE demain: Glycoprotein.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | **STEARSBERGY B. 1. Strausberg B. 1. Str                                                                                                                                                                                                           | Strausberg R.; Strausberg R.; Strausberg R.; Strausberg R.; Submitted (FEE-2001) to the EMBL/GenBank/DDBJ databases. Submitted (FEE-2001) to the EMBL/GenBank/DDBJ databases.  EMBL; BCOUSELU; AAHUSELU]; HSSP; DROODS, 18F9. InterPro; IPROODSE; EGF-11. InterPro; IPROUDSE; EGF-11. InterPro; IPROUDSE; EGF-11. InterPro; IPROUDSE; EGF-11. SWAFT, SWOODSE; EGF-1. SWAFT, SWOODSE; EGF-1. FEE-STE; EGF-1. FEE-STE; EGF-2. FEE-STE; ESGLESE; EGF-2. FEGF-11Ke demain; Glycoprotein.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
| SEQUENCE FROM N.A.  SEQUENCE FROM N.A.  STRANSPORT R.;  SUBLANDA;  SUBLANDALLED (FEB-2001) to the EMBL/GenBank/DDBJ databases.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | SEQUENCE FROM N.A.  SEQUENCE FROM N.A.  Strausberg R.; Strausberg  | SEQUENCE FROM N.A.  SEQUENCE FELLANOMA.A.  SETAUSDERGY SUBJECT R.,  SUBLALLEGG (FEB-2001) LO UBE EMBL/GenBank/DDBJ databases.  EMBL, BGCUSALD, AAHUSALD, 1.  EMBL, BCCUSALD, AAHUSALD, 1.  HSSP, PORTOS, 18F9.  InterPro; IPROUNTANE; FASB-C.  PRINTS, PROUNTANE; FASB-C.  PRINTS, PROUNTANE; FASB-C.  PRINTS, PROUNTANE; FASB-C.  PRINTS, PROUNTANE; FASB-C.  PRINTS, SMOOTS, ESF, 1.  SWAFT, SMOOTS, ESF, 1.  FESSIE; FSGLESS, ESF, 1.  FESSIE; FSGLESS, ESF, 2.  FESSIE; FSGLESS, ESFS-C.  FESSIE; FSGLESS, FASB-C.  FASB                                                                                                                                                                                                                                               | SEQUENCE FROM N.A.  SITUATED NO. N.A.  STRAUSBERGEN R.;  SUBLIANDRA.;  STANDED R.;  SUBLICE OF R.;  SUBLICE OF R.;  SUBLICE OF R.;  EMBL;  EMB                                                                                                                                                                                                           | SEQUENCE FROM N.A.  SLOWELENDENDEAL  STEAUSDERGY  SUBJECT  
| SEQUENCE FROM N.A. TISSUE-MELLANDMA.; SLEARSBERG R.; SLEARSBERG R.; SLEARSBERG R.; SLEARSBERG R.; SLEARSBERG R.; SHALLLE-G (FEB-2001) to the EMBL/GenBank/DDBJ databases                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | SEQUENCE FROM N.A. TISSUE MELLANDMA.; SLICABLE MELLANDMA.; SULABLE OF R.; SULABLE OF R.; SULABLE CONTAINS I F5/8 TYPE C FOMAIN. EMBL; BCUJSID: AAHUSED(1); INTEPPO: IPRO0056: BGF-II. INTEPPO: IPRO0056: BGF-II. INTEPPO: IPRO0042: FARE.C. PRINTS; PROODIG: EGF-II. INTEPPO: IPRO0142: FARE.C. PRINTS; PROODIG: EGF-II. INTEPPO: IPRO0142: EGF-II. INTEPPO: IPRO0142: EGF-II. INTERPO: IPRO0142: EGF-II. INTER | SEQUENCE FROM N.A. TISSUE MELLANDMA.; SLEAUSDERFORMA.; SLUBSELOND, SUBMILLED (FEB-2001) to the EMEL/GenBank/DDBJ databases: SAMILARITY: CONTAINS 1 FS/8 TYPE C FOWAIN: SAMILARITY: CONTAINS 1 FS/8 TYPE C FOWAIN. HSSP: P08709; 18F9. InterPro: 1PR000561; ESF-1ike. InterPro: 1PR000561; ESF-1ike. InterPro: 1PR000561; FANB_C. PRINTS, PRONTO; FRFRIAND SMAPT. SMOOTH ESF-IIKe. 1. SMAFT. SMOOTH, ESF-IIKe. 1. SMAFT. SMOOTH, ESF-IIKe. 1. SMAFT. SMOOTH, ESF-IIKe. 1. FROSTER: SGILEE; ESGILEE;                                                                                                                                                                                                                                                      | SEQUENCE FROM N.A. TISSUE MELLANDMA.; SLICABLE ABLANDMA.; SLICABLE OF R.; SLICABLET R.; SLICABLET R.; SIMILARITY: CONTAINS I F5/8 TYPE C FOMAIN. EMBL; BCUGSOLO; AAHUSOLO!; Interpro: IPROUSES: BGF-like. INTERPRO: BGF-like. BF-LIKE. BGF-LIKE. BGF-L                                                                                                                                                                                                           | SEQUENCE FROM N.A. TISSUE MELLANDMA.; SLEAUSBERT R., SILDMILLED (FEB-2001) to the EMEL/GenBank/DDBJ databases: SIMILARITY: CONTAINS 1 FS/8 TYPE C FOWAIN: SIMILARITY: CONTAINS 1 FS/8 TYPE C FOWAIN. HSSP; P08709; 1BF9. InterPro: PRE000561; BGF-1ike. InterPro: IPR000561; BGF-1ike. InterPro: IPR000501; FANB_C. PRINTS, PRONOTO: FANB_C. PRINTS, PRONOTO: FANB_C. PRINTS, PRONOTO: FANB_C                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
| TISSUE-MELANOMA.) Strausberg M. A. TISSUE-MELANOMA.) Strausberg M. A. Strausberg M. A. Strausberg M. D. Che EMBL/GenBank/DDBJ databases                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | TISSUE-MELANOMA.; Strausberg N. A. TISSUE-MELANOMA.; Strausberg N. A. TISSUE-MELANOMA.; Strausberg N. B. Strausberg N. B. TISSUE-MELANOMA.; Strausberg N. B. TISSUE-MELLUG (FEB.2001) LO Ube EMBL/GenBank/DDBJ databasesSIMILARITY: CONTAINS I FS/8 TYPE C FOMAINSIMILARITY: CONTAINS I FS/8 TYPE C FOMAIN                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | PEQUENCE FROM N.A.  Strausberg A.  HEBL; BCU0401, AAH03610.1;  HEBL; BCU04010; AAH03610.1;  HESP; DC06709; 18F9.  InterPro; IPR001651; BGF-11.  InterPro; IPR001651; BGF-11.  InterPro; IPR00161; BGF-11.  InterPro; IPR00161; BGF-11.  SMAPT; SMO0181; EGF, 1.  SMAPT; SMO0181; EGF, 1.  SMAPT; SMO0181; EGF, 1.  SMAPT; SMO0181; EGF, 1.  ERSILE; ESGLESS; EGF 2.  HENSITE; RSGLESS; EGF 2; 1.  HENSITE; RSGLESS; EGF 2; 1.  ERSILE; ESGLESS; EASSCL.; 1.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | TISSUE-MELANOMA.; Strausberg N. A. TISSUE-MELANOMA.; Strausberg N. A. Strausberg N. Stra                                                                                                                                                                                                           | TISSUE MELANDA.;  TISSUE MELANDA.;  SURUCHER ROW N.A.  TISSUE MELANDA.;  SURIALLY: COUNTY.  EMBL, GenBank/DDBJ databases.  SIMIALLY: COUNTY.  EMBL, BCUUSOLO;  AAHUSOLO;  INTEPPO: IPROUGSE: EGF-Like.  EMAFT: SMOOTOL: EGF-Like.  EMAFT: ENGLIES: EGF-LI.  EMOSTEE: FSGLLES: EGF-LI.  EMOSTEE: FSGLLES: EASECL: 1.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| [1] Strausberg A. TISSUE-MELANOMA.; Strausberg A. Strausberg A. Submilled (FEB-2001) to the EMEL/GenBank/DDBJ databases. Submilled (FEB-2001) to the EMEL/GenBank/DDBJ databases                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | [1] Stransberg B. Siransberg B | [1] Supplement From N.A. Strausberg R.; Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | [1] Strausberg P. Strausberg B. Strausberg B. Strausberg B. Strausberg B. Submitted (FE. 2001) to the EMEL/GenBank/DDBJ databases. Submitted (FE. 2001) to the EMEL/GenBank/DDBJ databases                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | [1] SEQUENCE FROM N.A. SEQUENCE FROM N.A. Strausberg R.; Strausberg R.; Strausberg R.; Strausberg R.; Strausberg R.; Submitted (EEE-2001) to the EMBL/GenBank/DDBJ databases. Submitted (EEE-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BCOUSEID: AAHUSEID: 1. INTERPOSED 18 FROM 1                                                                                                                                                                                              |
| SEQUENCE FROM N.A.   SEQUENCE FROM N.A.   Stransberg R.;   Stransberg R.;   Stransberg R.;   Submilled (FEB 2001) to the EMBL/GenBank/DDBJ databases.   HSSP; PO8709; BF9;   InterPro; PR000561; BGF-like.   InterPro; PR000561; BGF-like.   InterPro; PR0001421; FASB_C.   PRUNTS; PR00010; EGF_LIKe. I.   SWAPT; SW00181 EGF_LIKe. I.   SWAPT; SW00181 EGF_LIKe. I.   SWAPT; SW00181 EGF_LIKe. I.   EMST: I.KE GENGIN: GLYCOPTOTOTO.   SEQUENCE 335 AA, 37553 MW, 20e84ESDB7RESS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | SEQUENCE FROM N.A.   SEQUENCE FROM N.A.   SEQUENCE FROM N.A.   Strausberg R.; A.   Strausberg R.   | [1] SEQUENCE FROM N.A. SEQUENCE FROM N.A. STISSE—BELANOMA.; Strausberg R.; EMBL, BCOUGHOLD, AAHUGHOLD.;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | 1]                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | (1) SEQUENCE FROM N.A. SINGLENCE FROM N.A. STANSBERG R.; SUBLANOMA.; STANSBERG R.; SUBLANOMA.; SUBLALE (FEE 2001) LO UDE EMBL/GenBank/DDBJ databases. EMBL, BCOUSALD; AMADOSID.; FS/8 TYPE C FOMAIN. EMBL; BCOUSALD; ARADOSID.; FS/8 TYPE C FOMAIN. INTERPROPORT IPPRODOSE; FSF-11ke. FSWAFT, SWOOGOT, ESF-11ke, 1. SWAFT, SWOOGOT, ESF-11ke, 1. SWAFT, SWOOGOT, ESF-11ke, 1. FROSTER; FSG1285; FSSSC-1; 1. FROSTER; FSG1285; FASSC-1; 1. FROSTER; FSG1285; FASSC-1; 1. FROSTER; FSG1285; FASSC-1; 1. FROSTER; FSG1285; FASSC-1; 1.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
| NFH LAXINGGED BY THE WEBLE BY THE BENEFIT BY THE BENEFIT BY THE B | NFH LAXINGAGES  NFH LAXINGAGES  SEQUENCE FROM N.A.  TISSUE MELLANDAA;  SLITALDEAG (FEB-2001) to the EMBL/GenBank/DDBJ databases.  SLAMALLEAG (FEB-2001) to the EMBL/GenBank/DDBJ databases.  SLAMALLEAG (FEB-2001) to the EMBL/GenBank/DDBJ databases.  SLAMALLEAG (FEB-2001) to the EMBL/GenBank/DDBJ databases.  EMBL; SOUTSOLD; AAHUSED(1);  Interpro; IPRO00561; BGF-11ke.  Interpro; IPRO00583; BGF-11ke.  Interpro; IPRO00583; BGF-11ke.  PRINTS; PRO00101; BGF-11ke.  FRAFT, SMONO101;  | WHILMAXINAGED BY MATHEMATICAL BY MATHEMATINAGED BY MATHEMATICAL BY MATHEMATICA                                                                                                                                                                                                                                               | WITH_TAXINGGED.  SEQUENCE FROM N.A.  TISSUE MELLANDA.;  SLICABLE ROW N.A.  TISSUE MELLANDA.;  SUBMALLED (FEB-2001) to the EMBL/GenBank/DDBJ databases.  SLICABLE CONTAINS I F5/8 TYPE C FOWAIN.  EMBL; BCOUSELD: AAHUSELD.1;  EMBL; BCOUSELD: RGF-Like.  INTEFPO: IPROUSES: RGF-Like.  FROM TISSUE                                                                                                                                                                                                              | WHILMAXINAGED AND WATER AND                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| NCRI_TaxTD=9606; Still                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | NCRI_TaxTD=9606;  Strausberg N.A.  TISSUE-MELANOMA.; Strausberg N.A.  TISSUE-MELANOMA.; Strausberg N.A.  TISSUE-MELANOMA.; Strausberg N.A.  **L' SIMILARITY: CONTAINS I FS/8 TYPE C FOMAIN.  **L' SIMILARITY: CONTAINS I FS/8 TYPE C FOMAIN.  **EMBL. BGUOUS-BLU, AAHUAS-BLU, I.A.  **INTERPRO. IPROUGS-BLU, BGF-II.  **PRINTS; PROUGH-R: BGF-II.  **EMATT. SMOOGU, EGF-II.  **EMATT. SM | NCRI_TaxTD=9606; SEQUENCE FROM N.A. TISSUE_MELANOMA.; Strausberg P.; Strausberg P.; Subaltued (FEB-2001) to the EMBL/GenBank/DDBJ databases. Strausberg P.; SMILARITY: CONTAINS I F5/8 TYPE C FOMAIN. EMBL; BGUUSBLU; CONTAINS I F5/8 TYPE C FOMAIN. INTERPO: 18P000041; FS-11Ke. INTERPO: 1PR0000431; FS-11Ke. INTERPO: 1PR0000431; FS-11Ke. INTERPO: 1PR0000431; FS-11Ke. INTERPO: 1PR00001; EGE-11Ke. INTERPO: 1PR00001; EGE-11Ke. INTERPO: 1PR00001; EGE-11Ke. INTERPO: 1PR00001; EGE-11Ke. EMBL; SMO0001; EGE-11Ke. EMBL; EMBL; SMO0001; EGE-11Ke. EMBL; EM                                                                                                                                                                                                                                               | NCRI_TaxTD=9606;  [1]  Strawberg No. N. A.  TISSUE-MELANOMA.;  Strawberg RE. 2001  **Lister Contains to the EMBL/GenBank/DDBJ databases.**  **Interposit PRO00561; EGF-1ike.**  **Interposit PRO00561; EGF-1ike.**  **Interposit PRO00561; EGF-1ike.**  **PRON0501; EGF-1ike.**  **EMBL' SMON0501; EGF-1ike.**                                                                                                                                                                                                             | NCRI_TaxTD=9606;  SEQUENCE FROM N.A. TISSUE_MELANDAA.; SITUATOR OF SECURITY CONTAINS I F5/8 TYPE C FOMAIN.  EMBL: BCOUSELD TY: CONTAINS I F5/8 TYPE C FOMAIN.  EMBL: BCOUSELD SECURITY CONTAINS I F5/8 TYPE C FOMAIN.  INTERPO: IPPRO00561: EGF-1ike.  INTERPO: IPPRO0061: EGF-1ike.  EMAFT: SMOOTO: EGF-1ike.  EMAFT: SMOOTO: EGF-1ike.  EMAFT: SMOOTO: EGF-1ike.  EMAFT: SMOOTO: EGF-1ike.  EMAFT: EMOOTO: EMAFT: EMOOTO: EMAFT: EMOOTO: EMOOTO: EMAFT: EMAFT: EMOOTO: E |
| NOTITE TO TO THE COLOR TO THE C | MOTHER 187, DULLELING FIRMATES, CALAITHILE, HOWITHINGS, DOUGHLINGS, CALAITHILE, HOWITHINGS, DULLELINGS, CALAITHILE, HOWITHINGS, CALAITHILE, HOWITHINGS, CALAITHINE, HOWITHINGS, CALAITHINE, HOWITHINGS, CONTAINS, BENGARAN, ASTALLEW (FEB-2001) to Uhe EMBL/GenBank/DDBJ databases.  Submitted (FEB-2001) to Uhe EMBL/GenBank/DDBJ databases.  EMBL, BCOMAIN, AAHUSDU, A. HSSP, PORTOS, 1BF9.  InterPro; PRO00561; BGF-11.  InterPro; IPHOUGA, 1; FASB_C.  PRINTS, PRO00501; EGF-11.  SMAPT, SMOOSOT, EGF-11.  FEST, SMOOSOT,  | MOTHER TO A CONTROLL OF THE CONTROL OF THE C                                                                                                                                                                                                                                               | MONTH TAY TO A GOOD THE TAY THE TOWN THE TOWN TO A GOOD THE TAY TO A A GOOD THE TAY TO A A GOOD THE TAY TO A A GOOD THE TAY TOWN THE TAY THE TAY THE TAY THE TAY THE TAY TOWN THE TAY T                                                                                                                                                                                                           | MOUNTAINT AND TO THE TOWN NOT TOWN TO THE TOWN TO THE TOWN NOT TOWN TO THE TOWN NOT TOWN TOWN TOWN TOWN TOWN TOWN                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| Mammalia: Eutheria; Flimates; Catarrhini; Hominidae; Bomo. [1] SEQUENCE FROM N.A.  FISSUE-MELANOMA.;  SUBLALIANOMA.;  SUBLALIA: CONTAINS 1 F5/8 TYPE C FOWAIN.  SUBLALIA: CONTAINS 1 F5/8 TYPE C FOWAIN.  SUBLALIA: CONTAINS 1 F5/8 TYPE C FOWAIN.  HSSP; PO8709; 18F9.  InterPro: PR000561; BGF-like.  ERSF-like Gomalin: Glycoprotein.  SEQUENCE: 335-AA, 37553 MW, 20e84ESDB78EBESS CRC64;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | Manualia: Eutheria; Filmates; Catarrhini; Hominidae; Homo. MATT-TaxTN=9606; [1] SEQUENCE FEON N.A. SEQUENCE FEON N.A. STERNSBERG R.; STEEL CEMBLACEDBU databases. Strausberg R.; STEEL CONTAINS 1 F5/8 TYPE C FOMAIN. EMBL; BCU03610; AAHU3610.1; HSSP; P087099; IBF9. InterPro; IPR000561; EGF-II.6. InterPro; IPR000561; EGF-II.6. InterPro; IPR000661; EGF-II.6. InterPro; IPR000601; EGF-II.6. InterPro; IPR000601; EGF-II.6. INTERPRO; IPR000601; EGF-II.6. SWAPT; SW00181; EGF-II.6. SWAPT; SW00181; EGF-II.6. FESSIE; FS01285; EASSC_1; I. FESSIE; FS01285; EASSC_1; I. FESSIE; FS01285; EASSC_1; I. FENOSIE; FS01285; EASSC_1; I. FENOSIE; FS01285; EASSC_2; 2. EGF-II.6. EMPOSITE; FS01285; EASSC_2; 2. EGF-II.6. EGF-    | Mammadia: Eutheria; Filmates; Catarrhini; Hominidae; Bouno. [1] SEQUENCE FROM N.A. SEQUENCE FROM N.A. STISSUE-MELANOMA.; Stransberg R.; Submitted (FEB 2001) to the EMEL/GenBank/DDBJ databases. Elemented (FEB 2001) to the EMEL/GenBank/DDBJ databases. Interproving 1 PRO00561; ESF 11 e.  HNSP: POROUSE1; FASP 11 e.  FASP 1 PROUPER: FASP 11 e.  EMAT: SMOOGU; ESF 11 e.  EMAT: SMOOGU; ESF 11 e.  FROM TO STORES EN EMERICANIA.  FROM TO STORES EN EMERICANIA.  FROM TO STORES EN EMBRICANIA.  FROM TO STORES EN EMBRICAN                                                                                                                                                                                                                                               | Mammalia; Eutheria; Filmates; Catarrhini; Hominidae; Homo. MATT_TAXTN=9606; [1] SEQUENCE FROM N.A. SEQUENCE FROM N.A. STATUSUE—BLANDMA.; Strausberg R.; Stra                                                                                                                                                                                                           | Mammadia: Eutheria; Filmates; Catarrhini; Hominidae; Bouno. [1] SEQUENCE FROM N.A. SEQUENCE FROM N.A. STANDARA; STANDARA; STANDARA; STANDARA; STANDARA; STANDARA; STANDARA; STANDARA; STANDARANDARA; STANDARANDARA; STANDARANDARA; STANDARANDARA; SMILLAG(FEB.2001) to the EMBL/GenBank/DDBJ databases                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| Catarrhini: Hominidae; BL/GenBank/DDBJ databa<br>B TYPE C DOMAIN. WM_1.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | Catarrhini; Hominidae; BL/GenBank/DDBJ databa<br>B TYPE C DOMAIN. WM_1.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | Catairhini; Hominidae; BL/GenBank/DDBJ databa<br>B TYPE C DOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | Catarrhini; Hominidae; BL/GenBank/DDBJ databa<br>B TYPE C DOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | Catarrhini; Hominidae;<br>BL/GenBank/DDBJ databa<br>B TYPE C DOMAIN.<br>WN_1.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
| Catarrhini, Wolfuchiuta, Catarrhini, Hominidaes<br>BL/GenBank/DDBJ databa<br>B TYPE C LOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | Catarrhini; Moninidaes<br>BL/GenBank/DDBJ databa<br>8 TYPE C FOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | olamata, Verteblata,<br>Catarrhini: Hominidae,<br>BL/GenBank/DDBJ databa<br>B TYPE C EOMAIN.<br>WM_1.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | Juliuta, Veltebluta,<br>Catarrhini; Hominidaes<br>BL/GenBank/DDBJ databa<br>8 TYPE C FOMAIN.<br>WM_1.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | olanda, Verteblada.<br>Gatarrhini: Hominidae.<br>EL/GenBank/DDBJ databa<br>E TYPE C FOMAIN.<br>WN_1.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
| FURTHER M. Lactas Chard 11st, Claridata, Voltebrala, Futeleostomic Manadias Eutherias Finates; Catarthini; Hominidae; Bonco. Month Tay The 4606; Finates; Catarthini; Hominidae; Bonco. Tractomedia: Eutherias Finates; Catarthini; Hominidae; Bonco. Figure Recom N.A. FISCUE-MELANOMA.A. FISCUE-MELANOMA.A. Stransberg M. P.; FS/B TYPE C LOWAIN. EMBL. BEUD.1; SIMILARITY: CONTAINS I FS/B TYPE C LOMAIN. EMBL. BECO.1; FIRESP. PORTOS; BEF. 11. FIRESP. PORTOS; ERFERON. BEF. 11. FIRESP. PROMOTO: ERFERON. BEFREVA. SMOROSI: ERFERON. BERNOW. BEFREVA. SMOROSI: ERFERON. BERNOW. BEFREVE. SMOROSI: ERFERON. BERNOW. B       | Catarrhini: Mominidae;<br>Catarrhini: Mominidae;<br>BL/GenBank/DDBJ databa<br>B TYPE C DOMAIN.<br>WM_1.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | Catarrhini: Hominidae; Catarrhini: Hominidae; BL/GenBank/DDBJ databa B TYPE C DOMAIN. 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| Clubidus, Verteblata, Calarrhini; Hominidaes, Calarrhini; Hominidaes, BL/GenBank/DDBJ databa<br>BTYPE C FOMAIN. 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| Cluminidae,<br>Calarrhini; Hominidae,<br>Calarrhini; Hominidae,<br>BL/GenBank/DDBJ databa<br>B TYPE C FOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | Cluminidae,<br>Calarrhini; Hominidae,<br>Calarrhini; Hominidae,<br>BL/GenBank/DDBJ databa<br>B TYPE C FOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | Cluminidae,<br>Catarrhini, Hominidae,<br>Catarrhini, Hominidae,<br>BL/GenBank/DDBJ databa<br>B TYPE C FOMAIN.<br>WM_1.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | Cluminta, Verteblata, Catarrhini; Hominidae, Catarrhini; Hominidae, BL/Genbank/DDBJ databag TYPE C FOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | Cluminidae,<br>Catarrhini, Hominidae,<br>Catarrhini, Hominidae,<br>BL/GenBank/DDBJ databa<br>B TYPE C FOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
| Cluminta, Vertebruta, Catarrhini; Hominidae, BL/GenBank/DDBJ databa 8 TYPE C FOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | Oluminta, Vertebruta,<br>Catarrhini, Hominidae,<br>BL/GenBank/DDBJ databa<br>B TYPE C EOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | Clariata, Verteblata,<br>Catarrhini; Hominidae;<br>EL/GenBank/DDBJ databa<br>E TYPE C FOMAIN.<br>D0x84E5DB78E8E25 CRC5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | Cluminta, Verteblata, Catarrhini, Hominidae, Catarrhini, Hominidae, ETYPE C EOMAIN. 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DO&84E5DB78E8E25 CRC5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | Et annotation update) E FACTOR 8 PROTEIN. Clumintar, Vertebrata, Catarrhini; Hominidae; EL/GenBank/DDBJ databa 8 TYPE C FOMAIN. WM_I.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | Et annotation update) E FACTOR B PROTEIN. Colariuts, Vertebrats, Catarrhini; Hominidae; BL/GenBauk/DDBJ databa B TYPE C FOMAIN.  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Clumintar, Vertebrata, Catarrhini; Hominidae; EL/GenBank/DDBJ databa B TYPE C DOMAIN. MM_1.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | Et annotation update) E FACTOR B PROTEIN. Catarrhini; Hominidae; EL/GenBank/DDBJ databa B TYPE C LOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
| st annobation update) F FACTOR B PROTEIN. Catarrhini: Hominidae; EL/GenBank/DDBJ databa F TYPE C FOMAIN. 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Catarrhini: Hominidae; Catarrhini: Hominidae; WM_1. 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Clumintal, Vertebrata, Catarrhini, Hominidae; EL/GenBank/DDBJ databa E TYPE C EGMAIN. 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| st sequence update)  F raction update)  F raction update)  Cluminta, Vertebrata,  Catarrhini; Hominidae,  EL/GenBank/DDBJ databa  F TYPE C FOMAIN.  DOE84E5DB78E8E25 CRC5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | st sequence update)  Fraction update)  Fraction update)  Claridat, Verteblata,  Catarrhini; Hominidae;  BL/GenBank/DDBJ databa  B TYPE C FOMAIN.  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DOE84ESDB78EBE25 CRC5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | st sequence update) ct ancotation update) ct ancotation update) ct ancotation update) Clariata, Verteblata, Catarrhini; Hominidae; BL/GenBauk/DDBJ databa B TYPE C FOMAIN. COEBULE UPDBJ GATABA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | st sequence update) F constation update) F PACTOR & PROTEIN. 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| st sequence update) ct annotation update) ct annotation update) Claridta, Verteblata, Catarrhini; Hominidae, EL/GenBauk/DDBJ databa B TYPE C FOMAIN.  20284E5DB78E8E25 CRC5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | st sequence update) ct annotation update) ct annotation update) Clanidta, Verteblata, Catarrhini, Hominidae, Gararrhini, Hominidae, Gararrhini, ElygenBank/DDBJ databa 8 TYPE C DOMAIN. DOES4ESDB78E8E25 CRC5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | st sequence update) ct annotation update) ct annotation update) classiats, Verteblats, Catarrhini; Hominidae; EL/GenBank/DDBJ databa B TYPE C FOMAIN.  WN_1.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | st sequence update) ct annotation update) F ACTOR & PROTEIN. CLAILLA, Vertebiala. Calarrhini; Hominidae. 8 TYPE C EOMAIN. MM_1.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | st sequence update) ct annotation update) ct annotation update) Cluminta, Vertebrata, Catarrhini; Hominidae; EL/GenBank/DDBJ databa B TYPE C DOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
| St. Sequence update) st. anocation update) F. FACTOR & PROTEIN. Clumiata, Verteblata, Catarrhini; Hominidae; EL/GenBank/DDBJ databa B. TYPE C. EOMAIN. DORB4ESDB78E8E25 CRC5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | St. Sequence update) st. sequence update) r tanocation update) F FACTOR & PROTEIN. Clusiata, Verteblata, Catarrhini; Hominidae; EL/GenBank/DDBJ databa B TYPE C FOMAIN.  DUESTEENS?EREESS CROS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | st sequence update) st sequence update) practice appoint. Catarrhini: Hominidae; EL/GenBank/DDBJ databa g TYPE C DOMAIN.  DOM84ESDB78E8E25 CRC5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | St. Sequence update) st. anocation update) F. FACTOR 8 PROTEIN. Catarrhini: Hominidae; EL/GenBank/DDBJ databa 8 TYPE C. DOMAIN. MM_1.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | st sequence update) st sequence update) F FACTOR 8 PROTEIN. Catarrhini: Hominidae; EL/GenBank/DDBJ databa 8 TYPE C DOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
| eates) esteed esteed ct annotation update) ct annotation update) F PACTOR 8 PROTEIN. Clumintial Wortchbula, Catarrhini: Hominidae; EL/GenBank/DDBJ databa B TYPE C EOMAIN. DOL84E5DB78E8E25 CRC5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | eates) eates) esteen es | eates) eates) est sequence update) et annotation update) F FACTOR 8 PROTEIN. Clumiatus Vertebratas, Catarrhini; Hominidae; EL/GenBank/DDBJ databa B TYPE C FOMAIN. DD&84ESDB7eE8E25 CRC5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | eates) eates) esteen es                                                                                                                                                                                                           | eates) eates) esteen ct ancotation update) E FACTOR 8 PROTEIN. Clumintar, Vertebrata, Catarrhini; Hominidae; EL/GenBank/DDBJ databa B TYPE C FOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
| eates) st sequence update) st sequence update) st anoctation update) F FACTOR 8 PROTEIN. Clanidta, Verteblata, Catarrhini: Howinidae; EL/GenBank/DDBJ databa B TYPE C FOMAIN. 20284E5DB78E8E25 CRC5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | eates) st sequence update) st sequence update) F FACTOR 8 PROTEIN. Clumidation Vertebrata, Catarrhini; Hominidation B TYPE C DOMAIN. COLSTEE DOMAIN. COLSTEE DOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | eates) st sequence update) st sequence update) st uncollion update) F PACHOP 8 PROTEIN. Clumidat, Vertebrata, Catarrhini: Hominidate, Catarrhini: Homi                                                                                                                                                                                                                                               | ealed<br>st sequence update)<br>st sequence update)<br>F FACTOR B PROTEIN.<br>Clusidata Vertebala.<br>Catarrhini: Hominidae;<br>Catarrhini: Hominidae;<br>Catarrhini                               | eates) st sequence update) st sequence update) st annotation update) F PACHOP 8 PROTEIN. Clumiata, Vertebrata, Catarrhini: Hominidae; EL/GenBank/DDBJ databa 8 TYPE C FOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
| eated) St Sequence update) St Sequence update) F FACTOR B PROTEIN. Clumiatu, Voltoblatu, Catarrhini: Hominidae; EL/GenBank/DDBJ databa B TYPE C DOMAIN. COLB41E5DB78E255 CRC5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | eated) St Sequence update) St Sequence update) F FACTOR B PROTEIN. Clumiati, Vorteblata, Catarrhini: Hominidae, Catarrhini: Hominidae, MM_1.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | eated) St sequence update) St sequence update) F FACTOR 8 PROTEIN. Clumiata, Vertebrata, Catarrhini; Howinidae; EL/GenBank/DDBJ databa B TYPE C FOMAIN. DO&84ESDB78EBE25 CRC5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | eated) St sequence update) St sequence update) F FACTOR 8 PROTEIN. Clumiata, Vertebrata, Catarrhini; Hominidaes EL/GenBank/DDBJ databa B TYPE C FOMAIN. COER4FSURZEEESS CROSS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | eated) St sequence update) St sequence update) F FACTOR B PROTEIN. CLALLALA, VELTEBLALA. CALARTHINI: HOWINIGARY BL/GenBank/DDBJ databa B TYPE C FOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
| eated) st sequence update) st annotation update) r Facrop 8 PROTEIN. Clarida, Vertebrata, Catarrhini; Hominidae, EL/GenBank/DDBJ databa 8 TYPE C FOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | eated) st sequence update) st annotation update) r Facrop 8 PROTEIN. Clariata, Verteblata, Catarrhini; Hominidae; EL/GenBank/DDBJ databa B TYPE C FOMAIN. DDE84E5DB78E8E25 CRC5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | eated) st sequence update) st annotation update) F PACTOR 8 PROTEIN. Clumiation Vortechals. Catarrhini: Hominidae. EL/GenBank/DDBJ databa E TYPE C DOMAIN. DOM84ESDB78EEBESS CRCS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | eated) st sequence update) st ancotation update) r Facrick 8 PROTEIN. Clariata, Verteblata. Catarrhini; Hominidae. BL/GenBauk/DDBJ databa B TYPE C FOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | eated) st sequence update) st annotation update) F PACTOR 8 PROTEIN. CLIMINIA WOLTCCHALL, CALARTHINI, HOMINIGACE EL/GenBank/DDBJ databa E TYPE C FOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
| eated) st sequence update) ct annotation update) ct annotation update) Cluidia. Cluidia. Vertebiala. Calarrhini; Hominidae. BL/GenBauk/DDBJ databa B TYPE C FOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | eated) st sequence update) ct annotation update) ct annotation update) Clanidta, Verteblata, Catarrhini; Hominidae, Catarrhini; Hominidae, Catarrhini; Comain.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | st sequence update) st annotation update) st annotation update) st annotation update) st annotation update) claiding PROFEIN. Catarrhini; Hominidae; catarrhini; Hominidae; envicenbank/DDBJ databa B TYPE c FOMAIN.  DOWSTESDB78EEBESS CRC5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | eated) st sequence update) st sequence update) st annotation update) F FGTGP 8 PROTEIN. Claridia, Vertebiala, Catarrhini; Hominidae, GTYPE C EOMAIN. MM_1.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | eated) st sequence update) st anotation update) st anotation update) Standard PROFEIN. Clarital Verteblata. Catarrhini; Hominidae. BL/GenBank/DDBJ databa B TYPE C DOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
| eated) St. Sequence update) St. anotation update) F FACTOR 8 PROTEIN. Clumiata, Verteblata, Catarrhini, Hominidae; EL/GenBank/DDBJ databa 8 TYPE C FOMAIN. 20284E5DB78E8E25 CRC5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | eated) St. Sequence update) St. anotation update) F FACTOR & PROTEIN. Clumiatu, Vertebiatu, Catarrhini; Hominidae; EL/GenBank/DDBJ databa B TYPE C EOMAIN. DUESTEE DOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | eated) St. Sequence update) Et anocation update) F. FACTOR 8 PROTEIN. Catarrhini: Hominidae; Catarrhini: Hominidae; WM_1.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | eated) St. Sequence update) St. anotation update) F FACTOR & PROTEIN. Clumiatu, Vertebiatu, Catarrhini; Hominidae; EL/GenBank/DDBJ databa B TYPE C FOMAIN. COERTES CROSS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | eated) St. Sequence update) Et anocation update) F.FACTOP 8 PROTEIN. Catarrhini: Hominidae; Catarrhini: Hominidae; WM_1.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
| st sequence update) st sequence update) F PACHOR 8 PROTEIN. Clumiatu, Vertebbula, Catarrhini; Hominidae; BTYPE C EOMAIN. 20284E5DB78E8E25 CRC5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | st sequence update) st sequence update) F FACTOR 8 PROTEIN. Catarrhini: Mominidae; EL/GenBank/DDBJ databa F TYPE C DOMAIN. MM_1.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | eated) st sequence update) st annotation update) F PACTOR 8 PROTEIN. Clumiata, Vertebrata, Catarrhini; Hominidae; Catarrhini; Hominidae; FYPE C FOMAIN. DO&84ESDB78E8E25 CRC5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | st sequence update) st sequence update) st annotation update) F PACTOR 8 PROTEIN. Catarrhini: Mominidae; Catarrhini: Hominidae; EL/GenBank/DDBJ databa B TYPE C FOMAIN. 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Clumint, Vertebruta, Catarrhini; Hominidae; EL/GenBank/DDBJ databa B TYPE C FOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
| eated) st sequence update) st sequence update) F FACTOR 8 PROFEIN. Clumintal, Vertebrata, Catarrhini; Hominidae; ELYGENBANK/DDBJ databa F TYPE C FOMAIN. DOL84E5DB78E8E25 CRC5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | eated) st sequence update) st sequence update) st annotation update) F FACTOR 8 PROTEIN. Clumintar, Vertebruta, Catarrhini; Hominidae; EL/GenBank/DDBJ databa 8 TYPE C FOMAIN. 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D0x84ESDB78E8E25 CRC5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | eated) ested) Et sequence update) Et annotation update) E FACTOR B PROTEIN. Clumiatu, Vertebratu, Catarrhini; Hominidae; EL/GenBank/DDBJ databa B TYPE C DOMAIN. COEB44ESUKZEEESS CROSS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | eated) ested) ct amoutation update) ct amoutation update) F FACTOR 8 PROTEIN. 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| ealed) st sequence update) st sequence update) st annotation update) F FACTOR 8 PROTEIN. Clumiata, Verteblata, Catarrhini: Hominidae; EL/GenBank/DDBJ databa B TYPE C FOMAIN. 20284E5DB78E8E25 CRC5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | ealed) st sequence update) st sequence update) st sequence update) F FACTOR B PROTEIN. Clusidata, Verteboula, Catarrhini; Hominidae; EL/GenBank/DDBJ databa B TYPE C DOMAIN. COLBYESUB?BESUS CROS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | eated) st sequence update) st sequence update) st sequence update) F PACTOR B PROTEIN. Clumiata, Vertebrata, Catarrhini; Hominidae; BL/GenBank/DDBJ databa B TYPE C FOMAIN. 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Colarinta, Verteblata, Catarrhini; Hominidae; GATARRADBJ databa B TYPE C DOMAIN. COLBATESHARRESS CROSS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | eated) st sequence update) st sequence update) st sequence update) F FACTOR 8 PROTEIN. Clumiata, Vertebrata, Catarrhini, Hominidae; EL/GenBank/DDBJ databa E TYPE C FOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
| PRI) 330 AA. eated) St Sequence update) St annotation update) F PACTOR 8 PROTEIN. Clumiation Voltethala. Catarrhini: Hominidae. BL/GenBank/DDBJ databa B TYPE C DOMAIN. DOLB41E5DB78EBE25 CRC5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | PRI) 330 AA. eated) St. Sequence update) St. Sequence update) F. FACTOR 8 PROTEIN. Classiata, Vertebrata, Catarrhini; Hominidae; EL/GenBank/DDBJ databa 8 TYPE C EOMAIN. DOESTEEDS CROS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | PRI) 330 AA. eated) st sequence update) st annotation update) F FACTOR 8 PROTEIN. Catarrhini: Howinidae; Catarrhini: Howinidae; EL/GenBank/DDBJ databa 8 TYPE C FOMAIN. D0284ESDB78E8E25 CRC5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | PRI) 330 AA. eated) St Sequence update) St annotation update) F PACTOR 8 PROTEIN. Cluminta, Vertechild. Catarrhini; Hominidae; EL/GenBank/DDBJ databa B TYPE C DOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | PRI) 330 AA. sated) st sequence update) st annotation update) F FACTOR 8 PROTEIN. Catarrhini: Howinidae; EL/GenBank/DDBJ databa 8 TYPE C FOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
| PRT; 35 AA. eated) st sequence update) st annotation update) r racing 8 PROTEIN. Clarida, Vertebilda, Catarrhini; Hominidae; BL/GenBank/DDBJ databa 8 TYPE C FOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | PRT; 35 AA. eated) st sequence update) st annotation update) r Facrick 8 PROTEIN. Clariata, Vertebiata, Catarrhini; Hominidae; BL/GenBank/DDBJ databa B TYPE C FOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | PRT: 35 AA. eated) st sequence update) st sequence update) ft annotation update) F PACTOR 8 PROTEIN. Clumidting Worlochidiae; Catarrhini: Hominidae; BL/GenBank/DDBJ databa 8 TYPE C DOMAIN. DOM84ESDB78E8BESS CRC5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | PRT: 35 AA. eated) st sequence update) st ancotation update) r Factor B PROTEIN. Clariata, Verteblata. Catarrhini; Hominidae. BL/GenBauk/DDBJ databa B TYPE C FOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | PRT; 35 AA. eated) st sequence update) st annotation update) F FACTOR 8 PROTEIN. Clumidti, Vortechala. Catarrhini: Hominidae. EL/GenBank/DDBJ databa E TYPE C FOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
| PRT: 335 AA. eated) st sequence update) st anotation update) st anotation update) st anotation update) st racing # PROTEIN. Claridia. Vertebiala. Catarrhini: Hominidae: BL/GenBauk/DDBJ databa # TYPE C FOMAIN. 20284E5DB78E8E25 CRC5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | PRT: 335 AA. eated) st sequence update) cl anotation update) F FACTOR B PROTEIN. Claridta, Vertebiala. Catarrhini; Hominidae. BL/GenBank/DDBJ databa B TYPE C DOMAIN. CAUSTAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | PRT: 335 AA.  cated) st sequence update) st annotation update) r tannotation update) r FACTOR 8 PROTEIN.  Claritata, Vertebala,  Catarrhini; Hominidae,  EL/GenBank/DDBJ databa B TYPE C FOMAIN.  MM_1.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | PRT: 335 AA. eated) st sequence update) cl anotation update) F FACTOR B PROTEIN. Claridta, Vertebiala. Catarrhini; Hominidae. BL/GenBank/DDBJ databa 8 TYPE C DOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | PRT: 335 AA. eated) st sequence update) st ancotation update) st tannotation update) st PACTOR CLULIALA, VELEBLALA, Catarrhini; Hominidae; BL/GenBank/DDBJ databa B TYPE C DOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
| PRT: 335 AA. eated) st sequence update) ct annotation update) F FACTOR 8 PROTEIN. Claridta, Vertebiala. Catarrhini; Hominidae. BL/GenBauk/DDBJ databa 8 TYPE C FOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | PRT: 335 AA. eated) st sequence update) st sequence update) ct annotation update) F FACTOR 8 PROTEIN. Claridia, Vertebiala. Calarrhini; Hominidae. STYPE C DOMAIN. MM_I.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | PRT: 335 AA. eated) st sequence update) st annotation update) st tannotation update st tannotation update) st tann                                                                                                                                                                                                                                               | PRT: 335 AA. eated) st sequence update) st sequence update) ct annotation update) F PACHOR B PROTEIN. Claridia, Vertebiala. Calarrhini; Hominidae. BL/GenBank/DDBJ databa 8 TYPE C EOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | PRT: 335 AA. eated) st sequence update) st annotation update) st tannotation update) st tan |
| 9FT19 9FT19 9FT19 9FT19 1-JUN-2001 (TFEMBLED1.17, Created) 1-JUN-2001 (TFEMBLED1.17, Last sequence update) 1-JUN-2001 (TFEMBLED1.17, Last sequence update) 1-JUN-2001 (TFEMBLED1.17, Last sequence update) 1-SEC-2001 (TFEMBLED1.19, Last annotation update) 1-SEC-2001 (TFEMBLED1.19, Last sequence update) 1-SEC-2001 (TFEMBLED1.19, Howitidae) 1-SEMILARITY: CONTAINS 1 F5/8 TYPE C DOMAIN. 1-SIMILARITY: SMOOTOR: ESSELIT. 1-SIMILARITY: SMOOTOR: ESSELIT. 1-SIMILARITY: SMOOTOR: ESSELIT. 1-SIMILARITY: PSOLUSS: FASSCLIT. 1-SIMILARITY: PSOLUSS: | 9FT19 9FT19 9FT19 9FT19 1-JUN-2001 (TFEMBLED1.17, Created) 1-JUN-2001 (TFEMBLED1.17, Last sequence update) 1-JUN-2001 (TFEMBLED1.17, Last sequence update) 1-JUN-2001 (TFEMBLED1.17, Last sequence update) 1-SEC-2001 (TFEMBLED1.19, Last annotation update) 1-SEC-2001 (TFEMBLED1.19, Last sequence update) 1-SEC-2001 (TFEMBLED1.19, Last sequence update) 1-SEC-2001 (TFEMBLED1.10, Last sequence update) 1-SEU-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 99FIL9 9PRELIMINARY; PRT; 335 AA. 99FIL9; 1-JUN-2001 (TFEMBLEEL. 17, Greated) 1-JUN-2001 (TFEMBLEEL. 17, Last sequence update) 1-JUN-2001 (TFEMBLEEL. 17, Last sequence update) 1-DUN-2001 (TEMBLEEL. 17, Last sequence                                                                                                                                                                                                                                                | 9FTL9 1-JUN-2001 (TFEMBLrel. 17, Last sequence update) 1-JUN-2001 (TFEMBLrel. 17, Last sequence update) 1-FT-2001 (TFEMBLrel. 19, Last sequence update) 1-FT-2001 (TFEMB                                                                                                                                                                                                           | 99FIL9 9PRELIMINARY; PRT; 335 AA. 99FIL9; 1-JUN-2001 (TFEMBLEC1.17, Greated) 1-JUN-2001 (TFEMBLEC1.17, Last sequence update) 1-JUN-2001 (TFEMBLEC1.17, Last sequence update) 1-DUN-2001 (TFEMBLEC1.17, Last sequence update) 1-DEC-2001 (TFEMBLEC1.18, Last sequence update) 1-DEC-2001 (TFEMBLEC1.18, Last sequence update) 1-DEC-2001 (TEMBLEC1.18, LAST sequ |
| 9HTL9 PRELIMINARY; PRT; 335 AA, 9HTL9 PRELIMINARY; PRT; 335 AA, 9HTL9 1-JUN-2001 (TFEMBLrel. 17, Last sequence update) 1-JUN-2001 (TFEMBLrel. 17, Last sequence update) 1-JUN-2001 (TFEMBLrel. 17, Last sequence update) 1-FFC-2001 (TFEMBLrel. 19, Last annotation update) 1-FFC-2001 (TFEMBLrel. 19, Last sequence update) 1-FFC-2001 (TFEMBLrel. 19, TIMELS, HOWITHING SET SEQUENCE FROM N.A. 1-SIMILARITY: CONTAINS 1 F5/8 TYPE C FOMAIN. 1-SIMILARITY: SMOOTOR: EGFL-11. 1-SIMILARITY: SMOOTOR: EGFL-11. 1-SIMILARITY: FSG1128: | 9HTL9 PRELIMINARY; PRT; 335 AA, 9HTL9 PRELIMINARY; PRT; 335 AA, 9HTL9 1-JUN-2001 (TFEMBLrel. 17, Last sequence update) 1-JUN-2001 (TFEMBLrel. 17, Last sequence update) 1-JUN-2001 (TFEMBLrel. 17, Last sequence update) 1-FF-2-001 (TFEMBLrel. 19, Last annotation update) 1-FF-2-001 (TFEMBLrel. 19, Last sequence update) 1-FF-2-101 (TF | 98TL9 98TL9 98TL9 98TL9 98TL9 98TL9 98TL9 98TL9 1-JUN-2001 (TERMELTOL. 17, Created) 1-JUN-2001 (TERMELTOL. 17, Last sequence update) 1-JUN-2001 (TERMELTOL. 17, Last sequence update) 1-JUN-2001 (TERMELTOL. 19, Last sequence update) 1-FFC-2001 (Hound) 1-FFC-2001 (TERMELTOL) 1-FECH STATES (FECH SECTION) 1-FECH SECTION NA. 1-FECH SECTION NA                                                                                                                                                                                                                                               | 9HTL9 PRELIMINARY; PRT; 335 AA. 9HTL9 PRELIMINARY; PRT; 335 AA. 9HTL9 1-JUN-2001 (TrEMBLrel. 17, Last sequence update) 1-JUN-2001 (TrEMBLrel. 17, Last sequence update) 1-JUN-2001 (TrEMBLrel. 17, Last sequence update) 1-FFC-2001 (TrEMBLrel. 19, Last annotation update) 1-FFC-2001 (TrEMBLrel. 19, CALARTHINI, Howinidaes) 1-FFC-2001 (FEE-2001) to the EMBL/GenBank/DBBJ databatera R. 1-SIMILARITY: CONTAINS 1 F5/8 TYPE C FOMAIN. 1-SIMILARITY: FANDONS 1 F5/8 TYPE C FOMAIN. 1-SIMILARITY: FANDONS 1 F5/8 TYPE C FOMAIN. 1-SIMILARITY: FANDONS 1 FANDO                                                                                                                                                                                                           | 9HTL9 PRELIMINARY; PRT; 335 AA. 9HTL9 19UL9; PRELIMINARY; PRT; 335 AA. 9HL9; 19UN-2001 (TFEMBLEOL. 17, Last sequence update) 1-5UN-2001 (TFEMBLEOL. 17, Last sequence update) 1-FEC-7001 (TFEMBLEOL. 17) 1-FEC-7001 (TFEMBLEOL. 18) 1- |
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| 9HTL9 PRELIMINARY; PRT; 335 AA, 9HTL9 PRELIMINARY; PRT; 335 AA, 9HTL9 1-JUN-2001 (TFEMBLrel. 17, Last sequence update) 1-JUN-2001 (TFEMBLrel. 17, Last sequence update) 1-JUN-2001 (TFEMBLrel. 17, Last sequence update) 1-FFC-2001 (TFEMBLrel. 19, Last annotation update) 1-FFC-2001 (TFEMBLrel. 19, Last sequence update) 1-FFC-2001 (TFEMBLrel. 19, TIMELS, HOWITHING SET SEQUENCE FROM N.A. 1-SIMILARITY: CONTAINS 1 F5/8 TYPE C FOMAIN. 1-SIMILARITY: SMOOTOR: EGFL-11. 1-SIMILARITY: SMOOTOR: EGFL-11. 1-SIMILARITY: FSG1128: | 9HTL9 PRELIMINARY; PRT; 335 AA, 9HTL9 PRELIMINARY; PRT; 335 AA, 9HTL9 1-JUN-2001 (TFEMBLrel. 17, Last sequence update) 1-JUN-2001 (TFEMBLrel. 17, Last sequence update) 1-JUN-2001 (TFEMBLrel. 17, Last sequence update) 1-FF-2-001 (TFEMBLrel. 19, Last annotation update) 1-FF-2-001 (TFEMBLrel. 19, Last sequence update) 1-FF-2-101 (TF | 98TL9 98TL9 98TL9 98TL9 98TL9 98TL9 98TL9 98TL9 1-JUN-2001 (TERMELTOL. 17, Created) 1-JUN-2001 (TERMELTOL. 17, Last sequence update) 1-JUN-2001 (TERMELTOL. 17, Last sequence update) 1-JUN-2001 (TERMELTOL. 19, Last sequence update) 1-FFC-2001 (Hound) 1-FFC-2001 (TERMELTOL) 1-FECH STATES (FECH SECTION) 1-FECH SECTION NA. 1-FECH SECTION NA                                                                                                                                                                                                                                               | 9HTL9 PRELIMINARY; PRT; 335 AA. 9HTL9 PRELIMINARY; PRT; 335 AA. 9HTL9 1-JUN-2001 (TrEMBLrel. 17, Last sequence update) 1-JUN-2001 (TrEMBLrel. 17, Last sequence update) 1-JUN-2001 (TrEMBLrel. 17, Last sequence update) 1-FFC-2001 (TrEMBLrel. 19, Last annotation update) 1-FFC-2001 (TrEMBLrel. 19, CALARTHINI, Howinidaes) 1-FFC-2001 (FEE-2001) to the EMBL/GenBank/DBBJ databatera R. 1-SIMILARITY: CONTAINS 1 F5/8 TYPE C FOMAIN. 1-SIMILARITY: FANDONS 1 F5/8 TYPE C FOMAIN. 1-SIMILARITY: FANDONS 1 F5/8 TYPE C FOMAIN. 1-SIMILARITY: FANDONS 1 FANDO                                                                                                                                                                                                           | 9HTL9 PRELIMINARY; PRT; 335 AA. 9HTL9 19UL9; PRELIMINARY; PRT; 335 AA. 9HL9; 19UN-2001 (TFEMBLEOL. 17, Last sequence update) 1-5UN-2001 (TFEMBLEOL. 17, Last sequence update) 1-FEC-7001 (TFEMBLEOL. 17) 1-FEC-7001 (TFEMBLEOL. 18) 1- |
| 9HTL9 PRELIMINARY; PRT; 335 AA, 9HTL9 1-JUN-2001 (TFEMBLEO1.17, Created) 1-JUN-2001 (TFEMBLEO1.17, Last sequence update) 1-JUN-2001 (TFEMBLEO1.17, Last sequence update) 1-SUN-2001 (TFEMBLEO1.17, Last sequence update) 1-FEC-2001 (TFEMBLEO1.19, Last annotation update) 1-FEC-2001 (TFEMBLEO1.19, Last annotation update) 1-FEC-2001 (TFEMBLEO1.19, Last sequence update) 1-FEC-2001 (TFEMBLEO1.10, Last Sequence update) 1-FEC-2001 (TFEMBLEO1.10, Last Sequence update) 1-FEC-2001 (TFEMBLEO1.10, Last Sequence update) 1-FEMBLEON N.A. 1 | 9HTL9 PRELIMINARY; PRT; 335 AA, 9HTL9 1-JUN-2001 (TFEMBLrel. 17, Last sequence update) 1-JUN-2001 (TFEMBLrel. 17, Last sequence update) 1-JUN-2001 (TFEMBLrel. 17, Last sequence update) 1-FFC-2001 (TFEMBLrel. 19, Last annotation update) 1-FFC-2001 (TFEMBLrel. 19, Last annotation update) 1-FFC-2001 (TFEMBLrel. 19, Last sequence update) 1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1-FFC-1- | 9FTL9 PRELIMINARY; PRT; 335 AA, 9JHL9; PRELIMINARY; PRT; 335 AA, 9JHL9; 1-JUN-2001 (TFEMBLEG1. 17, Last sequence update) 1-JUN-2001 (TF                                                                                                                                                                                                                                               | 9HTL9 PRELIMINARY; PRT; 335 AA, 9HTL9 9HTL9 19UL9; PRELIMINARY; PRT; 335 AA, 9HTL9 19UN-2001 (TrEMBLrel. 17, Last sequence update) 1-JUN-2001 (TrEMBLrel. 17, Last sequence update) 1-JUN-2001 (TrEMBLrel. 19, Last sequence update) 1-FOC-2001 (TrEMBLRel. 19, Last sequence update) 1-FO                                                                                                                                                                                                           | 9FTL9 9FTL9 19JUN-2001 (TFEMBLED1.17, Greated) 1-JUN-2001 (TFEMBLED1.17, Last sequence update) 1-JUN-2001 (TFEMBLED1.17, Last  |
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| 9FT19 9FT19 9FT19 9FT19 9FT19 1-JUN-2001 (TFEMBLED1.17, Created) 1-JUN-2001 (TFEMBLED1.17, Last sequence update) 1-JUN-2001 (TFEMBLED1.17, Last sequence update) 1-JUN-2001 (TFEMBLED1.17, Last sequence update) 1-SEC-2001 (TFEMBLED1.19, Last annotation update) 1-SEC-2001 (TFEMBLED1.19, Last sequence update) 1-SEC-2001  | 9FT19 9FT19 9FT19 9FT19 1-JUN-2001 (TFEMBLED1.17, Created) 1-JUN-2001 (TFEMBLED1.17, Last sequence update) 1-JUN-2001 (TFEMBLED1.17, Last sequence update) 1-JUN-2001 (TFEMBLED1.17, Last sequence update) 1-SEC-2001 (TFEMBLED1.19, Last annotation update) 1-SEC-2001 (TFEMBLED1.19, Last sequence update) 1-SEC-2001 (TFEMBLED1.19, Last sequence update) 1-SEC-2001 (TFEMBLED1.10, Last sequence update) 1-SEU-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 99FIL9 9PRELIMINARY; PRT; 335 AA. 99FIL9; 1-JUN-2001 (TFEMBLEEL. 17, Greated) 1-JUN-2001 (TFEMBLEEL. 17, Last sequence update) 1-JUN-2001 (TFEMBLEEL. 17, Last sequence update) 1-DUN-2001 (TEMBLEEL. 17, Last sequence                                                                                                                                                                                                                                                | 9FTL9 1-JUN-2001 (TFEMBLrel. 17, Last sequence update) 1-JUN-2001 (TFEMBLrel. 17, Last sequence update) 1-FT-2001 (TFEMBLrel. 19, Last sequence update) 1-FT-2001 (TFEMB                                                                                                                                                                                                           | 99FIL9 9PRELIMINARY; PRT; 335 AA. 99FIL9; 1-JUN-2001 (TFEMBLEC1.17, Greated) 1-JUN-2001 (TFEMBLEC1.17, Last sequence update) 1-JUN-2001 (TFEMBLEC1.17, Last sequence update) 1-DUN-2001 (TFEMBLEC1.17, Last sequence update) 1-DEC-2001 (TFEMBLEC1.18, Last sequence update) 1-DEC-2001 (TFEMBLEC1.18, Last sequence update) 1-DEC-2001 (TEMBLEC1.18, LAST sequ |
| PRT: 335 AA. eated) st sequence update) ct annotation update) F FACTOR 8 PROTEIN. Claridta, Vertebiala. Catarrhini; Hominidae. BL/GenBauk/DDBJ databa 8 TYPE C FOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | PRT: 335 AA. eated) st sequence update) st sequence update) ct annotation update) F FACTOR 8 PROTEIN. Claridia, Vertebiala. Calarrhini; Hominidae. STYPE C DOMAIN. MM_I.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | PRT: 335 AA. eated) st sequence update) st annotation update) st tannotation update st tannotation update) st tann                                                                                                                                                                                                                                               | PRT: 335 AA. eated) st sequence update) st sequence update) ct annotation update) F PACHOR B PROTEIN. Claridia, Vertebiala. Calarrhini; Hominidae. BL/GenBank/DDBJ databa 8 TYPE C EOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | PRT: 335 AA. eated) st sequence update) st annotation update) st tannotation update) st tan |
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DO&84E5DB78E8B25 CRC5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | PRT: 335 AA. eated) st sequence update) st anotation update) F FACTOR B PROTEIN. Clusiata, Vertebiata. Catarrhini; Hominidae; EL/GenBank/DDBJ databa 8 TYPE C DOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | PRT; 35 AA. eated) st sequence update) st annotation update) F PACTOR B PROTEIN. Clumints, Vertechild. Catarrhini; Hominidae; EL/GenBank/DDBJ databa F TYPE C FOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
| PRT; 335 AA. eated) st sequence update) st ancotation update) r Facrick 8 PROFEIN. Clariata, Vertebiata, Catarrhini; Hominidae; BL/GenBank/DDBJ databa 8 TYPE C FOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | PRT; 335 AA. eated) st sequence update) st annotation update) st Action 8 PROTEIN. Claridar, Verteblada. Catarrhini; Hominidae. BL/GenBauk/DDBJ databa 8 TYPE C FOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | PRT: 35 AA. eated) st sequence update) st annotation update) F PACTOR 8 PROTEIN. CLIMIAL, Vetteballa, Catarrhini: Hominidae; EL/GenBank/DDBJ databa 8 TYPE C DOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | PRT: 335 AA. eated) st sequence update) st anotation update) st tarnotation update) st tarn                                                                                                                                                                                                           | PRT; 35 AA. eated) st sequence update) st annotation update) F PACTOR B PROTEIN. CLARITHINI; HOMINIGACE EL/GenBank/DDBJ databa E TYPE C FOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| PRT: 435 AA. eated) st sequence update) st sequence update) fr annotation update) fr PACTOR 8 PROTEIN. Cluminta, Vertebula, Catarrhini; Hominidae; BL/GenBank/DDBJ databa 8 TYPE C DOMAIN. 202841E5DB78E8E25 CRC5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | PRT: 435 AA. eated) st sequence update) st saquence update) st annotation update) st saquence update) st saquence update) st saquence update) st ranction update) st racing Vertebildat, Catarrhini; Hominidat, Catarrhini; Hominidate B TYPE C FOMAIN. DUR84E5DB78E8E25 CRC5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | PRT: 35 AA. eated) St sequence update) St annotation update) F PACTOR 8 PROTEIN. Catarrhini: Hominidae; Catarrhini: Hominidae; BL/GenBank/DDBJ databa 8 TYPE C FOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | PRT: 435 AA. eated) st sequence update) st annotation update) r racing 8 PROTEIN. Clariata, Vertebiata, Catarrhini; Hominidae, BL/GenBauk/DDBJ databa 8 TYPE C FOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | PRT; 35 AA. eated) St sequence update) St annotation update) F PACTOR 8 PROTEIN. Catarrhini: Hominidae; EL/GenBank/DDBJ databa 8 TYPE C DOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| PRIS 435 AA. eated) St sequence update) St sequence update) F FACTOR 8 PROTEIN. Classiata, Vertebouta, Catarrhini; Hominidae; BL/GenBank/DDBJ databa 8 TYPE C DOMAIN. 20284E5DB78E8E25 CRC5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | PRI) 35 AA. eated) St Sequence update) St Sequence update) F FACTOR 8 PROTEIN. Clumiata, Vertebula, Catarrhini; Hominidae, B TYPE C FOMAIN. MM_1.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | PRI) 35 AA. eated) St Sequence update) St annotation update) F FACTOR 8 PROTEIN. Catarrhini: Howinidae; Catarrhini: Howinidae; BL/GenBank/DDBJ databa 8 TYPE C FOMAIN. DOL84ESDB78E8E25 CRC5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | PRI) 35 AA. eated) St Sequence update) St annotation update) F FACTOR 8 PROTEIN. Clariata, Vertebiala, Catarrhini; Hominidae, BL/GenBank/DDBJ databa B TYPE C FOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | PRI; 33 AA. eated) st sequence update) st annotation update) F FACTOR 8 PROTEIN. Catarrhini: Hominidae; EL/GenBank/DDBJ databa 8 TYPE C FOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| eated) st sequence update) st sequence update) st annotation update) F PACTOR 8 PROTEIN. Clumidti, Vortetbulta, Catarrhini: Hominidae; BL/GenBank/DDBJ databa 8 TYPE C DOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | eated) St Sequence update) St Sequence update) St annotation update) F PACTOR 8 PROTEIN. Clumintal, Vortechala, Catarrhini; Hominidae; BL/GenBank/DDBJ databa 8 TYPE C DOMAIN. MM_1.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | eated) St sequence update) St sequence update) St annobation update) F FACTOR 8 PROTEIN. Clumidta, Vertebbata, Catarrhini: Howinidae; EL/GenBank/DDBJ databa B TYPE C FOMAIN. DO&84ESDB78E8E25 CRC5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | PRI) 330 AA. eated) St sequence update) St sequence update) F FACTOR 8 PROTEIN. Clumiata, Vertebrata, Catarrhini; Hominidaes BTYPE C FOMAIN. WM_1.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | eated) St Sequence update) St Sequence update) St ancocation update) F FACTOR 8 PROTEIN. Clumintat, Vertebbate, Catarrhini: Howinidae; EL/GenBank/DDBJ databa 8 TYPE C FOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| eated) St sequence update) St sequence update) St annotation update) F FACTOR 8 PROTEIN. Catarrhini: Hominidae; Catarrhini: Hominidae; WM_1.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | PRINT SOUTH AND MAN. Seated) St Sequence update) St Sequence update) F PACHOP 8 PROTEIN. Colsida, Vertebiala, Calarrhini; Hominidae; Calarrhini; Hominidae; WM_I.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | eated) st squence update) st squence update) st annotation update) F FACTOR 8 PROTEIN. Clumiata, Vertebrata, Catarrhini; Howinidae; EL/GenBank/DDBJ databa B TYPE C FOMAIN. 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Clumiata, Vertebrata, Catarrhini; Hominidae; GALARRHINI; Hominidae; GALARRHINI; HOMINIDAE; GALARRHINI; HOMINIDAE; GALARRHINI; HOMINIDAE; GALARRHINI; HOMINIDAE; GOERALESURFEESS, CROSS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | eated) st sequence update) st sequence update) st annobation update) F FACTOR 8 PROTEIN. Clamidta, Vertebrata, Catarrhini; Howinidae; EL/GenBank/DDBJ databa B TYPE C FOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
| eated)  st sequence update)  st sequence update)  st sequence update)  F PACTOR B PROTEIN.  Cluidate, Vettebrata,  Catarrhini; Hominidae;  ELYGENBANK/DDBJ databa  R TYPE C FOMAIN.  DOL84E5DB78E8E25 CRC5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | eated) eated) ct annotation update) ct annotation update) F FACTOR B PROTEIN. Clumintal, Vertebrata, Catarrhini; Hominidae; EL/GenBank/DDBJ databa B TYPE C DOMAIN. 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Clumidul, Vertebruta, Catarrhini; Hominidaes B TYPE C DOMAIN. 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Clumintal, Vertebrata, Catarrhini; Hominidae; EL/GenBank/DDBJ databa B TYPE C DOMAIN. 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Cluminta, Vertebrata, Catarrhini; Hominidae; EL/GenBank/DDBJ databa 8 TYPE C FOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
| eated)  Et sequence update)  Et annotation update)  E FACTOR B PROTEIN.  Clumintar, Vertebrata,  Catarrhini; Hominidae;  EL/GenBank/DDBJ databa  E TYPE C FOMAIN.  DOL84E5DB78E8E25 CRC5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | eated)  st sequence update)  st sequence update)  st sequence update)  F FACTOR B PROTEIN.  Cluidate, Vertebiala,  Calarrhini; Hominidae;  Calarrhini; Hominidae;  WM_I.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | eated) set sequence update) st sequence update) st sequence update) st sequence update) F PACTOR B PROTEIN. Clubiata, Verteblata, Catarrhini; Hominidae; STYPE C LOMAIN.  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Cluminta, Vertebrata, Catarrhini; Hominidaes EL/GenBank/DDBJ databa 8 TYPE C DOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
| eated) st sequence update) st annotation update) F FACTOR 8 PROFEIN. Clumiatu, Vertebruta, Catarrhini; Hominidae; EL/GenBank/DDBJ databa E TYPE C FOMAIN. DOE84E5DB78E8E25 CRC5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | eated) st sequence update) st annotation update) F FACTOR 8 PROFEIN. Clumiata, Vertebrata, Catarrhini; Hominidae; ELYGENBANK/DDBJ databa R TYPE C FOMAIN. CORSTENDS CROS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | eated) st sequence update) st sequence update) st annotation update) F FACTOR 8 PROTEIN. Clubiata, Verteblata, Catarrhini; Hominidae; EL/GenBauk/DDBJ databa 8 TYPE C FOMAIN. D0x84ESDB78E8E25 CRC5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | eated) st sequence update) st amoutation update) F FACTOR 8 PROFEIN. Clumiatu, Vertebrata, Catarrhini; Hominidae; EL/GenBank/DDBJ databa 8 TYPE C FOMAIN. COER4FSURZERESS CROSS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | eated) st sequence update) ct annotation update) F FACTOR B PROTEIN. Clubidata Verteblata. Catarrhini: Hominidae; EL/GenBank/DDBJ databa B TYPE C LOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
| eated) st sequence update) st annotation update) F PACTOR 8 PROTEIN. Clumiatu, Vettebruta, Catarrhini; Hominidae; EL/GenBank/DDBJ databa B TYPE C EOMAIN. 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Clumiatu, Vertebruta, Catarrhini; Hominidae; ELYGENBANK/DDBJ databa F TYPE C FOMAIN. CORRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUBTRESUB | eated) st sequence update) st annotation update) F FACTOR 8 PROTEIN. Clumidital Vertebrata, Catarrhini; Hominidae; EL/GenBank/DDBJ databa R TYPE C FOMAIN. D0x84ESDB78E8E25 CRC5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | eated) st sequence update) st annotation update) F FACTOR 8 PROTEIN. Clumiatu, Vertebruta, Catarrhini; Hominidae; ELYGENBANK/DDBJ databa B TYPE C EOMAIN. COER4ESHK?REEES CROSS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | eated) st sequence update) st annotation update) F FACTOR 8 PROTEIN. Clumintal, Vertebrata, Catarrhini; Hominidae; EL/GenBauk/DDBJ databa B TYPE C FOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
| st sequence update) st sequence update) F PACTOR 8 PROTEIN. Catarrhini: Hominidae; EL/GenBank/DDBJ databa F TYPE C DOMAIN. 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Clumiatu, Vettebruta, Catarrhini; Hominidae; EL/GenBank/DDBJ databa F TYPE C FOMAIN. DOESTEENSTEREDS CROS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | eated) st sequence update) st annotation update) F FACTOR 8 PROTEIN. Clumiatu, Vertebratu, Catarrhini; Hominidae; EL/GenBank/DDBJ databa B TYPE C FOMAIN. 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Clumiatu, Vettebruta, Catarrhini; Hominidae; ELYGENBANK/DDBJ databa F TYPE C FOMAIN. 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| eated) st. sequence update) st annotation update) F PACTOR 8 PROTEIN. Catarrhini: Mominidae; EL/GenBank/DDBJ databa B TYPE C FOMAIN. 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Catarrhini: Hominidae; EL/GenBank/DDBJ databa F TYPE C FOMAIN.  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Clumiata, Vertebrata, Catarrhini; Hominidae; Catarrhini; Hominidae; EL/GenBank/DDBJ databa 8 TYPE C FOMAIN. 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Catarrhini: Hominidae; Catarrhini: Hominidae; ELYGENBANK/DDBJ databa B TYPE C FOMAIN. COERTESTINGEREES CROSS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | eated) st sequence update) st annotation update) F FACTOR 8 PROTEIN. Clumiatu, Vertebrata, Catarrhini; Hominidae; EL/GenBank/DDBJ databa 8 TYPE C FOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
| st sequence update) st sequence update) F PACHOR 8 PROTEIN. Clumiatu, Vertebbula, Catarrhini; Hominidae; BTYPE C EOMAIN. 20284E5DB78E8E25 CRC5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | st sequence update) st sequence update) F FACTOR 8 PROTEIN. Catarrhini: Mominidae; EL/GenBank/DDBJ databa F TYPE C DOMAIN. 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Clumiata, Vertebrata, Catarrhini; Hominidae; Catarrhini; Hominidae; FYPE C FOMAIN. DO&84ESDB78E8E25 CRC5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | st sequence update) st sequence update) st annotation update) F PACTOR 8 PROTEIN. Catarrhini: Mominidae; Catarrhini: Hominidae; EL/GenBank/DDBJ databa B TYPE C FOMAIN. 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Clumint, Vertebruta, Catarrhini; Hominidae; EL/GenBank/DDBJ databa B TYPE C FOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
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Catarrhini: Hominidae; EL/GenBank/DDBJ databa FYPE C FOMAIN. 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Clumiatu, Vertebruta, Catarrhini; Hominidae; FYPE C DOMAIN. DOWSTEE C DOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | st sequence update) st sequence update) F PACTOR & PROTEIN. Catarrhini: Hominidae; EL/GenBank/DDBJ databa F TYPE C DOMAIN. MM_1.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | st sequence update) st sequence update) F FACTOR 8 PROTEIN. Clumiatu, Vertebruta, Catarrhini; Hominidae; EL/GenBank/DDBJ databa 8 TYPE C EOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
| eated) St. Sequence update) Et annotation update) F FACTOR & PROTEIN. Clumiatu, Vertebiatus, Catarrhini; Hominidae; EL/GenBank/DDBJ databa E TYPE C EOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | eated) St. Sequence update) Et annotation update) F FACTOR & PROTEIN. Clumiatu, Verteblata, Catarrhini: Hominidae; EL/GenBank/DDBJ databa B TYPE C FOMAIN. DURB4E5DB78E8E25 CRC5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | st sequence update) st sequence update) F FACTOR 8 PROTEIN. Catarrhini: Hominidae; EL/GenBank/DDBJ databa R TYPE C DOMAIN. DOWSTESS CROS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | eated) St. Sequence update) Et anocation update) F FACTOR & PROTEIN. Catarrhini: Hominidae; EL/GenBank/DDBJ databa FYPE C FOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | st sequence update) st sequence update) F FACTOR 8 PROTEIN. Catarrhini: Hominidae; Catarrhini: Hominidae; WM_1.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| eated) St. Sequence update) St. anotation update) F FACTOR 8 PROTEIN. Clumiata, Verteblata, Catarrhini, Hominidae; EL/GenBank/DDBJ databa 8 TYPE C FOMAIN. 20284E5DB78E8E25 CRC5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | eated) St. Sequence update) St. anotation update) F FACTOR & PROTEIN. Clumiatu, Vertebiatu, Catarrhini; Hominidae; EL/GenBank/DDBJ databa B TYPE C EOMAIN. DUESTEE DOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | eated) St. Sequence update) Et anocation update) F FACTOR 8 PROTEIN. Catarrhini: Hominidae;                                                                                                                                                                                                                                               | eated) St. Sequence update) St. anotation update) F FACTOR & PROTEIN. Clumiatu, Vertebiatu, Catarrhini; Hominidae; EL/GenBank/DDBJ databa B TYPE C FOMAIN. COERTES CROSS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | eated) St. Sequence update) Et anocation update) F.FACTOP 8 PROTEIN. Catarrhini: Hominidae; Catarrhini: Hominidae; WM_1.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
| eated) st sequence update) st annotation update) Francialus, Professuras, Calarrhini; Hominidaes EL/GenBank/DDBJ databa E TYPE C FOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | eated) st sequence update) st annotation update) F PACHOR B PROTEIN. Claidia, Vertebiala. Catarrhini; Hominidae. BL/GenBank/DDBJ databa 8 TYPE C FOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | eated) st sequence update) ct annotation update) ct annotation update) ct annotation update) Cluridin Vertebials, Calarrhini; Hominidae, Calarrhini; Hominidae B TYPE C DOMAIN.  MN_1.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | eated) st sequence update) st annotation update) F PACHOR B PROTEIN. Claniata, Verteblata, Catarrhini; Hominidae, EL/GenBank/DDBJ databa B TYPE C EOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | eated) st sequence update) ct amotation update) ct amotation update) Cluminta, Vertebruta, Catarrhini; Hominidae; EL/GenBank/DDBJ databa B TYPE C DOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
| eated) st sequence update) st annotation update) F FACTOR B PROTEIN. Claridar, Verteblada, Catarrhini; Hominidae; EL/GenBank/DDBJ databa B TYPE C FOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | eated) st sequence update) st annotation update) st transtant sequence update) st transtant vertebials, catarrhini; Hominidae; styre c romain. DURSTEELSESS CROS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | eated) st sequence update) st annotation update) F FACTOR 8 PROTEIN. Clumintu, Vertebruta, Catarrhini, Hominidae, EL/GenBank/DDBJ databa 8 TYPE C FOMAIN. D0x84E5DB78E8E25 CRC5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | eated) st sequence update) st annotation update) st annotation update) st annotation update) st sequence u                                                                                                                                                                                                           | eated) st sequence update) st ancotation update) F Facrope 8 PROFEN. Clariata, Vertebrata, Catarrhini; Hominidae; EL/GenBank/DDBJ databa F TYPE C FOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
| eated) St Sequence update) St annotation update) F PACTOR 8 PROTEIN. Cluminta, Vertebrata, Catarrhini, Hominidae, EL/GenBank/DDBJ databa 8 TYPE C DOMAIN. 20284E5DB78E8E25 CRC5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | eated) st sequence update) st sequence update) F FACTOR 8 PROTEIN. Clumiata, Vertebrata, Catarrhini; Hominidae, EL/GenBank/DDBJ databa 8 TYPE C FOMAIN. DOES4ESDB78E8E25 CRC5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | eated) st sequence update) st sequence update) F PACTOR 8 PROTEIN. Clumidia. Verteblats. Catarrhini: Hominidae. EL/GenBank/DDBJ databa 8 TYPE C DOMAIN. DOM84ESDB78E8BESS CRCS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | eated) st sequence update) st annotation update) F FACTOR 8 PROTEIN. Clariata, Vertebrata, Catarrhini; Hominidae; BL/GenBauk/DDBJ databa 8 TYPE C FOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | eated) St Sequence update) St Sequence update) F FACTOR 8 PROTEIN. Clumintal, Verteblata. Catarrhini: Hominidae. EL/GenBank/DDBJ databa E TYPE C DOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
| eated) St. Sequence update) St. Sequence update) F. PACTOR 8 PROTEIN. CLUMINAL, Vertebrata, Catarrhini: Hominidae; EL/GenBank/DDBJ databa B. TYPE C. DOMAIN. DOL841E5DB78EBE25 CRC5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | eated) St. Sequence update) St. Sequence update) F FACTOR 8 PROTEIN. Clumintal, Vettebruta, Catarrhini; Hominidae; EL/GenBank/DDBJ databa 8 TYPE C EOMAIN. MM_1.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | eated) st sequence update) st annotation update) F FACTOR 8 PROTEIN. Clumint. Vertebbula. Catarrhini: Hominidae; EL/GenBank/DDBJ databa 8 TYPE C FOMAIN. DOWSTERNI.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | eated) St. Sequence update) St. Sequence update) F. Factor B PROTEIN. Clubiata, Vettebrata, Catarrhini, Hominidae; EL/GenBank/DDBJ databa B TYPE C DOMAIN. COMBINE COMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | eated) st sequence update) st annotation update) F FACTOR 8 PROTEIN. Clumint. Vortebbula. Catarrhini: Hominidae; BL/GenBank/DDBJ databa 8 TYPE C FOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
| eated) St Sequence update) St Sequence update) F FACTOR B PROTEIN. Clumiatu, Voltoblatu, Catarrhini: Hominidae; EL/GenBank/DDBJ databa B TYPE C DOMAIN. COLB41E5DB78E255 CRC5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | eated) St Sequence update) St Sequence update) F FACTOR B PROTEIN. Clumiati, Vorteblata, Catarrhini: Hominidae, Catarrhini: Hominidae, MM_1.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | eated) St sequence update) St sequence update) F FACTOR 8 PROTEIN. Clumiata, Vertebrata, Catarrhini; Howinidae; EL/GenBank/DDBJ databa B TYPE C FOMAIN. DO&84ESDB78EBE25 CRC5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | eated) St sequence update) St sequence update) F FACTOR 8 PROTEIN. Clumiata, Vertebrata, Catarrhini; Hominidaes EL/GenBank/DDBJ databa B TYPE C FOMAIN. COER4FSURZEEESS CROSS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | eated) St sequence update) St sequence update) F FACTOR B PROTEIN. CLALLALA, VELTEBLALA. CALARTHINI: HOWINIGARY BL/GenBank/DDBJ databa B TYPE C FOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
| eated) St sequence update) St sequence update) F FACTOR 8 PROTEIN. Clamidta, Verteblata, Catarrhini: Hominidae; EL/GenBank/DDBJ databa B TYPE C FOMAIN. 20284E5DB78E2B55 CRC5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | eates) st sequence update) st sequence update) st sequence update) F PACHOR B PROTEIN. Clumidta, Vertebrata, Catarrhini; Hominidae; Catarrhini; Hominidae; WM_L. COL84ESUB?BEBESS CROS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | eates) st sequence update) st sequence update) st anoction update) F FACTOR 8 PROTEIN. Clumiata, Vertebrata, Catarrhini, Hominidae; EL/GenBank/DDBJ databa 8 TYPE C FOMAIN. DO&84ESDB78E8E25 CRC5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | eated) St sequence update) St sequence update) St annotation update) F PACHOR B PROTEIN. Calarrhini; Hominidae; Ca                                                                                                                                                                                                           | ealed) st sequence update) st anoctation update) F FACTOR 8 PROTEIN. Cluminta, Vertebrata, Catarrhini, Hominidae; EL/GenBank/DDBJ databa E TYPE C FOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
| eates) st sequence update) st sequence update) st anoctation update) F FACTOR 8 PROTEIN. Clanidta, Verteblata, Catarrhini: Howinidae; EL/GenBank/DDBJ databa B TYPE C FOMAIN. 20284E5DB78E8E25 CRC5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | eates) st sequence update) st sequence update) F FACTOR 8 PROTEIN. Clumidation Vertebrata, Catarrhini; Hominidation B TYPE C DOMAIN. COLSTEE DOMAIN. COLSTEE DOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | eates) st sequence update) st sequence update) st uncollion update) F PACHOP 8 PROTEIN. Clumidat, Vertebrata, Catarrhini: Hominidate, Catarrhini: Homi                                                                                                                                                                                                                                               | ealed<br>st sequence update)<br>st sequence update)<br>F FACTOR B PROTEIN.<br>Clusidata Vertebala.<br>Catarrhini: Hominidae;<br>Catarrhini: Hominidae;<br>Catarrhini                               | eates) st sequence update) st sequence update) st annotation update) F PACHOP 8 PROTEIN. Clumiata, Vertebrata, Catarrhini: Hominidae; EL/GenBank/DDBJ databa 8 TYPE C FOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
| eates<br>sates<br>st sequence update)<br>st sequence update)<br>F FACTOR 8 PROTEIN.<br>Claritain Vertebrata.<br>Catarrhini; Hominidae;<br>EL/GenBank/DDBJ databa<br>B TYPE C FOMAIN.<br>DOL84E5DB78E8E25 CHC5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | eates  st sequence update)  ct annotation update)  F FACTOR B PROTEIN.  Clariata, Vertebrata,  Catarrhini; Hominidae;  EL/GenBank/DDBJ databa  B TYPE C FOMAIN.  ZOE84E5UB78E8E55 CRUS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | eates) ested sates) ct annotation update) ct annotation update) F FACTOR B PROTEIN. Clubidata, Vertebbala, Calarrhini; Hominidae; GALARRHINI; Hominidae; GALARRHINI; Hominidae; GALARRHINI; Hominidae; GALARRHINI; HOMINIGAE; GALARRH                                                                                                                                                                                                                                               | eates  stranguence update)  ct annotation update)  F FACTOR B PROTEIN.  Clariata, Vertebiata,  Catarrhini; Hominidae;  EL/GenBank/DDBJ databa  B TYPE C DOMAIN.  COER4FSURFRESS CROSS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | eates) estes) est sequence update) ct annotation update) F FACTOR 8 PROTEIN. Calarrhini; Hominidae; calarrhini; Hominidae; s TYPE C DOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
| cates  sates  sates  transcation update)  stranscation update)  Fraction apparent  Cluniatu, Vertebiuta,  Catarrhini; Hominidae;  EL/GenBank/DDBJ databa  ETYPE C. FOMAIN.  DOL84E5DB78E8E25 CRC5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | eates strangered stran | cates  sates  sates  to anotation update)  E FACTOR 8 PROTEIN.  Claridata Vertebiala,  Catarrhini; Hominidae;  EL/GenBank/DDBJ databa  B TYPE C FOMAIN.  D0x84ESDB78E8E25 CRC5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | eates  sates  sates  ct ancotation update)  ct ancotation update)  F FACTOR 8 PROFEIN.  Claritata Vertebiala,  catarrhini; Hominidae;  EL/GenBank/DDBJ databa  B TYPE C FOMAIN.  COER4FSIM72EFFES CROSS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | eates) eates) st sequence update) st annotation update) F FACTOR B PROTEIN. Calarrhini; Hominidae; EL/GenBauk/DDBJ databa B TYPE C FOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
| cates  sates  sates  transcation update)  stranscation update)  Fraction apparent  Cluniatu, Vertebiuta,  Catarrhini; Hominidae;  EL/GenBank/DDBJ databa  ETYPE C. FOMAIN.  DOL84E5DB78E8E25 CRC5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | eates st sequence update) st annotation update) F FACTOR 8 PROFEIN. Cluminta, Vertebrata, Catarrhini; Hominidae; EL/GenBank/DDBJ databa F TYPE C FOMAIN. COERTE C FOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | cates  sates  sates  to anotation update)  E FACTOR 8 PROTEIN.  Claridata Vertebiala,  Catarrhini; Hominidae;  EL/GenBank/DDBJ databa  B TYPE C FOMAIN.  D0x84ESDB78E8E25 CRC5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | eates  sates  sates  ct ancotation update)  ct ancotation update)  F FACTOR 8 PROFEIN.  Claritata Vertebiala,  catarrhini; Hominidae;  EL/GenBank/DDBJ databa  B TYPE C FOMAIN.  COER4FSIM72EFFES CROSS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | eates) eates) st sequence update) st annotation update) F FACTOR B PROTEIN. Calarrhini; Hominidae; EL/GenBauk/DDBJ databa B TYPE C FOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
| eates  st sequence update)  ct ancotation update)  F FACTOR 8 PROFEIN.  Clumintar, Vertebruta,  Catarrhini; Hominidae;  EL/GenBank/DDBJ databa  E TYPE C FOMAIN.  DOL84E5DB78E8E25 CRC5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | eates  st sequence update)  ct ancotation update)  F FACTOR 8 PROTEIN.  Clariata, Vertebrata,  Catarrhini; Hominidae;  EL/GenBank/DDBJ databa  8 TYPE C FOMAIN.  ZOE84ESUB78EBEDS CROS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | eates  sates  sates  ca amodation update)  ca amodation update)  F PACTOR 8 PROTEIN.  Calarrhini; Hominidae;  EL/GenBauk/DDBJ databa  8 TYPE C FOMAIN.  D0x84ESDB78E8E25 CRC5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | eates  sates  sates  to amoutation update)  E FACTOR 8 PROTEIN.  Cluniatu, Vertebiatu,  Catarrhini; Hominidae;  EL/GenBank/DDBJ databa  B TYPE C DOMAIN.  COER4FSURZERESS CROSS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | eates) eates) estes) est sequence update) et annotation update) F FACTOR B PROTEIN. Calarrhini; Hominidae; estarrhini; Hominidae; erype C FOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| eates<br>sates<br>st sequence update)<br>st sequence update)<br>F FACTOR 8 PROTEIN.<br>Claritain Vertebrata.<br>Catarrhini; Hominidae;<br>EL/GenBank/DDBJ databa<br>B TYPE C FOMAIN.<br>DOL84E5DB78E8E25 CHC5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | eates  st sequence update)  ct annotation update)  F FACTOR B PROTEIN.  Clariata, Vertebrata,  Catarrhini; Hominidae;  EL/GenBank/DDBJ databa  B TYPE C FOMAIN.  ZOE84E5UB78E8E55 CRUS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | eates) ested sates) ct annotation update) ct annotation update) F FACTOR B PROTEIN. Clubidata, Vertebbala, Calarrhini; Hominidae; GALARRHINI; Hominidae; GALARRHINI; Hominidae; GALARRHINI; Hominidae; GALARRHINI; HOMINIGAE; GALARRH                                                                                                                                                                                                                                               | eates  stranguence update)  ct annotation update)  F FACTOR B PROTEIN.  Clariata, Vertebiata,  Catarrhini; Hominidae;  EL/GenBank/DDBJ databa  B TYPE C DOMAIN.  COER4FSURFRESS CROSS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | eates) estes) est sequence update) ct annotation update) F FACTOR 8 PROTEIN. Calarrhini; Hominidae; calarrhini; Hominidae; s TYPE C DOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
| eates) ested sates) ct amoutation update) ct amoutation update) F FACTOR B PROTEIN. Clumintary Catarrhini; Hominidae; EL/GenBank/DDBJ databa B TYPE C FOMAIN.  DOLS4E5DB78E8E25 CRC5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | eates) eates) ct annotation update) ct annotation update) F FACTOR B PROTEIN. Clumintal, Vertebrata, Catarrhini; Hominidae; EL/GenBank/DDBJ databa B TYPE C DOMAIN. COL84ESUB78E8ESS CROS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | eates) st sequence update) st sequence update) st annotation update) F PACTOR 8 PROTEIN. Clumidt, Vertebrata, Catarrhini; Hominidae; Gatarrhini; Hominidae; Gatarrhini; Hominidae; Gatarrhini; Hominidae; Catarrhini; Hominidae; Cata                                                                                                                                                                                                                                               | eates) eates) ct anotation update) ct anotation update) ct anotation update) F FACTOR B PROTEIN. Clumintatory Catarrhini; Hominidae; Cata                                                                                                                                                                                                           | eates) st sequence update) st sequence update) st sequence update) F FACTOR 8 PROTEIN. Cluminta, Vertebrata, Catarrhini; Hominidae; GTYPE C FOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
| eates<br>sates<br>st sequence update)<br>st sequence update)<br>F FACTOR 8 PROTEIN.<br>Claritain Vertebrata.<br>Catarrhini; Hominidae;<br>EL/GenBank/DDBJ databa<br>B TYPE C FOMAIN.<br>DOL84E5DB78E8E25 CHC5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | eates  st sequence update)  ct annotation update)  F FACTOR B PROTEIN.  Clariata, Vertebrata,  Catarrhini; Hominidae;  EL/GenBank/DDBJ databa  B TYPE C FOMAIN.  ZOE84E5UB78E8E55 CRUS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | eates) ested sates) ct annotation update) ct annotation update) F FACTOR B PROTEIN. Clubidata, Vertebbala, Calarrhini; Hominidae; GALARRHINI; Hominidae; GALARRHINI; Hominidae; GALARRHINI; Hominidae; GALARRHINI; HOMINIGAE; GALARRH                                                                                                                                                                                                                                               | eates  stranguence update)  ct annotation update)  F FACTOR B PROTEIN.  Clariata, Vertebiata,  Catarrhini; Hominidae;  EL/GenBank/DDBJ databa  B TYPE C DOMAIN.  COER4FSURFRESS CROSS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | eates) estes) est sequence update) ct annotation update) F FACTOR 8 PROTEIN. Calarrhini; Hominidae; calarrhini; Hominidae; s TYPE C DOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
| eates  st sequence update)  ct ancotation update)  F FACTOR 8 PROFEIN.  Clumintar, Vertebruta,  Catarrhini; Hominidae;  EL/GenBank/DDBJ databa  E TYPE C FOMAIN.  DOL84E5DB78E8E25 CRC5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | eates  st sequence update)  ct ancotation update)  F FACTOR 8 PROTEIN.  Clariata, Vertebrata,  Catarrhini; Hominidae;  EL/GenBank/DDBJ databa  8 TYPE C FOMAIN.  ZOE84ESUB78EBEDS CROS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | eates  sates  sates  ca amodation update)  ca amodation update)  F PACTOR 8 PROTEIN.  Calarrhini; Hominidae;  EL/GenBauk/DDBJ databa  8 TYPE C FOMAIN.  D0x84ESDB78E8E25 CRC5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | eates  sates  sates  to amoutation update)  E FACTOR 8 PROTEIN.  Cluniatu, Vertebiatu,  Catarrhini; Hominidae;  EL/GenBank/DDBJ databa  B TYPE C DOMAIN.  COER4FSURZERESS CROSS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | eates) eates) estes) est sequence update) et annotation update) F FACTOR B PROTEIN. Calarrhini; Hominidae; estarrhini; Hominidae; erype C FOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| eates  st sequence update)  ct ancotation update)  F FACTOR 8 PROFEIN.  Clumintar, Vertebruta,  Catarrhini; Hominidae;  ELYGENBANK/DDBJ databa  E TYPE C FOMAIN.  DOL84E5DB78E8E25 CRC5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | eates  st sequence update)  ct ancotation update)  F FACTOR 8 PROTEIN.  Clariata, Vertebrata,  Catarrhini; Hominidae;  EL/GenBank/DDBJ databa  8 TYPE C FOMAIN.  ZOE84ESUB78EBEDS CROS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | eates  sates  sates  ca amodation update)  ca amodation update)  F PACTOR 8 PROTEIN.  Calarrhini; Hominidae;  EL/GenBauk/DDBJ databa  8 TYPE C FOMAIN.  D0x84ESDB78E8E25 CRC5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | eates  sates  sates  to amoutation update)  E FACTOR 8 PROTEIN.  Cluniatu, Vertebiatu,  Catarrhini; Hominidae;  EL/GenBank/DDBJ databa  B TYPE C DOMAIN.  COER4FSURZERESS CROSS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | eates) eates) estes) est sequence update) et annotation update) F FACTOR B PROTEIN. Calarrhini; Hominidae; estarrhini; Hominidae; erype C FOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| eates  st sequence update)  ct ancotation update)  F FACTOR 8 PROFEIN.  Clumintar, Vertebruta,  Catarrhini; Hominidae;  ELYGENBANK/DDBJ databa  E TYPE C FOMAIN.  DOL84E5DB78E8E25 CRC5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | eates  st sequence update)  ct ancotation update)  F FACTOR 8 PROTEIN.  Clariata, Vertebrata,  Catarrhini; Hominidae;  EL/GenBank/DDBJ databa  8 TYPE C FOMAIN.  ZOE84ESUB78EBEDS CROS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | eates  sates  sates  ca amodation update)  ca amodation update)  F PACTOR 8 PROTEIN.  Calarrhini; Hominidae;  EL/GenBauk/DDBJ databa  8 TYPE C FOMAIN.  D0x84ESDB78E8E25 CRC5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | eates  sates  sates  to amoutation update)  E FACTOR 8 PROTEIN.  Cluniatu, Vertebiatu,  Catarrhini; Hominidae;  EL/GenBank/DDBJ databa  B TYPE C DOMAIN.  COER4FSURZERESS CROSS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | eates) eates) estes) est sequence update) et annotation update) F FACTOR B PROTEIN. Calarrhini; Hominidae; estarrhini; Hominidae; erype C FOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| eates  st sequence update)  ct ancotation update)  F FACTOR 8 PROFEIN.  Clumintar, Vertebruta,  Catarrhini; Hominidae;  ELYGENBANK/DDBJ databa  E TYPE C FOMAIN.  DOL84E5DB78E8E25 CRC5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | eates  st sequence update)  ct ancotation update)  F FACTOR 8 PROTEIN.  Clariata, Vertebrata,  Catarrhini; Hominidae;  EL/GenBank/DDBJ databa  8 TYPE C FOMAIN.  ZOE84ESUB78EBEDS CROS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | eates  sates  sates  ca amodation update)  ca amodation update)  F PACTOR 8 PROTEIN.  Calarrhini; Hominidae;  EL/GenBauk/DDBJ databa  8 TYPE C FOMAIN.  D0x84ESDB78E8E25 CRC5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | eates  sates  sates  to amoutation update)  E FACTOR 8 PROTEIN.  Cluniatu, Vertebiatu,  Catarrhini; Hominidae;  EL/GenBank/DDBJ databa  B TYPE C DOMAIN.  COER4FSURZERESS CROSS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | eates) eates) estes) est sequence update) et annotation update) F FACTOR B PROTEIN. Calarrhini; Hominidae; estarrhini; Hominidae; erype C FOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| eates  st sequence update)  ct ancotation update)  F FACTOR 8 PROFEIN.  Clumintar, Vertebruta,  Catarrhini; Hominidae;  ELYGENBANK/DDBJ databa  E TYPE C FOMAIN.  DOL84E5DB78E8E25 CRC5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | eates  st sequence update)  ct ancotation update)  F FACTOR 8 PROTEIN.  Clariata, Vertebrata,  Catarrhini; Hominidae;  EL/GenBank/DDBJ databa  8 TYPE C FOMAIN.  ZOE84ESUB78EBEDS CROS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | eates  sates  sates  ca amodation update)  ca amodation update)  F PACTOR 8 PROTEIN.  Calarrhini; Hominidae;  EL/GenBauk/DDBJ databa  8 TYPE C FOMAIN.  D0x84ESDB78E8E25 CRC5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | eates  sates  sates  to amoutation update)  E FACTOR 8 PROTEIN.  Cluniatu, Vertebiatu,  Catarrhini; Hominidae;  EL/GenBank/DDBJ databa  B TYPE C DOMAIN.  COER4FSURZERESS CROSS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | eates) eates) estes) est sequence update) et annotation update) F FACTOR B PROTEIN. Calarrhini; Hominidae; estarrhini; Hominidae; erype C FOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| eates  st sequence update)  ct ancotation update)  F FACTOR 8 PROFEIN.  Clumintar, Vertebruta,  Catarrhini; Hominidae;  ELYGENBANK/DDBJ databa  E TYPE C FOMAIN.  DOL84E5DB78E8E25 CRC5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | eates  st sequence update)  ct ancotation update)  F FACTOR 8 PROTEIN.  Clariata, Vertebrata,  Catarrhini; Hominidae;  EL/GenBank/DDBJ databa  8 TYPE C FOMAIN.  ZOE84ESUB78EBEDS CROS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | eates  sates  sates  ca amodation update)  ca amodation update)  F PACTOR 8 PROTEIN.  Calarrhini; Hominidae;  EL/GenBauk/DDBJ databa  8 TYPE C FOMAIN.  D0x84ESDB78E8E25 CRC5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | eates  sates  sates  to amoutation update)  E FACTOR 8 PROTEIN.  Cluniatu, Vertebiatu,  Catarrhini; Hominidae;  EL/GenBank/DDBJ databa  B TYPE C DOMAIN.  COER4FSURZERESS CROSS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | eates) eates) estes) est sequence update) et annotation update) F FACTOR B PROTEIN. Calarrhini; Hominidae; estarrhini; Hominidae; erype C FOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| eates  st sequence update)  ct ancotation update)  F FACTOR 8 PROFEIN.  Clumintar, Vertebruta,  Catarrhini; Hominidae;  ELYGENBANK/DDBJ databa  E TYPE C FOMAIN.  DOL84E5DB78E8E25 CRC5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | eates  st sequence update)  ct ancotation update)  F FACTOR 8 PROTEIN.  Clariata, Vertebrata,  Catarrhini; Hominidae;  EL/GenBank/DDBJ databa  8 TYPE C FOMAIN.  ZOE84ESUB78EBEDS CROS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | eates  sates  sates  ca amodation update)  ca amodation update)  F PACTOR 8 PROTEIN.  Calarrhini; Hominidae;  EL/GenBauk/DDBJ databa  8 TYPE C FOMAIN.  D0x84ESDB78E8E25 CRC5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | eates  sates  sates  to amoutation update)  E FACTOR 8 PROTEIN.  Cluniatu, Vertebiatu,  Catarrhini; Hominidae;  EL/GenBank/DDBJ databa  B TYPE C DOMAIN.  COER4FSURZERESS CROSS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | eates) eates) estes) est sequence update) et annotation update) F FACTOR B PROTEIN. Calarrhini; Hominidae; estarrhini; Hominidae; erype C FOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| eates  st sequence update)  ct ancotation update)  F FACTOR 8 PROFEIN.  Clumintar, Vertebruta,  Catarrhini; Hominidae;  ELYGENBANK/DDBJ databa  E TYPE C FOMAIN.  DOL84E5DB78E8E25 CRC5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | eates  st sequence update)  ct ancotation update)  F FACTOR 8 PROTEIN.  Clariata, Vertebrata,  Catarrhini; Hominidae;  EL/GenBank/DDBJ databa  8 TYPE C FOMAIN.  ZOE84ESUB78EBEDS CROS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | eates  sates  sates  ca amodation update)  ca amodation update)  F PACTOR 8 PROTEIN.  Calarrhini; Hominidae;  EL/GenBauk/DDBJ databa  8 TYPE C FOMAIN.  D0x84ESDB78E8E25 CRC5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | eates  sates  sates  to amoutation update)  E FACTOR 8 PROTEIN.  Cluniatu, Vertebiatu,  Catarrhini; Hominidae;  EL/GenBank/DDBJ databa  B TYPE C DOMAIN.  COER4FSURZERESS CROSS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | eates) eates) estes) est sequence update) et annotation update) F FACTOR B PROTEIN. Calarrhini; Hominidae; estarrhini; Hominidae; erype C FOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| eates  stranguence update)  stranguence update)  Fraction update)  Fraction update)  Clumint. Vertebruta,  Catarrhini: Hominidae;  EL/GenBank/DDBJ databa  ETYPE C. FOMAIN.  DOL84E5DB78E8E25 CRC5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | eates st sequence update) st annotation update) F FACTOR 8 PROFEIN. Cluminta, Vertebrata, Catarrhini; Hominidae; EL/GenBank/DDBJ databa F TYPE C FOMAIN. COERTE C FOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | cates  sates  sates  to anotation update)  E FACTOR 8 PROTEIN.  Claridata Vertebiala,  Catarrhini; Hominidae;  EL/GenBank/DDBJ databa  B TYPE C FOMAIN.  D0x84ESDB78E8E25 CRC5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | eates  sates  sates  ct ancotation update)  ct ancotation update)  F FACTOR 8 PROFEIN.  Claritata Vertebiala,  catarrhini; Hominidae;  EL/GenBank/DDBJ databa  B TYPE C FOMAIN.  COER4FSIM72EFFES CROSS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | eates) eates) st sequence update) st annotation update) F FACTOR B PROTEIN. Calarrhini; Hominidae; EL/GenBauk/DDBJ databa B TYPE C FOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
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Clumiatus Vertebratas, Catarrhini; Hominidae; EL/GenBank/DDBJ databa B TYPE C FOMAIN. DD&84ESDB7eE8E25 CRC5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | eates) eates) esteen es                                                                                                                                                                                                           | eates) eates) esteen ct ancotation update) E FACTOR 8 PROTEIN. Clumintar, Vertebrata, Catarrhini; Hominidae; EL/GenBank/DDBJ databa B TYPE C FOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
| earce<br>transcation update)<br>ct annotation update)<br>F PACTOR 8 PROTEIN.<br>Catarrhini: Mominidae;<br>Catarrhini: Hominidae;<br>EL/GenBank/DDBJ databa<br>8 TYPE C EOMAIN.<br>20284E5DB78E8E25 CRC5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | earce<br>tr. sequence update)<br>ct. annotation update)<br>F. FACTOR 8 PROTEIN.<br>Catarrhini: Hominidae;<br>Catarrhini: Cataba                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | earce update) earchor sequence update) ft annotation update) F PACTOR 8 PROTEIN. Clumiata, Vertebruta, Catarrhini; Hominidae; EL/GenBank/DDBJ databa 8 TYPE C FOMAIN. DD&84ESDB78E8E25 CRC5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | earce<br>st sequence update)<br>of amotation update)<br>F Pacrop 8 PROTEIN.<br>Catarrhini: Hominidae;<br>Catarrhini: Hominidae;<br>EL/GenBank/DDBJ databa<br>B TYPE C FOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | earce<br>earce<br>ct amodation update)<br>ct amodation update)<br>F PACTOR B PROTEIN.<br>Claritain Vertebrata,<br>Catarrhini; Hominidae;<br>Catarrhini; Hominidae;<br>EL/GenBank/DDBJ databa<br>B TYPE C FOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
| st sequence update) st sequence update) F FACTOR 8 PROTEIN. Clumiatu, Vertebbula, Catarrhini; Hominidae; EL/GenBank/DDBJ databa B TYPE C EOMAIN. DOR84E5DB78E8E25 CRC5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | st sequence update) st sequence update) F FACTOR 8 PROTEIN. Clumiatu, Vertebbula, Catarrhini; Hominidae; BTYPE C EOMAIN. MM_1.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | st sequence update) st sequence update) E FACTOR 8 PROTEIN. Cludiata, Verteblata. Catarrhini: Hominidae. BL/GenBank/DDBJ databa 8 TYPE C DOMAIN. DOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | st sequence update) st sequence update) F FACTOP 8 PROTEIN. Catarrhini: Hominidae; EL/GenBank/DDBJ databa 8 TYPE C DOMAIN. MM_1.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | st.sequence update) st.sequence update) E FACTOR 8 PROTEIN. Clumiatu, Vertebruta, Catarrhini; Hominidae; EL/GenBank/DDBJ databa 8 TYPE C EOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
| St Sequence update) st anotation update) F PACTOR & PROTEIN. Clumiata, Verteblata, Catarrhini; Hominidae; EL/GenBank/DDBJ databa F TYPE C EOMAIN. 202841E5DB78E2855 CRC5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | St. Sequence update) st.anotation update) F.FACTOR B PROTEIN. Clumiata, Verteblata, Catarrhini; Hominidae; EL/GenBank/DDBJ databa B TYPE C EOMAIN. MM_1.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | St Sequence update) st annotation update) F FACTOR 8 PROTEIN. Catarrhini: Hominidae; Catarrhini: Hominidae; WM_1.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | St Sequence update) st anotation update) F FACTOP 8 PROTEIN. Cludiata, Verteblata, Catarrhini; Hominidae; EL/GenBank/DDBJ databa 8 TYPE C FOMAIN. 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Catarrhini: Hominidae; Catarrhini: Hominidae; WH_L:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
| st sequence update) ct anotation update) F PACTOR B PROTEIN. Clarida, Vertebiala, Catarrhini; Hominidae; BL/GenBank/DDBJ databa 8 TYPE C DOMAIN. MM_1.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | st sequence update) ct anotation update) F PACTOR B PROTEIN. Claniata, Verteblata, Catarrhini, Hominidae; EL/GenBank/DDBJ databa F TYPE C EOMAIN. DDES4ESDB78E8E25 CRC5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | st sequence update) ct anotation update) F FACTOR & PROTEIN. Clanidta, Verteblata, Catarrhini; Hominidae; EL/GenBank/DDBJ databa # TYPE C FOMAIN.  DO&#15DB78E8E25 CRC5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | st sequence update) ct anotation update) F PSTYPE & PROTEIN. Catarrhini: Hominidae: EL/GenBank/DDBJ databa FYPE C EOMAIN. MM_1.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | st sequence update) ct annotation update) ct annotation update) Freigh B PROTEIN. Calarrhini; Hominidae; Calarrhini; Hominidae; BL/GenBank/DDBJ databa B TYPE C DOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
| st sequence update) ct amotation update) ct amotation update) Cluridia. Cluridia. Verteblata. Catarrhini: Hominidae: EL/GenBauk/DDBJ databa B TYPE C FOMAIN.  20284E5DB78E8E25 CRC5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | st sequence update) ct annotation update) ct annotation update) Clusiatus Vertebiatus. Catarrhinis Hominidaes BTYPE C DOMAIN. WM_1.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | st sequence update) ct annotation update) ct annotation update) Clumiata, Verteblata, Catarrhini; Hominidae, EL/GenBank/DDBJ databa B TYPE C FOMAIN.  MN_1.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | st sequence update) ct anotation update) ct anotation update) classidta, Vertebiata, catarrhini; Hominidae, smryee c romain. ww_l.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | st sequence update) ct annotation update) ct annotation update) Cluminta, Verteblata, Catarrhini; Hominidae, EL/GenBank/DDBJ databa B TYPE C FOMAIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |

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   MEDLINE 97061201; FubMcd-8905231;
Kanoko T., Sato S., Kofani H., Tanaka A., Asamiru E., Nakamura Y.,
Miyajima N., Hirosawa M., Susamoro S., Kimura T.,
Miyajima N., Hirosawa M., Sasamoro S., Kimura Y.,
Miyajima N., Hirosawa M., Sasamoro S., Karine A., Karine S., Chumura S.
Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
  6; Gaps
   "Sequence analysis of the genome of the univellular evandage origin Syncohocystis sp. strain PCC6803. II. Sequence determination of the cutire genome and assignment of potential protein confined regions ";
   Fukaryota, Meladda Chordata, Craniata, Vertebrata; Esteleostowi,
Mammalia; Eurheria; Perissodactyla; Equidae; Equus.
NYKL_TaxID=4746;
  85.2%; Score 46; DB 6; Length 363; 88.9%; Pred. No. 3.1;
  it Indels
  Gentzel M., Toepfer-Petersen B.;
Submitted (AGG-1998) to the EMMI/GenRack/DERI databases
EMBL: EMBL: CAA00010 1; CAA00010 1; HSSP; P00746; IEDM.
  363 AA: 40744 MW: 1FRB6395AF3233FD CPC54:
   Syncchocystis sp. (strain PCC 6803).
Bacteria: Cyanobacteria; Chroococcales; Synechocystis
NCBL_TaxID+1148;
   01-NoV-1998 (TrEMBLrel, 08, Created)
01-NoV-1998 (TrEMBLrel, 08, Last sequence update)
01-DEC-2001 (TrEMBLrel, 19, Last annotation update)
   01-FEB-1997 (TrEMBLrel, 02, Croated)
01-FEB-1997 (TrEMBLrel, 02, Last Sequence update)
01-JUN-2001 (TrEMBLrel, 17, Last annotation update)
  SPERM-MEMBRANE ASSOCIATED PROTEIN P47 (FRAGMENT).
  PRT; 453 AA.
  6; Mismatches
   Pram. Prant. Pract. PrePryte_C: 2. SMAPT: SMAD18: POF: 1. Pract. 
   InterPro; IPR000561; EGF-like.
InterPro; IPR050421; EA58_r
Pfam; PF00008; EGF; 1,
   EGF-like domain; Glycoprotein.
   PROSITE; PS01285; FA58C_1; 1.
   DNA Res. 3.109 136(1996).
EMBL: D90909; BAA17766 1; -
   Query Match
Rest Local Similarity 88.99
Matches R: Conservative
  PPELIMINAPY;
  PRELIMINARY;
   Equus caballus (Horse).
  363
  97 GLQHWVPEL 105
  102 GLORWVPEL 110
   SEQUENCE FROM N.A.
   SEQUENCE FROM N.A.
1 CLOHWVPEL 9
   1 CLOHWVPEL 9
  363
  DNA PHOTOLYASE.
   PHR OR SLL1629.
   TISSUE TESTIS;
   Tabata S.:
  SEQUENCE
  NON_TER
   077718;
  NON_TER
   177967;
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P77967
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Asgeirsson B., Andresson O.S.; "Primmary structure of cold-addred alkaline phosphatase from a Vibrio Sp., as deduced from the incientide sequence."; Hinchim Hinghys Arta u.u.eu(2001).
  0; daps
  Gaps
   Simpson A.I.G., Reinach F.C., Arrida P., Abreu F.A., Acencio M., Alvaronga P., Alves L.M., Alves L.M., Britas C.S., Berriss M.H., Bonarcersi E.B., Bordin R., Bove J.M., Briones M.R.S., Euron M.F.P., Calmarcer P., Conarce D.M., Carrett H., Colauto M.B., Colombe C.A., Costa M.C.R., Costa Neto C.M., Coutinho L.L., Cristofani M., Dias-Neto E., Doena C., El Derry H.,
  Vibrio sp. 615-21.
Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
  :
0
  Bacteria, Proteobacteria, gamma subdivision, Xanthomonas group;
  75.9%; Score 41; DB 16; Length 453; 75.0%; Prod No 29; tive 2; Mismatches 0; Indels
  75.9%; Score 41; DR 2; Length 521; 62.5%; Pred. No. 33;
   0; Indels
  453 AA; 52920 MW; CRESSERDOSCSESER CPC64;
  EMBL: AR35214, AAK94204.1; -.
SEQUENCE 571 AA: 57384 MW: @B9493@B4E9CP192 CPC64;
   01-021-2000 (TLEMBLRel. 15, Cleated)
01-021-2000 (TLEMBLRel. 15, Last sequence update)
01-DEC-2001 (TLEMBLRel. 19, Last annotation update)
  01-DEC-2001 (TrEMBLrel, 19, Created)
01-DEC-2001 (TrEMBLrel, 19, Last sequence update)
01-DEC-2001 (TrEMBLrel, 19, Last annotation update)
   PPT; 521 AA.
   PPT; 833 AA.
   3, Mismatches
HSSP; P05327; IQNP.
InterPro; IPRG00474; DNA_photolyase.
InterPro; IPRG02881; DNA_photolyase_1.
Plan; PF00875; DNA_photolyase; I.
ProDom; PD004390; DNA_photolyase; I.
PROSITE; PSG0394; DNA_Photolyase; I.
   MEDLINE-20365717; PubMed=10910347;
   Local Similarity 75 0º
les 6; Conservative
   Lyase; Complete proteome.
   PPFLIMINAPY;
  Conservative
   PPELIMINAPY;
  ATP-DEPENDENT HELICASE,
   ALKALINE PHOSPHATASE.
   Best Local Similarity
  Xylella fastidiosa.
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   1 GLQHWVPE 8
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   STRAIN-9A5C;
  SECUENCE
  Query Match
  Query Match
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   XF1229.
  ชี้ 2ปสชับ
  Q9PD29,
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141 GLEEWVPEV 149

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1 GLOHWVPEL 9

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Facinoani A P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
Fraga J.S., Franca S.C., Franco M.C., Frohmo M., Porlan I.P.,
A Garnier M. Goldman M.H.S., Gomes S.L., Gruber A.,
A D. L., Hohelsel J. W., Goldman M.H.S., Gomes S.L., Gruber A.,
A Krieger J.E., Kuramae E.E., Taigret F., Lambais M.R., Teite D.C.C.,
Lemos M.V., Lemos M.V.F., Topes S.A., Topes P., Martina J.P.,
A Marchado M.A., Madelia A.M.R.N., Martins E.M.F., Marchina C.L.,
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A Marchina M.A., Marchina M.M., Marchina M.M., Marchina M.M., Marchina M.M., Marchina M.M.,
   у.
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17
   SEQUENCE FROM N.A. Schler G. Aign N.A. Schler D., Fartmann R., Holland P. Nyakatura G., Mowes H.W., Manhaupt G., Submitted (APE-2000) For the EMBL/NewBank/1445 databases.
  "The genome sequence of the plant pathogen Xylella fastidiosa."; Nature 406:151\cdot159(2000) .
   c:
  Eskirjota, Pungi, Aserrjeeta, Periodrottina, Serdariompetes.
Sordariales, Sordariaceae; Neurospora
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  German Neurospoid genome project;
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  01-0CT-2000 (TrEMBLrel. 15, Created)
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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ا
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FMBL; AE003956; AAF84039.1;
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InterFro; IPR001650; Helicase_C.
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AMPRE: SM04401, HELICO; 1
ATP-Dinding, Complete professe, Helicase, SEQUENCE 833 AA, 32557 MW; ECCABU0844
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   Ouery Match
Best Local Similarity (6.74
5. Conservative
   6, Charitaithe
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SEQUENCE FROM N.A.
   Neurospora crassa.
   658 LKHWMPEL 665
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  2 LQHWVPET 9
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        :7
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SPAURNCE FROM N.A.
SIRAIN-EL 10k N15561 / SEKOIYPE 01;
MEDELINE-20406833; PubMed-1052301;
Heidelberg J.E. 1878 J.A. 1848 M.P. Clayton R.A. Gwinn M.L.,
Podson R.T., Haft D.H., Hickoy E.R., Potorson T.P., Hmayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tetterlin H., Richardson D.,
Ermolacva M.D., Vamalhovan J., Hass S., Qin H., Dragoi I., Sellers P.,
Merlonaid L., uttorback P., Pleischmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Coiwell R.P., Nierman W.C., White O.,
   Gaps
  Maratilla M., Agramayor M., Nunca A., Funcs J.M., Varas A.J.,
Loped Estebarand J.L., Esteban M., Martin-Callardo A.;
"A Random Kink Semperating, Computer Reseal Approach for the Generation
of a Gene Map of Molluscum Contagiosum Virus.",
virus Genes D.O.O.(1997)
  Molluscum contagiosam virus subtype 1 (MCVI).
Viruses; dsENA viruses, no ENA stage; Foxoridae; Choroepexvirinae;
  Bacteria: Profeepacteria: gamma subdivision: Vibrionaceae: Vibrio.
NCBL_TaxID-666;
  "DNA sequence of both chromosomes of the choiera pathogen Vibrio
   .;
Ç
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Prod. No. 27;
3; Mismatches 0; Indols
  SBSB7 MW, LOLBSBIGB/PSS/PRSS/PRSS94;
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01-07T-2000 (TrEMBLE), 15, Last sequence update)
01-087-2001 (TrEMBLE), 19, East annotation update)
   Last sequence update)
Last annotation update)
  337 AA
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(fow, PSO2666, PS_Granbs_lare, l
  Created)
                . Teta
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  PHOSPHATIDYLSERINE DECARROXYLASE,
   Nature 406:477-483(2000).
EMRL; AEOO4122; AAF93512 1; -
  74.18;
  01-JUL-1997 (TrEMBLrel. 04, 01-JUL-1997 (TrEMBLrel. 04, 01-JUL-1997 (TrEMBLrel. 04, 01-prc-2001 (TrEMBLrel. 19,
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  01-0PC-2001 (Tremplice)
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   Molluscipoxvirus.
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  7 GLQYWIPQ 14
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   1 SIQHWVPE 8
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   SECUENCE
  SECUENCE
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  011317;
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   011317
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   Matches
Q9KV19
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  011317
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С,
   Arabidopsis thaliana (Mouse-car cress).
Eukaryeta: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
Spermatophyta: Magnollophyta: endicetyledons: oute endicots. Residue:
eurosids II: Brassicales: Brassicaceae; Arabidopsis.
                                  O, Gaps
  Caps
   Eiglmeier K., Honore N., Woods S.A., Caudron B., Cole S.T., "Use of an ordered cosmid library to deduce the genomic organization of Myrobacterium leprae.";
Mol. Microbiol. 7:197-20.",
EMBL. Y1497, CAA7519R 1;
Hypothetical protein
SRQUENTE. 480 AA: 51400 MW, 3441940456779558 Props4;
   Actinomyrr'ales, Cerynebacterineae, Mycobacteriaceae, Mycobacterium
  FederSpiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F., Altati H., Aranjo P., Huizar L., Bowley D., Bushler E., Dunn P., Gonzalez A., Kremenetskala I., Kim C., Forz C., I.J., Tin S., Luros S., Schwartz J., Shinn P., Toriumi M., Vysorskala V.S., Walker M., Yu G., Erker J., Thrologis A., havis P.W.; Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
  0
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Eiglmeier K., Garnier T., De Rossi E., Fsihi H., Cole S.T.,
Submitted (And-1997) to the FMRI/GenRank/PoRT databases
74.1%; Score 40; DB 12; Length 337; 85.7%; Pred. No. 32;
  Ouery Match 74 1%; Score 40; DR 10; Longth 452; Best Local Similarity 75.0%; Pred. No. 43; Matches 6; Conservative 1, Mishatches 1, Indels
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  1, It.dels
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  452 AA; 50554 MW; 0878800211180413 08064,
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01-NVV-1999 (TFEMBLEG), 12, Last Sequence update)
01-DEC-2001 (TFEMBLEG), 19, Last annotation update)
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
HFFOHFTICAL 51.4 KDA PROTEIN.
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  480 AA
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   PRT;
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   MEDLINE-93188700; PubMed-8446027;
                                  6; Conservative
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  STRAIN CV. COLUMBIA;
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  SEQUENCE FROM N.A.
  SEQUENCE FROM N.A.
   115 LAHWVPEM 122
   NCB1_Tax1D-1769;
   2 LOHWVPEL 9
  :|||||||
52 RHWVPEI, 58
  3 CHWVPEL 9
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Query Match
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MEDINE 21128732; PutMod 11234002; Johnson N.R., Filmeier K., Parkhill J., James K.D., Thomson N.R., Wheeler P.R., Honcer N., Garnier T., Churcher G., Harriss D., Mangall K., Basham D., Brown D., Chillingworth T., Connor R., Manjall K., Basham D., Brown D., Feltwell T., Fraser A., Hamlin N., Harloyd S., Hornsby T., Jaqeis K., Laroriak C., Marlean J., Moule S., Murphy L., Oliver K., Quall M.A., Rajandream M.A., Rutherford K.M., Futler S., Seever K., Simcut S., Simmends M., Skelton J., Squares R., Squares S., Levens K., Taylor K., Whitehead S., Woodward J.K.,
                                    0; Caps
   0; daps
  Actinomycetales, Corynchaeterineae, Mycobacterlaceae, Mycobacterlann
NCFL_TaxID=1769,
   Molluscum contagiosum virus subtype l (MCVI).
Viruses, dSDNA viruses, no KWA stage, Foxviridae, Chordopoxvirinae;
Molluscipexvirus.
  MEDCINE 96325459; PubMed 8670425;
Senkevich F.G., Bugert J.J., Sisler J.R., Koonin E.V., Daral G.,
  Genome sequence of a human tumorigenic poxyirus: Prediction of
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01-FBB-1997 (TFEMBLrel. 02, Last sequence update)
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   "Massive gene decay in the legrosy bacillus.";
Nature 409:1007-1011(2001).
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   SEQUENCE FROM N.A.
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  MCOSSE
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   Matches
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Rest Local Similarity 62 30
Turn 57 Conservative
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Matches 5, Conservative
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   26 LMHWIPEV 33
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   99
   Job time: 471 sec
  I.M26.176.
  NON_TER
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  Query Mateh
  O9NMB6;
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  g
   NAME OF STREET O
  ·.
   ز:
  Gaps
   Stab
  "Cloning and sequence of the gene encoding a nevel orbitisher-hydrilizing betain temash (TX M ^{\circ}) from Excharmon, an Space Antimicrob. Agents Chemother, 44:1970-1973(2000)
  Senkevich T G , Rugert I.I., Sisler J.R., Koonin E.V., Darai G.,
   Sabate M., Tarrago R., Navarro F., Miro F., Verges C., Karbe J.,
Prats G.;
   Profesibarteria, gamma subdivision, Enterobarteriaceae,
   Sabate M., Navarro F., Barbe J., Miro E., Mirelis B., Prats G., "A movel complex sull type integron (In60) in Escherichia coli carrying the blacTX-M-9 ".
   .:
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   çù
   Cucry Match 74.1%; Score 40; DB 12; Length 748; Best Local Similarity 85.7%; Fred. Ho. 71, Matches 6; Conservative 1; Mismatches 0; Indels
   Score 40; DR 2; Longth 1005;
Pred. No. 96;
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  Setmitied (201-2001) to the EMBL/GenBank/DDBJ dutabases.
EMBL: AP174129; AAK60193.1; -.
Plasmid.
  1005 AA; 116157 MW; 726E107EFADA057F CRC64;
  Submitted (JUN-1996) to the EMBL/Skidkatk/Tidk: Jurahams.
EMBL: U60315, AACS5160.1,
SEQUENCE 748 AA: 84411 XM; 61A2741F6206A5BA 0R054;
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   61 AA.
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specific host response-evasion genes."; science 273:813-816(1996).
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   RESULT 14
Q947B5
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Eukaryota, Viridiplantuo, Stroptophyta, Embryophyta, Frachosphyta;
Spormatophyta, Magnellophyta, eudioptyledons, core eudioots; Rosidae,
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STRAIN-FRIEDLIN:
Marthy L. gorall M. Marris B. Rajandream M., Iveus A., Barrell B.;
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EMEL: AL160493: CAB97794.1; -.
  Eskarysta: Englenozoa, Kinetoplastida; Trypanosomatidae; Leishmania.
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   refretta 3., tabeatjan 3., Mckwicze f., Kunzi L., Giuliano 5.; "Tomato and bafey contain daplicated copies of cryptochrome 1."; Plant Gell Emriron, 24:991-997(2001).
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  NON_TER 61 61
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OM protein - protein search, using sw model

September 5, 2002, 15:27.35; Pearch time 58 86 Seconds (without alignments) 3,735 Million cell updates/sec Run on

75 09-744 864 39 54 Perfect score:

BLOSUM62 Gapop 16 0 , Gaprixt O S I GLÜHWVPEL 9 Scoring table: Sequence:

231628 scqs, 24425594 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Listing first 45 summaries Maximum Match 100% Post-processing· Minimum Ma+rh 0\*

Issued\_Patents\_AA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result |          | %<br>Ouerv |              |            |                      |                    |
|--------|----------|------------|--------------|------------|----------------------|--------------------|
| NO.    | Score    | Match      | Match Length | DB         | ID                   | Description        |
|        | 54       | 100.0      | 160          | -1         | (IS-08-162-4028-10   | Sequence 10, April |
| 64     | c#<br>L) | 100.0      | 7 H >        | :•         | US+08+152+4026-6     |                    |
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| ¥      | 39       | 72.0       | C.C.         | C 1        | 00 2345 80 Si        | ζ.                 |
| 7      | 3¢       | 77.5       | 4.14         | -1         | US U8-162-402B 9     |                    |
| Œ.     | ~ 7      | 2          | ir<br>Ži     | 7.1        | us-08-719 697-8      | Œ                  |
| 6      | 37       | 68.5       | 764          | 4          | US-U8-727-516A-8     | 8                  |
| 10     | 37       | 68.5       | 265          | C1         | 9-269 612-80-SA      | Ų                  |
| 11     | 3.7      |            | L<br>Vi      | 7          | US-08-727-616A 6     | ū                  |
| 12     | 3.7      |            | 5079         | -T         | PCT - US94 - 00198-4 | -7                 |
| 13     | 36       |            | 255          | 7          | US-08-484 905-110    | =<br>=             |
| 14     | 36       |            | E.<br>E.     | ·~         | US-08-481-985R-110   | 110,               |
| 15     | 36       | 66.7       | 255          | 4          | US-08-370-476-110    | 110,               |
| 16     | 36       | rr. 7      | 4,5,1        | 74         | ns-n8-484-905 113    | 113                |
| 17     | 36       | 66.        | 355          | <b>(~)</b> |                      | 113,               |
| 18     | 36       |            | 256          | 4          | US 08-370-476 113    | Sequence 113, App. |
| 19     | 36       |            | 500          | 4          | US-08-960-190A-25    | 25, A              |
| 20     | 36       |            | 514          |            | US-07-872-644 17     | 17,                |
| 21     | 36       |            | 514          | _          | •                    | 17,                |
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| 530 1 05-07-644-6 530 1 08-07-67-644-6 530 1 08-08-297-644-6 530 1 08-08-455-526-6 530 1 08-08-455-526-6 530 1 08-08-455-526-6 530 1 08-08-455-526-6 530 1 08-08-297-491-6 531 1 08-08-297-494-49 535 1 08-08-297-494-49 535 1 08-08-297-494-49 535 1 08-08-297-494-49 535 1 08-08-297-494-49 535 1 08-08-297-494-49 535 1 08-08-194-49 535 1 08-08-194-49 535 1 08-08-194-49 535 1 08-08-194-49 535 1 08-08-194-49 535 1 08-08-194-49 535 1 08-08-194-49 535 1 08-08-194-49 535 1 08-08-194-49 535 1 08-08-194-49 | sequence 6, Appli | Sequence 6, Appli | Sequence 6, Appli | Ď,              | Seguence 6, Appli | sequence 6, Appli | seguence 6, Appl1 | Sequence by Appli   | Sequence 49, Appl | 49,              | Sequence 49, Appl | Sequence 49, Appl | sequence 49, Appl  | 49,              | Sequence 49, Appl | 49,               | 7,                         | Sequence 7, Appli |
|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------|-------------------|-------------------|-----------------|-------------------|-------------------|-------------------|---------------------|-------------------|------------------|-------------------|-------------------|--------------------|------------------|-------------------|-------------------|----------------------------|-------------------|
| денеед »Уееенеек ©е                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | US-0/-8/2-644-6   | US-U8-297-494-6   | 05 08 297-510-6   | US-08-4/9-532-6 | US-08-455-526-6   | US-V8-455-525-b   | US-U9-139-491-6   | 1.777 (a.7780) I.S. | US-07-872-644-49  | US-08-297-494-49 | US-08-297-510-49  | 35.08.475.532.49  | 115-118-455-524-44 | US-08-455-525-49 | US-09-139-491-49  | PCT US92 03222 49 | 7 -> 7 F -> 15R - RO - Sig | US-08-803-972-7   |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | i<br>I            | 0                 | <br>0             |                 | 0                 | 1 n               | Ü 3               | -                   | ٦.                |                  | 5 1               |                   | <br>س              | 5 1              | ~                 | un<br>un          |                            | 4 1               |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | 66.1              | 66.7              | 66.7              | 66.7            | 66.7              | 1.00              | 0.00              | 1.1.                | 66.7              | 66.7             | 66.7              | 1.6.7             | 00 7               | 66.7             | 66.7              | 66.3              | 1 44                       | 66.7              |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | 36                | 36                | 98                | 36              | 36                | 36                | 36                |                     | 3.6               | 3.6              | 36                | 3.5               | 3.0                | 36               | 36                | 36                | ÷,                         | 36                |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | œ                 | 6                 | ر:                |                 | 2                 | Υ)                | 4                 | ¥.                  | Ç.                | 7                | œ                 | ٠,                | D                  | -1               | 7                 | 3                 | <del>-,-</del>             | 'n                |

## AL. I GNMENTS

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APPLICANT: CERIANI, ROBERTO L.
APPLICANT: PETERSON, JERRY A.
AFFLICANT: LANCCA, DAVID J.
TITLE OF INVENTION - 46 KOLLTON HUMAN MILK FAT
HILLE OF INVENTION: GLOBULE (HMFS) ANIISEN, FFASMENIS & FUSION PROIEIN
   100.0%; 330re 54; UB 2; Length 166, 100.0%; Pred. No. 0.015;
  OPERATING SYSTEM: DOS SOFTWARE; FastSEQ for Windows Version 2.0 cuppent application Data:
  AUDRESSEE: Pretty, Schroeder & Poplawski
STREET: 444 South Flower St., 19th Floor
CITY: Los Angeles
  UMBSE, US/US/TEL,401B
na perijaas
  RELECTION THOUSE: P.C. 38215
TELECTMMUNICATION INFORMATION:
TELEPHONE: -3: --5.22-7700
            US-08-162-402B-10
; Sequence 10, Application US/98162402B
; Patent No. 5972337
  NAME: Amzel, Viviana
EEGIFTBATTON NYMREE: 20,030
  1:0:
   IBM Compatible
  FILLING DATE, ALLOEMALLON.
  LENGIH: 160 amino acids
  29
  Diskette
  TELEFAX: 213-489-4210
  INFORMATION FOR SEQ ID NO
SEQUENCE CHARACIERISTICS:
  SS: unknown
unknown
  , MOLECULE IYPE, peptide US-08-162-402B-10
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  CLASSIFICATION: 435
FPIOF APPLICATION PATA,
AFPLICATION NUMBER.
   CORRESPONDENCE ADDRESS:
  NUMBER OF SEQUENCES:
  APECICATION NUMBER
FILING PAIE: 03 PE
   όνει, Μαίσί.
Best Local Similarity
   COMPUTER: IBM CON OPERATING SYSTEM:
   GENERAL INFORMATION:
   USA
  STRANDEDNESS:
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  90071
  STATE: CA
   TOPOLOGY:
  TELEX:
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  PEFEPENCE/DOCKET NUMBER- P67
TELECOMMUNICATION INFORMATION:
TELEPHONE: 213 622-7700
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  INFORMATION FOR SEQ ID NO: 8:
  IBM Compatible
   COMPUTER: IRM Compatible
  03-DEC-1993
  ATTORNEY/AGENT INFORMATION:
   SEQUENCE CHARACTERISTICS:
LENGTH: 465 amino acids
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9, Conservative
   SOG
  29
   TELEFAX: 213-489-4210
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   unknown
   Diskette
  Amzel, Viviana
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APPLICATION NUMBER:
   TOPOLOGY: unknown
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   COMPUTER REALIARIE FORMS
  PEGISTRATION NUMBER.
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  CITY: Los Angeles
STATE: CA
  Los Angeles
  COMPUTER: IBM COM
OPERATING SYSTEM:
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   US-08-162-402B-11
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   TITLE OF INVENTION: 45 KDALFON HUMAN MILK FAT
TITLE OF INVENTION: GLOBULE (HMEG) ANTIGEN, FRAGMENTS 5 FUSTON PROTEIN
NUMBER OF SEQUENCES: 29
   (Japs
  Gaps
 ċ
  Ö,
  100 0%; Score 54; PR 2; Length 387; 100 0%; Prod. No. 0 039;
 [nde]s
  0, Indels
ċ
  GENERAL INFORMATION:
APPLICANT: CERTANI, PORFPTO I.
APPLICANT: PEPERSON, IEPPY A
APPLICANT: LAFORCEA, DAVID 1
TITLE OF INVENTION: 46 KDALTON HUMAN MILK FAB
   SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/162,402R
  ADDRESSER: Prefly, Schlowder & Poplawski STREET: 444 South Flower St., 19th Floor CITY: Los Angeles
  6; Mismatches
0; Mismatches
   UMBER: US/08/162,402R
03-DEC-1993
   Sequence 6, Application US/08162402H
Patent No. 5972337
  Segmence 8. Application USynotle,4028
Patent No. 5972337
   APPLICANT: CERIANI, ROBERTO L. APPLICANT: PETERSON, JERRY A. APPLICANT: LABORCA, DAVID J
  REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: PAR
   TELECOMMINICATION INFORMATION:
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  MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
  ATTORNEY/AGENT INFORMATION:
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TELEFAX: 213-489-4210
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Host Local Similarity 100 o
'conservative'
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  003
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  NAME: Amzel, Viviana
   CLASSIFICATION: 435
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  FILING DATE:
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  US-08-162-402H-6
  US-08-162 402R 6
   US-08-162-402B-8
  COUNTRY:
   LENGTH:
 Matches
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   CIC)
                                     Š
  3
  ŝ
```

```
APPLICANT: CERTANI, ROBERTO L.
APPLICANT: PETERSON, JERRY A.
APPLICANT: IAPROCA, DAVID J.
TITLE OF INVENTION: GLOBULE (HMFG) ANTIGEN, FRAGMENTS & FUSION PROTEIN
TITLE OF INVENTION: CLORMLE (HMFG) ANTIGEN, FRACMENTS & FUSION PROTEIN
   Gaps
  ċ
  || jūū 0%; Score 54; DB 2; Length 465; || jūu.ū%; Pred No 0.047;
   O. Indels
  OPERATING SYSTEM: DOS
SOFTWARE: FastSPQ for Windows Version 2 0
CURRENT APPLICATION DATA:
  SOFTWARE: PastSEQ for Windows Version 2 0 CURPENT APPLICATION DATA:
  n; Mismatches
   ADDRESSE: Pretty, Schroeder & Poplawski STREET, 444 South Flower St., 19th Floor
  E: Pretty, Schroeder & Poplawski
444 South Flower St., 19th Floor
  USZURZIKZ, 4 0.2B
   P66 38215
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.. O

0; Gaps

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TITLE OF INVINCTOR. DEVELOPMENTALLY REGULATED ENDOTHELIAL FITLE OF INVENTION: CELL LOCUS-1 REMARKS OF SIQUIRERS: 29
  Overy Match 72.2%; Score 39; DB 2; Longth 320;
Best Local Similarity 77.8%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 2; Indels
  72.2%; Seere 39; PP 2; Length 320; 77.8%; Pred. No. 14;
   2; Indels
  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
AFLICATION THE HE, 78, 55, 235C FILING DATE: 05-JUN-1996
   0; Mismatches
   REFERENCE/CHOCKET NUMBER: 8907-0034-999 TELECOMMONICATION INFORMATION:
  ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CIIY: New York
  US-08-659-2356-20
: Sequence 20, Application US/086592356
: Patent No. 5877281
  COMPUTER: THM PC compatible OPERATING SYSTEM: PC PGS/MS-DOS
  Pennie & Edmonds LLP
  ; Sequence 9, Application US/08162402B
; Patent No. 5972337
   APPLICANT: Quertermous, Thomas APPLICANT: Hegan, Brigid
  APPLICANT: Snodgrass, H. Kalph
APPLICANT: Zupancic, Thomas J.
   TELEFAX: (212) 869 8864/9741
TELEX: 66141 Pennie
INFORMATION FOR SEQ ID NO: 20:
  28,462
  (212) 790-9090
   Floppy disk
   ATTORNEY/AGENT INFORMATION:
   NAME: Poissant, Brian M. REGISTRATION WIMMBER: 28.
  320 amino acids
   tY: United States
10036-2711
   Guery Match
Rest Local Similarity 77.89
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   ; MOLECULE TYPE: protein US-08-659-235C-20
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   1 GLQHWVPEL 9
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  US 08:480-229C-20
   US-08-162-402B-9
    TOPOLOGY:
   COUNTRY:
  STATE:
  RESULT
  <u>-</u>
   S
   APPLICANT: Querrermous, Thomas
APPLICANT: Godan, Brigid
APPLICANT: Shodyauss, B. Falgh
APPLICANT: Shodyauss, B. Falgh
APPLICANT: Shodyaus, Thomas J.
TITLE OF INVENTION: DEVELOPMENTALLY-REGULATED ENDOTHELIAL
TITLE OF INVENTION: CELL LOCUS 1
   Tatch 72.2%, Score 39, DB 2, Lougth 160, Local Similarity 77.8%; Pred. No. 6.7; concrruation of Mismatches 2, Indels
  Patentin Release #1.0, Version #1.30
  8907-0026-999
   1: Pennie & Edmonds LLP
1155 Avenue of the Americas
   REFERENCE/DOCKET NUMBER: P66 38215
TELEFOMMUNICATION INFORMATION:
TELEPHONE: 213-622-7700
  TE, 708/480, 2290
   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
   : Sequence 20, Application HS,AMBARDPac
: Patent No. 5874562
: GENERAL INFORMATION:
   : (212) 790-9090
(212) 869-8864/9741
  NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,445
REFERENCE/DOCKET NUMBER: 890
IELECOMMUNICATION INFORMATION:
   30,930
  INFORMATION FOR SECTION: 20:
SEQUENCE CHARACTERISTICS:
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   07-JUN-1995
N: 536
FILING DATE: 03-DEC-1993
CLASSIFICATION: 435
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APPLICATION NUMBER:
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: United States
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  SEQUENCE CHARACTERISTICS:
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  Viviana
  MOLECULE TYPE: peptide
   COMPUTER READABLE FORM:
  66141 Pennie
  CORRESPONDENCE ADDRESS:
   PPGISTRATION NUMBER:
  APPLICATION NUMPER:
   NUMBER OF SEQUENCES:
   anknown
   amino acid
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STRANDEDNESS: un!
   10036-2711
  New York
   CLASSIFICATION:
  ||| | || 1 || 1 || 29 GLQRWGPEL 37
  1 GLQHWVPEL 9
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  STRANDEDNESS
  MEDIUM TYPE:
  FILING DATE:
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  TELEX:
   Ouery Match
  Best Loca
Matches
  RESULT
```

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US-08-727-616A-8
  ã
   APPLICANT: Whitney, Michael A. TITIE OF TWENTIANS FOR SENSITIVE METHODS AND COMPOSITIONS FOR SENSITIVE TITLE OF INVENTION: AND RAPID. FUNCTIONAL TOPWITCH OF GENERAL PROPERTY OF GENERAL PROPERTY OF GENERAL PROPERTY OF THE OF THURSMITCH.
             APPLICANT: CERIANI, ROBERTO I.,
APPLICANT: PETERSON JERRY A.
APPLICANT: PROCYA, DAVID 1
ITHE OF INVENTION: 46 KDALTON HUMAN MILK FAT
ITHE OF INVENTION: GIGHUF (HMEG) ANTIGEN, FRAGMENTS & FUSION PROTEIN
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
   Ö
   Ouery Match 72.2%; Score 39; DB 2; Length 463; Best Local Similarity 77.8%; Pred. No. 21; Matches 7; Conservative 9; Mismatches 2; Indels
   OFEKATING SYSTEM: DOS
SOFTWARE: FastSEG for Windows Version 2.0
SOFTWENT APPLICATION DATE: US/98/162,4028
  ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
  ADDRESSEE: Pretty, Schroeder & Poplawski
STREET: 444 South Flower St., 19th Floor
CITY: Los Angeles
   KEFFERENCEZDOCKET NUMBER: P66 38215
TELECOMMINICATION INFORMATION:
   Sequence 8, Application US/08719697
Patent No. 5928888
GENERAL INFORMATION:
  NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
   E: Floppy disk
IBM PC compatible
   CLASSIFICATION: 435
PKOR APPLICATION DAILS
APPLICATION NUMBER:
  COMPUTER RENDABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPALIDE
  ATTORNEY/AGENT INFORMATION:
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   213-489-4210
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CORRESPONDENCE ADDRESS:
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  amino acid
   CENERAL INFORMATION:
  La Jolla
  1 GLOHWVPEL 9
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  USA
  STRANDEDNESS
   90071
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   TELEPHONE:
  STATE: CA
   US-08-162-402B-9
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  ToPoLoGY:
   TELEFAX:
   COUNTRY:
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  LENGTH:
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   Matches
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   Ś
```

```
.,
D
   Score 37; DB 2; Length 264;
Pred, No. 26;
0; Mismatches 2; Indels
  APPLICANT: Tsien, Roger Y.
APPLICANT: Tsien, Roger Y.
TITLE OF INVENTION: SUBSTRATES FOR BETA-LACTAMASE
CORRESPONDENCES: 10
CORRESPONDENCE ADDRESS:
              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: IS/08/719 697
   OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
  ATTRESSFE: Fish & Figherdson P.C. STREET: 4225 Executive Square, Suite 1400 CITY: La Jolla
   NAME: Haile, Lisa A. REJSTRATION NOMBER: 38,347
REFERENCE/LOCKET NUMBER: 08366/003001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678.5070
  0034001
  APPLICATION NUMBER: BSZ08,727,616A FILING DATE: 15-0CT-1996
OPERATING SYSTEM: PC-DOS/MS-DOS
  ; Sequence 8, Application US/08727616A; Patent No. 6291162; GENERAL INFORMATION:
   PRIOR APPLICATION DATA:
AFFLICATION NUMBER. 08/407,544
FILING DATE: 20-MAR-1995
ATTORNEY/AGENT INFORMATION:
   PEGISTRATION NUMBER: 38,347
EFFFFFWTF,0.07kFI NUMFFF GT
TELECOMMUNICATION INFORMATION:
   68.5%;
75.0%;
   INFORMATION FOR SHO ID NO: 8: SEQUENCE CHARACTERISTICS:
  INFORMATION FOR SEC ID NO: 8:
  CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
   COMPUTER: IBM Compatible OPERATING SYSTEM: Windows
   26-SEP-1996
  619/678-5070
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   619/678-5099
  MOLECULE TYPE: protein US-08-714-697-8
   NAME: Haile, Lisa A.
   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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  TYPE: amino acid
   linear
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|138 LDHWEPEL 145
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   US-08-727-616A-8
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   COUNTRY:
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   TYPE:
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Thu Sep

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ó
   APPLICANT. Whitney, Michael A. TITLE OF INVENTION: METHER AND COMPOSITIONS FOR SENSITIVE TITLE OF INVENTION: AND RAPID, FUNCTIONAL IDENTIFICATION OF GENOMIC TITLE OF INVENTION: FOTYHOUSFILDES AND SFICHFARY SCHEENING CAFASILITIES
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                                       0;
  0,
68.5%; Score 37; DB 4; Length 264; 75.0%; Pred. No. 26;
Live 0; Mismatches 2; Indels
  68.5%; Score 37; DB 2; Length 265. 75.0%; Pred. No. 26;
  2, Indels
  APPLICANT: Tsien, Roger Y.
APPLICANT: Tsien, Roger Y.
TITLE OF TSION: SUBSTRATES FOR BETA-LACTAMASE
NOMBER OF SEQUENCES: 10
CORPETE NORME ADDRESS:
  COMPUTER: IBM PC COMPACIDATE COMPACIFICATIONS SYSTEM: PC-DUS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30
   Er Fish & Pichardson P 7
4225 Executive Square, Suite 1400
   Pred. No. 26;
0; Mismatches
  19366,7003001
   Fish & Richardson F.C.
   , Sequence 6, Application 03/08727616A
; Patent No. 6291162
  ; Sequence 6, Application US/08719697
; Patent No. 5928888
   5: Floppy disk
IBM PC compatible
   ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
   TELECOMMUNICATION INFORMATION: TELEPHONE: 619/678-5070
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4225 Executive Square, Suite 1400
   0; Mismatches
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  APPLICATION NUMBER: PCT/US94/00198
   PRIOR APPLICATION DATA:
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  Sequence 4, Application PC/TUS9400198 GENERAL INFORMATION:
   APTICATION NUMBER, 88/407,544
FILING DATE: 20-MAR-1995
ATTORNEY/AGENT INFORMATION:
  SYSIEM: 6.0.8
Microsoft Word 5.1a
   NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
   REGISTRATION NUMBER: 32,743
   TELECOMMUNICATION INFORMATION:
   INFORMATION FOR SEQ ID NO: 6:
  ADDRESSEE: Schering Corp. STREET: 1 Girald Farms
   15-JAN-1993
  3: Diskette
IBM Compatible
   ATTORNEY/AGENT INFORMATION:
  Floppy disk
  265 amino acids
  APPLICANT: Schering Corp.
  THE NUMBER
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  TELLECHE. 619,678 507
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Matches 6, Conservative
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FRAGMENT TYPE: internal
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  New Jersey
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EIF. 94304-1104
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   CLASSITICATION:
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   GENERAL INFORMATION:
APPLICANT: MOLLEZ, ESTELLE
APPLICANT: Abastado, Jean-Pierre
APPLICANT: Kourilsky, Phillippe
APPLICANT: Kourilsky, Phillippe
TITLE OF INVENTION: An Altered Major Histocompatibility
TITLE OF INVENTION: Complex(MHC) Determinant and Methods for Using the
TITLE OF INVENTION: Determinant
  0; Caps
  Score 37, 58 5, Length 3079, 
prod No 3 9+02;
2, Mismatches 2; Indels
   NUMBER OF SEQUENCES: 127
COFFESSONENCE ALDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner
   SOFTWARE: Patentin Palease #1 0, Version #1 25
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   03495 DIBE-03080
  1300 I Street, N.W., Suite 700
  ORGANISM. Saccharomyces cerevisiae
   APPLICATION NUMBER: US 07/792,473
FILING DATE: 15-NOV-1991
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  Sequence 110, Application US/08484905
Patent No. 5976551
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TELEPHONE: (201)822-7255
THEMERAX: (201)822-7039
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FILLING DATE: 05-DEC-1991
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  ATTORNEY/AGENT INFORMATION:
  NAME: Potter, Jane E. R. REGISTRATION NUMBER: 33,
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STRANDEDNESS: single
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   OPERATING SYSTEM:
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|2418 CLSYWIPNE 2426
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   CITY:
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   Gaps
   APPLICANT: Mottez, Estelle
APPLICANT: Abastado, Jean-Pierre
APPLICANT: Kourilsky, Phillipe
TITLE OF INVENTION: Altered Major Histocompatibility Complex
TITLE OF INVENTION:
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  parch 66.7%, Score 36, DB 3, Length 255; Jocal Similarity 62.5%, Pred. No. 38; 1: indels 98. 5; Conservative 2: Misearches 1: indels
66.7%, Score 36, DB 2; Longth 255;
62.5%; Pred. No. 38;
   1; Indels
   ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
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FILING DATE: 05-DEC-1991
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15-NOV-1991
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PEPERENCE/DOCKET NUMBER 034
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   ATTORNEY/AGENT INFORMATION:
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  NAME: Meyers, Kenneth J
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  US-08-370-476-110
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   Query Mateb
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   0,
  GERERAL INCORNATION:

APPLICANT: Mottez, Estelle
APPLICANT: Abastado, Jean-Pierre
APPLICANT: Kourilsky, Phillipe
APPLICANT: Lone, Yu-Chun
APPLICANT: Ojcius, David
APPLICANT: Ojcius, David
APPLICANT: Ojcius, Armanda
TITLE OF INVENTION: Altered Major Histocompatibility Complex
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STREET: 1300 I Street, N.W., Suite 700
   SOFTWAPE: PatentIn Pelease #1.0, Version #1.35
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FILING DATE: 15-NOV-1991
ATTORNEY/AGENT INFORMATION:
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STATE: D.C.
Z1P: 20005-3315
  amino acid
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  FILING DATE:
   TELEPHONE:
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GenCore version 4.5
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OM protein - protein search, using sw model

(without alignments) 3 735 Million cell updates/sec September 5, 2002, (Fig.7 et , Search fige 58,89, September

US-09-744 804 40 Title: Perfect soure:

1 VQFVASYKV 9 Scoring table: Sedneuce:

BLOSUM62 Gapop 10 0 , gapext 0.5

Searched:

Total number of hits satisfying chosen parameters:

231628 seqs, 24425594 residues

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Listing first 45 summaries Post-processing: Minimum Match 0% Maximum Match 100%

Database

Pred. No. is the number of results predicted by charge to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| not tgi rosed              | Seminary 2, April 1 | · .                    | Sequence 12, Appl | œ,               | 3                | c i               | Sequence 3, Appli | ď                | Υ.               | Ċ               | Sequence 21, Appl | 2    | Sequence lo, Appl | 1:1               | -                 | ۲,                | Sequence 13, Appl | 20,               | ₽.                | Sequence 9, Appli | ٠.                | L٦               | 7,                                                                              | x                                            |                   | r.          | Sequence 7, Appli |
|----------------------------|---------------------|------------------------|-------------------|------------------|------------------|-------------------|-------------------|------------------|------------------|-----------------|-------------------|------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------------------|---------------------------------------------------------------------------------|----------------------------------------------|-------------------|-------------|-------------------|
| JD                         |                     | C 273 C 678 - 80 - 81. | 92-08-152-402B-12 | US-07-507-538C-3 | US-08-152 402B-3 | 112-07-507-5380-5 | US-08 142-402R-2  | 48-08 162 402R-F | #-E70# 757 RD-SD | #S-08 480-22921 | 08-08-659-5350-71 |      | 08-08-659-2350-10 | 75 08 480-2297-14 | US-08-659-2450-14 | 11S-08-111-939-25 | US 08-162-402B 13 | 78-68-480 2290-20 | 07-1547 NB4-80-Su | US-08-162-402B 9  | 1. 2622-084-80-80 | US-08 480 229C-5 | US - 08 - 480 - 119C 7                                                          | N. C. 4 4 10 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 | 118-08-654 2450-1 | 5-053-80-80 | US-08-659-235C-7  |
| 12                         | i<br>D              | 24                     | ~ i               | _                | cı               | _                 | C 4               | C:               | 4                | CI              | 24                | C1   | C 4               | ۲,                | ٠.                |                   | C4                | ٠.                | ٠,                | C I               | -1                | C1               | c4                                                                              | ٠,                                           | ٠.                | . 1         | Ċ1                |
| %<br>Query<br>Match bength | 1 6                 | д.                     | . v               | 217              | 217              | 218               | 218               | 797              | n                | 121             | 1,7               | 480  | 480               | ۲, ۲              | r<br>uh           | 100               | 157               | 3.20              | りごと               | 463               | 85                | u:<br>80         | 3<br>13<br>13<br>13<br>13<br>13<br>13<br>13<br>13<br>13<br>13<br>13<br>13<br>13 | x                                            | Œ.                | 30          | 85                |
| %<br>Query<br>Match        | 100 5               | 100.0                  | 100.0             | 100 O            | 100.2            | 100.0             | 100.0             | 100.0            | 901              | 7 cg            | 44 7              | 83.7 | 83.7              | 83 -              | 83.1              | 79 1              | 79.1              | 79.1              | 79.1              | 79.1              | 67.4              | 1.19             | £7.4                                                                            | 67 4                                         | F7 4              | 67.4        | 67.4              |
| Score                      | 43                  | 4.2                    | 43                | 43               | ~                | 43                | 43                | 43               | 2 +              | 36              | 36                | 36   | 36                | 36                | 36                | 34                | 34                | 34                | Ψ <sub>c</sub>    | 3.1               | 62                | ēं∂              | er<br>Ca                                                                        | 29                                           | e.<br>CI          | 67          | ರ್<br>೧೩          |
| Result<br>No.              | 1                   | ¢4                     | œ                 | 4                | u,               | ¥                 | 7                 | ω                | g,               | 10              | 11                | 12   | 13                | 14                | 15                | 16                | 17                | 18                | ۍ.<br>1 م         | 0                 |                   | CI<br>CI         | e<br>e                                                                          | ä                                            | C1<br>R1          | (A)         | 27                |

|                                                                                                                                                                                                                                                         | Sequence 10, Appl<br>Sequence 10, Appl<br>Sequence 3, Appli<br>Sequence 24, Appli |
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| ្ន-ប្រាស្សសក្ <del>សុ</del> (-(របស់ស)                                                                                                                                                                                                                   | m m m ++                                                                          |
| 8 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1                                                                                                                                                                                                                 | 1477                                                                              |
| 247-10-00-00-00-00-00-00-00-00-00-00-00-00-                                                                                                                                                                                                             | 67.5                                                                              |
| 00000000000000000000000000000000000000                                                                                                                                                                                                                  | 67.73                                                                             |
| ######################################                                                                                                                                                                                                                  | 8838                                                                              |
| 6 7 7 7 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8                                                                                                                                                                                                                 | त्त्र क्ष<br>विक्ष                                                                |

### ALIGNMENTS

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APPLICANT: Quertermous, Thomas
APPLICANT: Quertermous, Thomas
APPLICANT: Hogan, Brigid
APPLICANT: Strenglass, H. Balph
APPLICANT: Zupancic, Thomas J.
APPLICANT: APPLICANT: CHERTER HELIALITIES ENDOTHELIAL
ILILE OF INVENTION: CELL LOCUS-1
   SOFTWARE: Farefill Politich #1.0, Version #1.30 CUBRENT APPLICATION BATA.
  Pres. 7 100 24 14 19
   4: Pennie & Edmonds LLP
1755 Averue of the Americas
  APPLICATION MUMBER: US/UE/480,229C
FILING DATE: 07-JUN-1995
GLASSIFICATION: 536
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  ; Sequence 2, Application US, 08480229C; Patent No. 5874562
  (212) 790+989
(212) 869-8864/9741
  NAME. POISSANC, BILAN M. PROTETRATON TUMBER 28,462
ELEPENDE, ANGEST NUMBER STORES TELECOMMUNICATION. TREPENDATION.
  MEDIUM TYPE: Floppy disk
  ATTORNEY/AGENT INFORMATION:
   TELEX. 60141 Pennie
INFERMATION FOR SEG ID NO
SEQUENCE CHARACTERISTICS:
LENGTH: 85 amino acids
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: United States
  NUMBER OF SECORNOES. 29
COREESCONFORD ALDRESS:
   , rorotogy, unknown
, Molbedub TYPB, peptide
US-08-480 7090 2
   COUNTRY: United State 21P: 10036-2711 COMPUTER PERADARLE FORM:
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   GENERAL INFORMATION:
  SIFFFI: 1155 Av
CITY: New York
STATE: New York
  STRANDEDNESS
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                         US-08-480-229C-2
  TELEPAX.
PESULT
```

edeb Specy Match Best Local Similarity 100:0%, From No. 0:03, Matches 4, Conservative 9, Mismatches 9, (ndels

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444 South Flower St , 19th Ploor
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   NAME: Amzel, Viviana
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   Ċ
   APPLICANT: CERTAIN, ROBERTO L.
APPLICANT: PETERSON, JERRY A.
APPLICANT: LAROCCA, DAVID J.
TITLE OF INVENTION: 46 KDALION HUMAN MILK FAT
TITLE OF INVENTION: GLOBULE (HMFG) ANTIGEN, FPAGMENTS & FUSION PROTEIN
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   APPLICANT: Quertermous, Thomas
APPLICANT: Hogan, Brigid
APPLICANT: Shoddrass, H. Kalph
APPLICANT: Zupancic, Thomas J.
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  Pretty, Schroeder & Poplawski
  8407-0034-999
  E: Pennie & Edmonds LLP
1155 Avenue of the Americas
  омвек: Оз/38/655,2353
05-JUN-1996
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   : (212) 790-9090
(212) 869-8864/9741
   NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,452
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  TELECOMMUNICATION INFORMATION:
  TELEX: 66141 Pennie
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  ATTORNEY/AGENT INFORMATION:
   New York
. United States
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   SOFTWARE:
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  FACTORS V AND VIII LIGHT-CHAIN HOMOLKGIES,
FUSION PROTEIN, POLYMCLEGYTDE AND POLYRTHRO-
NUCLEOTIDE ENCOPING THE POLYPEPTIDE, ANTI-
POLYPEPTIDE ANTIBODIES, KITS AND METHODS OF
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   Peterson Dr., Jerry A.
Larocca, David J.
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TELEPHONE: (510) 943-1189
TELEFAX: (510) 943-1189
  APPLICANT: Ceriani Dr., Roberto I.
APPLICANT: Peterson Dr., Jerry A.
APPLICANT: Larocca, David J.
  Sequence 2, Application US/07607538C Patent No. 5455031
  NAME: Viviana Amzel
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   Coory Word.
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7 9, Conservative
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CITY: Los Angeles
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TELEPHONE: 213-622-7700
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03-DEC-1993
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; Patent No. 5972337
  APPLICANT: CERTANI, RCHERTO L. APPLICANT: PETERSON, JERRY A. APPLICANT: LAROCCA, DAVID J
  Viviana
Viviana
In. 30,930
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REFERENCE THOMPHY: THE
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   . (510) 943-1931
(510) 943-1189
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Best Local Similarity | 100 ...
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  MOLECULE TYPE: protein FRAGMENT TYPE:
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   CLASSIFICATION: 435
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[on or energy 47, PH 2, Length 217]
100.0%; Pred. No. 0.081;
tive 0, Mismatches 0; Indels
  COMPUTER: 1BM PC COMPATIBLE
OPERATING SYSTEM: PC-FPG/MS-POS 5.0
SYSTWARE: PATCHIN PCLOSS #1.0, Version #1.25
CURENT APPLICATION DATA:
APPLICATION NUMBER: 05/07/607,538C
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```
ō.
   APPLICANT: CEKIANI, ROBERTO L.
APPLICANT: PETERSON, JEPPY A
APPLICANT: LAROCCA, DAVID J.
TITLE OF INVENTION: 46 KDALTON HUMAN MILK EAT
TITLE OF INVENTION: GLORUIF (HMFG) ANTIGEN, FPAGMENTS & FUSION PPOTEIN
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
  TITLE OF INVENTION: 46 KDALTON HUMAN MILK FAT
TITLE OF INVENTION: GLOBULE (HMFG) ANTIGEN, FRACMENTS & FUSTON PROFEIN
   0; Gaps
   100.0%; Score 43; PB 2; Length 218; 100.0%; Pred No. 0 081;
   ē; Indels
  SGFTWARF FASTSEQ for Windows Version 2.6
CHRRINT APPLICATION DATA:
  ...orkSSEE: Pretty, Schroeder & PoplawSki
STREET: 444 South Flower St., 19th Floor
CITY: Los Angeles
STATE: CA
COMPRESSE
  COPRESSION FINE STREETS. Schroeder & Puplawski STREET: 444 South Plower St., 19th Floor
   fr; Mismatches
   HS/08/162,402B
  PA6 38215
   Sequence 6, Application HS/08162402B
Patent No. 5972337
            Sequence 2, Application US/08152402E
Patent No. 5972337
  GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: CERRANI, ROBERTO L.
APPLICANT: PETERSON, JEKEY A
APPLICANT: TAROCCA, DAVID I
  TORNEY AGAIN ... NAME: Amzel, Viviana
  REPERPIN'E ADOLKET NÜMBER – ÞA
TELESDOMUNLAGTTON I UPOPMATTON:
TELEBEDONE: 213-622-7700
TELEBEAX: 213-489-4210
  INFORMATION FOR SEQ ID NO: 2:
   : Diskette
IBM Compatible
  03-DEC-1993
  ATTORNEY/AGENT INFORMATION:
   218 amino acids
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Matches 9; Conservative
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  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Diskett
   APPLICATION NUMBER
   NUMBER OF SEQUENCES:
   APPLICATION NUMBER.
   unknown
  TYPE: amino acid STRANDEDNESS: unk
  OPERATING SYSTEM:
   GENERAL INFORMATION:
  1 VOFVASYKV 9
  FILING DATE:
  FILING DATE:
  90071
   COMPUTER:
US-08-162 402B 2
  US-08-162-402B-2
   US-08-162-402B-6
   TOPOLOGY:
   COUNTRY
   LENGTH:
   Query Match
  TELEX
  RESULT
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Gaps
   .
  | 100 08, Soor= 43, PR 2, Longth 387, 100 08, Prod No 0 15, tive 0; Mismatches 0; Indels
   CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: 18,08/2162,402B

FILLING DATE: 03-DEC-1002
   SCHTWAPF, EastSEQ for Windows Version 2.0 chppsnt Application DATA:
APPLICATION NUMBER: US/08/162,402B
  ADDRESSEE: Pretty, Schrouder & Poplawski
STREET: 444 South Flower St., 19th Floor
CITY: Los Angeles
STATE: CA
   P66 38215
   US-08-162-402B-8
; Sequence 8, Application US/08162402B
; Patent No. 5972337
  NAME: Amzel, Viviana
PEGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P66
  TELEPHONE: 213 622-7700
TELEFAX: 213-489-4210
   COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
  E: Diskette
IRM Compatible
   APPLICATION NUMBER: USZOB
FILING DATE: 03-DEC-1993
  FILING DATE: ALTOKNEY/AGENT INFORMATION:
  Guery Match
Hear Local Similarity the
9, Conservative
   LENGTH: 387 amino acids
   INFORMALION FOR SEQ ID NO SHOURNCE CHARACTERISTICS:
  29
   unknown
   Diskette
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  MOLECULE TYPE. peptide
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  COMPUTER READABLE FORM:
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  CLASSIFICATION: 435
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CilY: Lus Angeles
   TOPOLOGY: unknown
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  313 VQFVASYKV 321
  1 VQFVASYKV 9
   USA
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   90071
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Gaps
   į.
  100.0%; Score 43; DB 2; Lenqth 465; 100.0%; Pred. No. 0.18; tive 0; Mismatches 0; Indels
  APPLICANT: Quertermous, Thomas
APPLICANT: Hogan, Brigid
APPLICANT: Snodqrass, H. Baiph
APPLICANT: Znodqrass, H. Baiph
APPLICANT: Znodqrass, Thomas J.
TITLE OF INVENTION: DEVELOPMENTALLY-PEGULATED ENDOTHELIAL
TITLE OF INVENTION: CELL LOCUS-1
   Patentin Release #1.0, Version #1.30
   8907-0026-999
  1155 Avenue of the Americas
  REFERENCE/DOCKET NUMBER: P66 38215
TELECOMONISTATION INFORMATION:
TELEPHONE: 213-622-7700
TELEFAS: 213-489-4210
   CURRENT APPLICATION DATA:
APPLICATION NUMBER: 05,08,480,2007
  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
  Sequench 21, Application US/084802295
Patent No. 5874562
GENERAL INFORMATION.
   Pennie & Edmonds LLP
  PEGISTPATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 799 0000
TELEFAX: (212) 840 8844,7434;
                                      30,530
   TELEX: 66141 Pennie
INPORMATION FOR SEQ ID NO: 21:
   Floppy disk
  07-JUN-1995
ATTORNEY/AGENT INFORMATION:
   ATTOPNEY/AGENT INFORMATION:
  NAME: Poissant, Brian M.
PEGISTPATION NUMBER: 28,
  : 321 amino acids
amino acid
  465 amino acids
  COUNTRY: United States
2IP: 10036-2711
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   SEQUENCE CHARACTERISTICS:
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   CORRESPONDENCE ADDRESS:
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   391 VOFVASYKV 399
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   US-08-480-229C-21
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  US-08-162-402B-8
  SOFTWARE:
  LENGIH:
  LENGTH:
  STREET:
   STATE:
   Matches
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or daps
   Caps
  APPLICANT: Hogan, Brigid
APPLICANT: Snodgrass, H. Ralph
APPLICANT: Zupancic, Thomas J.
TITLE OF INVENTION: DEVELOPMENTALLY-REGULATED ENDOTHELIAL
TITLE OF INVENTION: CELL LOCUS 1
NUMBER OF SEQUENCES: 29
   83.7%, Score 36, DB 2; Length 321; 77.8%, Pred, No. 3.6; tire 1; Michalaches 1; Indels
83.7%; Score 36; DB 2; Length 321; 77.8%; Pred. No. 3.6;
                                     1; indels
   1; Indels
  OPERATING SYSTEM: PCLOOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                   1; Mismatches
   REFERENCE/DOCKET NUMBER: 8907-0034-999
TELECOMMONICATION INFORMATICAL:
TELEPHONE: (212) 790-9090
   ADDRESSEE: Pennic a numerical STREET: 1155 Avenue of the Americas
  US/709,7659,235C
  Sequence 21, Application 98/08659245C
Patent No. 5877281
  Sequence 10, Application 05/084802290
Patent No. 5974562
  GENERAL INFORMATION:
APPLICANT: Quertermous, Thomas
APTLICANT: Hogan, Brigid
APPLICANT: Snodgrass, H. Kaiph
APPLICANT: Zupancic, Thomas J.
   IELEFAX: (212) 869-8864/9741
TELEX: 66141 Pennie
INFORMATION FOR SEQ ID NO. 21:
  Quertermous, Thomas
  E. Floppy disk
IBM PC compatible
   28,462
  05-JUN-1996
   ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M.
  321 amino acids
   Query Match
Hest Local Similarity 77.0%
17. Conservative
   United States
Ouery Match
Best Local Similarity 77.89
Matches 7: Conservative
  SHQUENCE CHARACTERISTICS:
  MOLECULE TYPE: protein
   CORRESPONDENCE ADDRESS:
  COMPUTER READABLE FORM:
MEDIUM TYPE, Floppy
   REGISTRATION NUMBER:
  APPLICATION NUMBER:
FILING DATE: 05-JUN
  unknown
  COMPUTER: 18M PC
OPERATING SYSTEM:
SOFTWARE: PatentI
  amino acid
   New York
New York
  GENERAL INFORMATION:
   246 VQFVGSYKL 254
   216 VOFVGSYKL 254
   COUNTRY: United
21P: 10036-2711
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   1 VQFVASYRV 9
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  RESULT 12
US-08-480-229C-10
  US-08 659 235C-21
  TOPOLOGY:
  APPLICANT:
  LENGTH:
   STATE:
  RESULT 11
   ć
   ŝ
```

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ATTORNEY/AGENT INFORMATION:
  Query Match
   Sales
TITLE OF INVENTION. DEVELOPMENTALLY-REGULATED ENDOTHELIAL
  APPLICANT: Snodgrass, H. Ralph
PPLICANT: Zupancic, Thomas J.
TITLE OF INVENTION: DEVELOPMENTALY-PECHIATED ENDOTHELIAL
TITLE OF INVENTION: CELL LOCUS-1
  83.7%, Score 36, DB 2, Length 480; 77.8%; Prod. No. 5 5; Live 1, Mismatches 1, Indels
   SOFTWARE: Patentin Release #1.0. Version #1 30 CURRENT APPLICATION DATA:
  Patentin Release #1.0, Version #1.30
  NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28.462
REFERENCE/HONNET NUMBER: 0007-0026-999
TELFORMINICATION INFORMATION:
  ..., Ve. ..
   ADDRESSEE: Pennie & Edmonds IL.P
STREET: 1155 Avenue of the Americas
   E: Pennie & Edmonds LLP
1155 Avenue of the Americas
   APPLICATION NUMBER: US/08/480, 229C
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
  8: Floppy disk
IBM PC compatible
SYSTEM: PT-FOS/MS-FGS
  Sequence 10, Application US/U8659235C Patent No. 5877281
GENERAL INFORMATION:
  PC-DOS/MS-DOS
  CELL LOCUS-1
   TELEPHONE: (212) 790-9090
FELEFAX: (212) 869-8864/9741
   APPLICANT: Quertermous, Thomas APPLICANT: Hogan, Brigid
  COMPUTER: IBM PC compatible
  INFORMATION FOR SEQ ID NO: 10:
  ATTORNEY/AGENT INFORMATION:
   Floppy disk
  LENGTH: 480 amino acids
  CURRENT APPLICATION DATA:
   New York
: United States
  SEQUENCE CHARACTERISTICS.
  Query Match
Best Local Similarity 77.8°
Matches 7; Conservative
  COUNTRY: United States
   MOLECULE TYPE: protein
  NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
   NUMBER OF SEQUENCES: 2'
   COMPUTER READABLE FORM:
   66141 Pennie
   APPLICATION NUMBER.
  OPERATING SYSTEM:
  OPERATING SYSTEM:
   amino acid
   linear
  TITLE OF INVENTION:
  New York
: New York
   402 VQFVGSYKL 410
  10036 2711
   New York
   CLASSIFICATION:
   1 VUEVASYKV 9
   MEDIUM TYPE:
   FILING DATE:
   COUNTRY: Ur
ZIP: 10636
  US-08-659-235C-10
   ADDRESSEE:
   US-08-480-229C-10
   COMPUTER:
   TYPE: ami
TOPOLOGY:
  SOFTWARE:
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   STATE
  TELEX:
  STATE:
  RESULT 13
   .<u>.</u>
   3
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```
Gaps
   APPLICANT: Querrermous, Thomas
APPLICANT: Hogan, Brigid
APPLICANT: Snodgrass, H. Ralph
APPLICANT: Supancic, Thomas J.
TITLE OF INVENTION: DEVELOPMENTALLY-FREGULATED ENDOTHELIAL
ILITLE OF INVENTION: CELL LOCUS-1
   83.7%; Score 36; DB 2; Longth 480; 77.8%; Pred. No. 5.5; tive 1; Mismatches 1; Indels
  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
  8907-0026-999
   ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
   118/08/480,229C
  Sequence 14, Application "Symmatoggs Patent No. 5874562
GENERAL INFORMATION:
   COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DGS/MS-DOS
  TELEPHONE: (212) 750-5040
TELEFAX: (212) 869-8864/9741
TELEX: 66141 Pennic
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
   : (212) 790-9090
(212) 869-8864/9741
                 REGISTRATION NUMBER: 28,462
REFERENCE/TONCKET NUMBER: 890
TELECOMMONICATION INFORMATION:
  REGISTRATION NUMBER: 28,462
REFERENCE/EGGKET NUMBER: 890
TELECOMMUNICATION INFORMATION:
   TELEX: 66141 Pennie
INFORMATION FOR SEQ ID NO: 14:
   Floppy disk
   07-JUN-1995
   ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M.
Poissant, Brian M.
   LENGTH: 480 amino acids
   513 amino acids
   Best Local Similarity 77,89
Matches 7; Conservative
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ZIP: 10036-2711
  SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE: protein
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   , MOLECULE TYPE: protein US-08-480-229C-14
   CORRESPONDENCE ADDRESS:
  NUMBER OF SEQUENCES:
  APPLICATION NUMBER.
   amino acid
  linear
  amino acid
   402 VOFVGSYKI, 410
  New York
   CLASSIFICATION:
  New York
  1 VQFVASYKV 9
  STRANDEDNESS:
   MEDIUM TYPE:
   FILING DATE:
  08-08-659-2350-10
  US-08-480-229C-14
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  TOPOLOGY:
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  STATE:
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83.7%; Score 36; DB 2; Length 514;

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0;
   0; Gaps
                               Gaps
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O
   APPLICANT: Querrermous, Thomas
APPLICANT: Hogan, Brigid
APPLICANT: Snodgrass, H. Ralph
APPLICANT: Zupancic, Thomas J.
TITLE OF INVENTION: DEVELOPMENTALLY REGULATED ENDOTHELIAL
TITLE OF INVENTION: CELL LOCUS-1
   Overy Match 83.7%; Score 36; DB 2; Length 513; Best Local Similarity 77.8%; Pred. No. 5.9; Matches 7; Conservative 1; Mismatches 1; Indels
                          1; Indels
  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION DATA: OR 08.059,235C FILING DATE: 05-JUN-1996 CLASSIFICATION: 435
Best Local Similarity 77.8%; Pred. No. 5.9;
Matches 7; Conservative 1; Mismatches
  NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/FOCKFT NUMBER: 8907-00:4-999
TELECOMMUNICATION INFORMATION:
   Search completed: September 5, 2002, 15:27:36
Job time: 321 sec
   ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CIIY: New York
STATE: New York
COUNTRY: United States
ZIP: 10036-2711
   Sequence 14, Application 05/08659235C; Patent No. 5877281; CENERAL INFORMATION:
   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
   TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 Pennie
INFORMATION FOR SEQ ID NO: 14:
  ATTORNEY/AGENT INFORMATION:
  SEQUENCE CHARACTERISTICS:
LENGIH: 513 amino acids
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   STRANDEDNESS: unknown
   ...rology: linear
MOLECTLE TYPE: protein
US-08-659-235C-14
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  DD 435 VQFVGSYKL 443
   |||| ||| ||| 435 VQFVGSYKL 443
   1 VQFVASYKV 9
  1 VQFVASYKV 9
  US-08-659-235C-14
   RESULT 15
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GenCare version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - profein search, using sw model

September 5, 2002, 15:26:31; Search time 158.43 Seconds (without alignments) 6.310 Million cell updates/see Pun on:

US-09-744-804-40 1 VCFVASYKV 9 Title: Perfect score: Sequence:

Gapop 10 0 , dapoxt 0,5 BLOSUM62 Scoring table:

747574 segs, 111073796 residues Searched.

Total number of hits satistying chosen parameters:

Maximum DB seq length: 2000000000 Minimum DB seq length: 0

1008 Post-processing: Minimum Match 0% Mayimum Match Database

Listing first 45 summaries

2. STECT PROBLET TO THE CONTROL OF CONTROL AND WIND TAXABLE TO STEET THE CONTROL OF CONT 781081 Susadat ash ish spenses primer amprombly AAT satt (AAT) at 781081 Section data ash ish spenses primer ampromosy, AAT 998 LOT (AAT) at 4001 dependency open exemptor and saturation dependency open exemptor and saturation dependency. As the triplate of the interpretations on the south AA was taken (STESLO) polaria, hind general (Aginosee) pearling additional (Antonomial). (STESLO) polaria, hendergenese (Aginosee) pearling (ANTONOMIA). 

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

|    | Description                | Lactadherin (BA-46 | Discoidin i/factor | HMFC 46 kDa anti | HMFG 46 kDa antige | HMPG 46 kba anti | Human lactadheri | Peptide #11766 enc | Protein #9130 cr | Human brain expr | Human brain expr |          |
|----|----------------------------|--------------------|--------------------|------------------|--------------------|------------------|------------------|--------------------|------------------|------------------|------------------|----------|
|    | ID                         | AAY82845           | AAW94690           | AAR77253         | AAR77254           | AAR77252         | AAY94453         | ABB44260           | ABB27131         | AAM58323         | AAM65298         | 10001134 |
|    | DB                         | 21                 | 2.0                | 16               | 16                 | 16               | 2.1              | C1                 | C)               | CI               | C1               | 000      |
|    | Query<br>e Match Length DB | 5                  | 38.5               |                  | 218                |                  | 387              | 25                 | C1<br>U1         | 52               | Ç.               | 6        |
| صو | Query<br>Match             | 100.0              | 100.0              | 100.0            | 100.0              | 100.0            | 100.0            | 83.7               | 83.7             | 83.7             | 83.7             | 0.0      |
|    | Score                      | 4.3                | C #7               | 43               | 4.3                | 43               | 43               | 36                 | 36               | 36               | 3.6              | 3.0      |
|    | Result.                    | -                  | :14                | ~                | 4                  | ហ                | 9                | 7                  | ∞                | Φ                | 10               | 11       |

| Peptide #8323 enco                     | Peptide #12252 end | Human milk fat glo | Mouse developmenta | Murice Del-1 prote | Human developmenta | Human Del-1 protei | reptide SEQ ID NO: | Mouse lactadherin | (24-Arg) MCP-1, H | Methanococcus mari | Drosophila melanog | Drosophila melanog | A partial core 2 b                      | Bacteriophage Dp-1 | Drosophila melanog | Arabidopsis thalia | Arabidopsis thalia |          | Arabidopsis thalla |          |          | Arabidopsis thalia | Arabidopsis thalia | Arabidopsis thalia | Tobarco PRPP-amido | prosophila melanod | pel-1 discoidin 1- | 2        | Discoldin L/factor | issestan flactor | i.e.s.i.n.i, tactor                     | Bushar that a doma | Rheats Colla I dom |
|----------------------------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|-------------------|--------------------|--------------------|--------------------|-----------------------------------------|--------------------|--------------------|--------------------|--------------------|----------|--------------------|----------|----------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|----------|--------------------|------------------|-----------------------------------------|--------------------|--------------------|
| AAM21889                               | AAM38215           | AAW91097           | AAW10364           | AAW94683           | AAW10365           | AAW94685           | AAW38891           | AAY94454          | AAR87676          | AAY04367           | ABB65653           | AB868395           | AAR18996                                | AAB16698           | ABB62376           | AAG15435           | AAC 16456          | AA043413 | AAC36455           | AAC13412 | AAG15434 | AAG15433           | AAG36454           | AAG4 34 1 1        | AAB70846           | ABR69750           | AAW10367           | AAW94689 | AAW94693           | AAW 41+ +1       | AAW -11                                 | AA1 82 543         | AATBZADU           |
| 21                                     | C1                 | 0                  | 18                 | 20                 | 8                  | 20                 | 50                 | <u></u>           | 16                | 50                 | 급<br>라             | C1<br>C1           | ======================================= | 5                  | C1                 | 5                  | 2                  | គ        | <u>-</u>           | គ        | 2        | 2                  | <u>-</u> 2         | 21                 | 22                 | C1<br>C1           | 18                 | 50       | 0.7                | ÷.               | :                                       | -                  | - 7                |
| C1                                     | CI<br>UN           | 22                 | 480                | 480                | 481                | 513                | 320                | 436               | 97                | 533                | 483                | 919                | 199                                     | 279                | 134                | 380                | 283                | <br>     | 386                | 286      | 287      | 0.68               | 967                | 368                | 573                | 315                | æ2                 | ဆ        | မ<br>ထ             | 7                | 1,11                                    |                    | : p :              |
| ~                                      | 83.7               | 8                  | 83.7               | 83.7               | 83.7               | 81.7               | 7.9.3              | 7.9.7             | 16.7              | 76.7               | 74.4               | 74.4               | , .<br>; .                              | 72.1               | 8.69               | 8.69               | 8.69               | 8.63     | 69.8               | 8.69     | 8.69     | 69.8               | 69.8               | 8.69               | 8.69               | 69.8               | 67.4               | 67.4     | 67.4               |                  | <br>-                                   |                    | £1.79              |
| 3.6                                    | <u>_</u>           | 3.6                | 36                 | 36                 | 3.6                | 3.6                | P ć                | <u>87</u>         | 33                | 3.3                | C.                 | C1                 | 2                                       | 31                 | 30                 | 0.5                | 3.0                | S.       | 3.0                | 30       | 30       | 30                 | 30                 | 30                 | 30                 | 0,5                | 59                 | 6Z       | Ç4                 | •                | ٠,                                      | 1                  | F)                 |
| ;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;; | ~                  | 1.1                | 15                 | 16                 | 17                 | 18                 | 5.                 | 20                | 21                | C4                 | 88                 | \$7.               | 61<br>C1                                | 26                 | 53                 | a)                 | 35<br>CH           | 3:0      |                    | C1       | **       | 3.4                | 3.5                | 3.6                | 37                 | ဆ                  | 58                 | 40       | 4.1                | .+               | • • • • • • • • • • • • • • • • • • • • | ::                 | .n                 |

#### ALL:NMFNIS

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Lartadberro (KA-4E) peptide tragment (tomour associated abiliquo).
  Treatment, presention, once, and chamber such me, actualses; treats for the series of 
   isment assertated antiqen peptide; TAA; cancer; carcinoma;
  AAYMJH45 Standard; peptide: 9 AA.
   (first ontry)
   W0200006723-A1.
  Homo sapiens.
   19-JUN-2000
   AA162845;
   AAY82845
Fr SULT
  HILL A PANER ON THE STANFAR RESERVENCE ON THE STANFAR STANFAR ON THE STANFAR S
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99WO 11.00417. 29 JUL 1999,

10-FEB-2000.

(YEDA ) YEDA RES & DEV CO LID. 381L 0125608. 30 JUL 1998,

Pat A. Pridkin M; Bar Eain E, Carmos L. Tirosh B. (BIOT ) BIG TECHNOLOGY GER CORP. Fiscubach L, C. Fitzer-attas C,

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Hogan B, Quertermous T, Snodgrass HR, Zupancic 73;
   W09515171-A.
  08-JUN-1995.
   Sednence
  AAR77253;
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  Matched
  AAR77253
   PESULT
SX COLOR OF COLOR OF BY A PRINCIPLE SX X COLOR OF COLOR O
   ċ
  The amino acids located at positions 2 and 9 of the tumors associated antigens are the archor residues which particleated in the binding to MHC class I molecules, more specifically HTA-2. Mere tumors are described in GENESED records AAYE2805. Those tumour associated antiques are described in GENESED records AAYE2805. YR2A24 and AAYE2825. YR2A29 are derived from Groplakin, such as Oroplakin II, proposition to the area of registed from prostate specific antigen records AAYE2825. YR2A29 are derived from prostate specific antigen frecords AAYE2825. These described in records AAYE2835 are derived from prostate specific antigen (PAA). Those described in records AAYE3835 are derived from COAYE.
  records YF82816 AAY82839 are derived from prostate acid phosphotase (PAP). Those described in records AAY82846 are derived from lactacherin (BA-46). Those described in records AAY82847-Y82854 are derived from Mucin and those described in records AAY82847-Y828854 are derived from Mucin and those described in records AAY82811-Y828854 are derived from Teratocarchoma derived growth factor (CRIF10-1).
  Tumor associated antigen peptides, especially derived from uroplakin,
   discoldin I, factor VIII like domain, epidermal arowth factor; EGF; diabetic retinopathy; rheumatoid arthritis; endometriosis;
  Tuncour associated autien pertides (TAA) may be used for the treatment, prevention and cure of cancer or cancer metastases. The cancer may be breast, bladder, prostate, pancreas, ovary, thyroid, colon, stomach, head or neck cancer or a carcinoma. The tumour associated antiqens are presentable to the immune system by HEA A2
  Pel-1; developmentally regulated endothelial cell locus 1; cancer;
   molecules and are generally between 8 to 10 amino acids in length.
  useful as vaccines to prevent or cure cancers including breast,
   ċ
   Those described in
   bladder, prostate, pancreas, evary, thyroid, colon and stomach
  100.0%; Score 43; DB 21; Length 9;
   Indels
   ; Pred. No. 6.4e+05;
0; Mismatches 0;
   prostate specific membrane antiqen (PSMA).
   Discoidin 1/factor VIII like domain #2.
  Claim 17; Page 100; 113pp; English.
   AAW94690 standard; peptide; 85 AA
   Best Local Simijarity 100.0%;
Matches 9; Conservative 0
  9508-0480229.
  9608-0659235
  05-MAY-1999 (first entry)
  (UYVA-) UNIV VANDERBILT.
  (PROG-) PROGENITOR INC.
                              WPI; 2000-205463/18.
  1 VOFVASYKV 9
  G AA:
  l vqtvasykv 9
  Homo sapiens.
  (5-JHN-1996;
  05-JHN-1996;
  13561-Nin-1668;
  anglodenesis
   02-MAR-1999.
  US5877281-A.
  Synthetic.
  Segnetion
  Query Match
  AAW94690;
  ~
   Matches
  94690 AAM94690
  RESULT
```

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The present sequence represents a discoidin (flactor VIII like domain. The present invention describes developmentally-requiated endothelial cell locus! (Bel 1), Bel has epidermal growth factor like domains and discoidin [//dactor VIII-like domains. The Bel ] protectins have an inhibitiony effect on applicatorsis (blood present provib), this inficial and may be useful clinically to prevent nevascularisation of tissues such as timent nodaices and prevention of metastusces. The anti-andioquenic activity of led [may be used to treat abundand conditions that result from anadioquesis, including cancer, diabetic retinepathy, theumatoid arthritis and endometricasis. Since Del-1 promotes and togenesis it can be seed to treat asset to treat exists. The absolute and beginned health and peripheral vascular disease. Bel its also useful for promoting bone formation, Del-1 binds to alpha Vera 3 integrin, and is an apoptosis
   HMFG, human milk fat globule; antiqen; immanogen; vaccine; virucide; epithelium; tumor; breast cancer; monoclonal antibody; MAb.
   A partial cDNA clone BA46-1 (AAQ91199) for the 46 kbs HMFG antiqen, a major component of the apical surface of the normal breast
  46 kD apparent molecular weight human milk fat globule antiqenused in assays to determine the presence of a cancerous tumour of epithelial origin, and in a vaccine against neoplastic tumours
   useful for treatment of cancer,
  diabetic retinopathy, rheumatoid arthritis and endometriosis
  100.0%; Score 43; DB-20; Benath 85; 100.0%; Pred, No. 0.13; 3re 0, Mismatches 0; Indels
   HMFG 46 kDa antigen C terminal region.
   Ceriani RL, Larocca DJ, Peterson JA;
   Example, Column 39-40, 73pp; English.
  (CANC-) CANCER RES FUND CONTRA COSTA.
  AAR77253 standard; Protein; 217 AA.
  Claim 7; Page 41; 68pp; English.
  93US-0162402.
  Del 1 polypeptide sequences
   94WO-US13967.
  21-NOV-1995 (first entry)
   Conservative
WPI; 1999-189720/16.
  WPI; 1995-215151/28.
  Query Match
Rest Logal Similarity
  85 AA;
  1 VQFVASYKV 9
  03-DEC-1993;
  05-DEC-1994;
  Homo sapiens.
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22 22 2 X 88

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9
   S
          Matches
   AAY94453
  AAR77252
   RESULT
   RESULT
  REAL PROPERTY OF THE PROPERTY 
   XX
XX
  0
  Gaps
   HMFG; human milk fat globule; antigen; immunogen, vaccine, virucide, epithelism; tumoi, breast cancer; monoclosal antibody; MAE.
  A partial cDNA clone 6A46-1 (AAQS1199) for the 40 KDa HMFG antigen, a major component of the apical surface of the normal breast epithelial cell, was obtained by PCR of cDNA from a lactating breast cDNA library.
opithelial sell, was obtained by PCR of cDNA from a lactating
breast cDNA library. The Giterminal region of the encoded protein
showed 43% identity to corresp regions of human Pactor-V and 38%
  46 KD apparent molecular weight human milk fat globule antigen used in assays to determine the presence of a cancerous tumour of epithelial origin, and in a vaccine against neoplastic tumours
  ċ
  100.0%; Score 43; DB 16; Length 217; 100.0%; Pred No 0.33;
   0; Indels
   /label= N-glycosylation_site
160..162
  /label= N-glycosylation_site
181..183
  /label- N-glycosylation_site
  /label= N-glycosylation_site
   Ú; Mismatches
  Peterson JA;
   Example 7; Page 38-40; 68pp; English.
   HMFG 46 kDa antigen partial sequence.
  (CANC-) CANCER RES FUND CONTRA COSTA
  Loration/Qualifiers
   AAR77254 standard, Frotein, 218 AA
   Ouery Match
Best Lonal Similarity 100 ...
Best Lonal Similarity 100 ...
  94WO-11513967
   9308-0162402
  21-NOV-1995 (first entry)
   158
  Larocca DJ,
  156
   WPI: 1995-215151/28
  143 vqfvasykv 151
  217 AA;
  218 AA;
   1 VQFVASYKV 9
   N-PSDB; AAQ91199
  to Factor-VIII.
   Modified-site
  Modified-site
   Modified-site
   Modified-site
   05 DEC-1994;
  33 - DEC - 1993;
   Homo sapiens
  Ceriani RL,
  WO9515171-A
  08-JUN 1995
   Sequence
   Segment
  AAR77254;
```

100.0%; Score 43; DB 16, Length 218; 100.0%; Pred No. 0.34;

Best Local Similarity

Query Match

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0
  Gaps
  Gaps
   HMFC; human milk fat globule; antigen; hæmunogen; vaccine; virucide; epithelium, tumot, breast cancer, monoclonal antibod;; MAb.
  compound of the apical surface of the normal breast epithelial cell, was obtained by PCR and RACE methods. CNA clones can be used to prepare MARS for use in immunisherapy, immonsheraphology, prognosis, disquests, inaging and therapy. Recombinate article can be expressed in prokaryotic of (qfycosylated) in eskuryotic cells.
  46 kD apparent molecular weight human milk fat globule antiqen used in assays to determine the presence of a cancerous tumour of epithelial origin, and in a varrine against neoplastic tumours
  c)
  A complete ofNA sequence for the 46 kFa HMF3 antigen, a major
   100.0%, Secret 43, DR 16, Tempth 387,
1so ow, Pred No e 51,
  e 61,
eas 0, Indels
   Human; lactadherin; MSF-E8; anti-tumour; immune response;
indels
  Janua, Prod s
ive 0, Mismatches
0, Mismatches
   Peterson JA;
   (CANC-) CANCER RES FUND CONTRA COSTA.
  AAP77252 standard; Protein; 387 AA.
   Claim 6; Page 46-47; 68pp; English.
   AAY94453 standard; Protein; 387 AA.
   94WO-US13967.
  930 F (F)402,
  Onery Match
Rest [was] Similarity | Teoms
tea | 9) | Conservative
  (first entry)
   11-SEP-2000 (first entry)
  Human lactadherin protein.
9, Conservative
  Larocca DJ,
  HMFG 46 kDa antigen.
   WP1; 1995 215151/28
   144 vqfvasykv 152
  Sequence 387 AA;
  I VQFVASYKV 9
  N-PSDB; AA091198.
   1 VQFVASYKV 9
  Homo sapiens.
  Carppy 1994;
   05-DEC-1994;
   21-NOV-1995
  W09515171-A.
  08-JUN-1995.
   Ceriani RL,
  AAY94453;
   AAR77252:
```

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09-AUG-2001.
  RESULT
  90
DEFENDED BY STANKEN STANK STAN
   0
   Lactadherin protein was found in exosomes produced by dendritic cells. The protein is inversed in the phase; tests of fatticulate artigens by dendritic cells. Exosomes produced by dendritic cells exposed to tumour antiqens induce potent immune responses. Lactadherin or variants of it may be used in the mediation of an immune response. Variants of lactadherin may be used to infibilities and/or stimulation of the cross priming of antiqens and stimulation of the phagocytosis of antiqens by dendritic cells. Compositions derived from lactadherin can also be used to monitor an immune response, more specifically a CTL (cytotexic T-lymphocyte) response and also to produce CTLs specific for a selected antigen. The present sequence is the human
  Chimeric isolated (human) lactadherin polypoptide that tunctions as an adaptor of cross-priming to eliminate pathogenic antigens, e.g. in
   gabs
  Human: fortal liver; gene expression, single exon muchele acid probe.
   .
C
  Peptide #11766 encoded by human foeta! liver single exon probe.
  100.0%; Score 43; DB 21; Length 387; 100.0%; Pred. No. 0.61; ive 0; Mismatches 0; Indels 0
  (INRM.) INSERM INST NAT SANTE & RECH MEDICALE.
  Tategris_bisding_site
  Secretion_signal
   Location/vualifiers
   /label- Lactadherin
  Example 3; Page 12; 20pp; English.
   ABB44260 standard; Peptide; 52 AA.
  98EP-0402935
   98EP-0402925
   04-FEB-2002 (first entry)
   9; Conservative
  1..23
/Iabel-
exosome; dendritic cell.
  24..387
  /label
   lactadherin protein.
   WPI; 2000-452597/31.
  INST CURIE.
   Rest Local Similarity
   313 vqfvasykv 321
  187 AA;
  N PSDB, AAA27140.
  1 VQFVASYKV 9
  W-200157277 AD
   Homo sapiens.
  24 - NOV - 15098 :
   24 NOV 1998;
   Homo sapiens
  Binding-site
   EP1004664-A1
  $1-MAY 2000.
  Sequence
   Query Match
  ABB44269;
   tumors .
  Pept.ide
   Protein
  Matches
   ABB44260
   Š
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measuring haman gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting necasuring and displaying quart expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from NIPO at the wipe int/published_pri_sequences.
   Protein #9130 encoded by probe for measuring heart cell gene expression.
   Gaps
   ...
   Human geneme-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver -
  The invention relates to a single even nucleic acid probe for
   Claim 27; SEQ ID NO 36895; 639pp + sequence listing; English.
  Human, gene expression, healt, microarray, vascular system, cardiovascular disease, hypertension, cardiac arrhythmia; congenital heart disease.
   83.7%; Score 36; DB 22; Longth 52; 77.8%; Pred No. 2.2;
13vc 1; Mismatches 1; Indels
  Penn SG, Hanzel DK, Chen W, Rank DR;
  ABB27131 standard; Protein; 52 AA.
  (MOLE-) MOLECULAR DYNAMICS INC
   20000S-0234687.
20000S-0236359.
  04 FUB 2000; 2000US-0180312.
26-MAY-2000; 2000US-0207456.
   2000US-0608408.
   2000US-0632366.
   04-00T-2000; 2000gp-0024263.
  30-JAN-2001; 2001W0-US00666.
  200008-0236359.
30-JAN-2001; 2001WO-US00669.
   2000018-0608408.
   2000008-0632366.
  23-JAN-2002 (first entry)
  7; Conservative
   WPI; 2001-483447,752.
   Rest Local Similarity
  23 vqfvgsykl 31
   F.2. AA;
   1 VQFVASYKV 9
   W0200157274-A2.
  26-MAY-2000;
30-JUN-2000;
   27-SEP-2000;
   21-SEP-2000;
27-SEP-2000;
  Homo sapiens
   03-AUG-2000;
   04 - FEB 2000,
   03-AUC-2000;
   30-JUN-2000;
  21-SEP-2000;
   ABB27131;
  Sequences
  Ouery Match
  Matches
  ABB27131
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epitepsy and cancers. The present september is a protein enoughd by mean
  Quer, Mater
  AAM65298
   brains
                       brains
  RESULT 10
   Matches
   AAM65298
  <u>∑</u>
  ö
  measuring human gene expression in a sample derived from human heart (see ABA2135 ABA41305). The present sequence is a protein encoded by one such grown expression in sample expecting, measuring and displaying gone expression in samples derived the human heart via microarrays. By measuring year expression, the prodes are useful for producting, diagnosing, grading, staning, mentioning and prognesing diseases of the human heart and vascular system e.g. cardiovascular diseases of the hypertension, cardiac arrhythmias and congenial heart disease. Note. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formet directly from when
  Human biain expressed single exon probe encoded protein SEQ 1D Nu: 39428.
   Single exon nucleic acid probes for analyzing gene expression in human
  Gaps
   The present invention relates to single exon nucleic acid probes for
  Human; brain expressed eyes, gene expression malysis, pecke, microania, Alcheimet's discuse, multiple scleresis; schipophrenia,
  0;
  83.7%; Score 36; DB 22; Length 52;
77.8%; Pred. No. 2.2;
   i, Indels
   at ftp.wipo.int/pub/published_pct_sequences.
   1, Mismatches
  Claim 15, SEQ ID No 28901, 530pp, English.
  Chen W, Rank DP;
   Rank CR,
  AAM58323 standard; Protein; 52 AA.
   (MOLE-) MOLECULAR DYNAMICS INC.
                     (MOLE-) MOLECHTAR DYNAMICS INC
   Cher W,
04-OCT-2500; 2000GB-0024263.
  21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
  2000GB-0024363.
  04-FEB-2000; 2000nS-0180312
  2000US 0207456.
   20408-0698408.
   2000005-0632366.
  30-TAN-2001; 2001WO USD0567
   05-NOV-2001 (first entry)
   Conservative
  Penn SG, Hanzel DK,
   Hangel DK,
   WPI; 2001 483446/f2
  WFI; 2001-488899/53
   Best Local Similarity
   23 vqfvgsykl 31
   1 VOFVASYKV 9
   epilepsy; cancel.
   W0200157275-A2.
  26-MAY-2000;
   House sapiets
   30- TUN-2000;
  03-A93-2000;
   04-0CT-2000;
   09-AUG-2001.
  Sequence
  AAM58323;
  Query Match
   Penn SG,
  hearts
   Matches
  AAM58323
   RESULT
δλ
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÷
   probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and impreved treatment of nervous grystem diseases such as Alzheiher's disease, muittiple seletosis, schizophrenia, epistepsy and cancers. The present sequence is a protein encoded by one of the probes of the invention.
   brain. They can be used to medsure gene expression in brain cell samples, which may enable the disquests and leproved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
  Human brain expressed single exon probe encoded protein SEG ID NO: 37403.
   probes which are derived free genemic sequences expressed in the human
Single exon nucleic acid probes for analyzing gene expression in human
  Single exen nucleic acid probes for analyzing gene expression in human
  Saps
  The present invention provides a number of single executable and
   The present invention provides a number of single exon nucleic acid
  Human; brain expressed exon; gene expression analysis; prote; microarray; Alchelmer's disease; multiple schetosis; schizophrenia;
   Example 4, SLy iD No. 30428, 650pp + Sequence Listing, English.
  -5
  Example 4, SEQ ID NO. 37403, 650pp + Sequence Listing; English.
  Score as, De JJ, Dength 52;
Fred, No. 2027
1: Mismatches 1: Indets
   Chen W, Runk DR;
  AAM65298 standard; Frotein; 52 AA.
  (MOLE-) MOLECULAR DYNAMICS INC
   83.7€,
77.8€;
   sa-JAN-Zaei; zealWa-Usausé7.
   04 FEP 2900; 2030US 0180312.
   .ngngs-g_07456.
zggdds-gb08408.
   03-AUG-2000; 2090US-0632366.
  2020018-02-04-897.
2020018-02-03-08-897.
   2000GB 0024263.
   (first entry)
   Conservative
  Penn SG, Hungel DK,
  WPI, 2001 483446/52
  Cocai Similarit_T es 7_T conserv
   epilepsy; cancer.
   1 VOFVASYKV 9
  WO200157275-A2.
   "TO TO SAM . "TO TO TO TO
   30-JUN-2000;
  (am)7 - JHS - [7]
   27 - SEP - 2909;
   04 OCT 2009.
   00 אייה 2001.
   Seguence
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Sequence
                                      AAM21889;
  Penn SG,
   AAM38215;
   Query Match
   ON AUG
  RESULT 12
   Matches
             AAM21889
   AAM38215
  0
   0
  The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure quie expression in bone marrow samples, which may number the improved distincts and treatment of cancers such as lymphoma, lenkaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention
   0; Gaps
  Gaps
   Human: bone marrow expressed exen; gene expression analysis; probe; microarray; cancer; loukacmia; lymphoma; myeloma.
   Human bone marrow expressed probe encoded protein SEQ ID Not 38303.
   ò
   Human genome-derived single exon nucleic acid probes useful for
  Example 4, SEv ID NO. 38303, 658pp + Sequence Listing; English.
   Score 36: DB 22: Longth 52:
Prod No 2 2:
1; Mismatches 1: Indels
   83.7%; Score 36; DB 22; Length 52;
77.8%; Pred. No. 2.2;
  1; Indels
  1, Indels
  analyzing gene expression in human bone marrow
   1, Mismatches
  Chen W, Bank DR
  AAM77997 standard; Protein; 52 AA.
  (MOLE-) MOLECULAR DYNAMICS INC.
   2000US-020466
2000US-0608408.
2000US-02346
the probes of the invention.
   83.78;
77.8%;
   もっとりをごけ・5110でしこ
  20000R 0024263
   30-JAN-2001; 2001W0-HS00668
   $5 FEB-2000 - 20005-01803-00
  (first entry)
   Conservative
   Conservative
  Penn SG, Hanzel DK,
                                     Onery Match
Host Local Similarity
Thosa 7; Conserva
   WPI; 2001-488900/53
   Best Local Similarity
   23 vqfvqsykl 31
                   52 AA;
   1 VOFVASYKV 9
   1 VQFVASYKV 9
   W0200157276 - A2.
   21-SEP-2000;
27-SEP-2000;
  06-NOV-2001
   Homo sapiens
   26-MAY-2000;
30-JUN-2000;
  03 - Ams - 2000;
  04-00T-2000;
   09-AUG-2001.
                     Sednence
  Sednence
   AAM77997;
   Query Match
   Matches
  AAM77997
  RESULT
2 × 2
   a
   ó
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The prefect insertion relates to haman simily exam nuclei, acid probes (SER), see AALIBOSE AALIBOTO). The present sequence is a petition concord by one such probe. The SERPS defined from the late of the concord of the used to probe a single examination of the which can be used to measuring human gene expression in a sample derived from human ecryteal epithelial cells. By measuring dene expression, the probes are therefore useful in grading and/or stading of deserves of the vervix, notably
  Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
  Portide #122F2 ergoded by probe for measuring placental gene expression.
  Peptide #8323 encoded by probe for measuring cervical gene expression.
   Gaps
  Probe; human; microarray; qene expression; cervical epithelial cell;
   Human genome-derived single exon machele and probes useful for analyzing gene expression in human cervical opithelial cells -
  ċ
   DB 22; Length 52;
  1; Indels
  at ftp.wipo.int/pub/published_pct_sequences.
  Pred. No. 2.2;
1, Mismatches
   Claim 27, SEQ ID No 26715; 487pp; English.
   Score 46;
   Chen W. Rank DR:
AAM21889 standard; Protein; 52 AA.
  AAM38215 standard, Protein; 52 AA.
   (MOLE-) MOLECULAR DYNAMICS INC
   84.7%;
   20000US-0180312.
2000US-0207456.
   2000US-0234687.
   2000US-0236359.
   200008-0024263.
   30-JAN-2001; 2001WO-US00670.
  2000US-0608408
   77.88;
  12 Off 2001 (first entry)
   17-0CT-2001 (first entry)
  Conservative
  Banzel DK,
  WPI; 2001-488901/53.
   Local Similarity
es 7, Conserv
   52 AA;
  23 vqfvgsykl 31
  1 VQFVASYKV 9
   cervical cancer.
   cervical cancer.
  WO200157278-A2.
   03 APO 2000;
21 SEP-2000;
27 SEP-2000;
  Homo sapiens.
   04-FEB-2000;
26-MAY-2000;
  30-JUN-2000;
   04-001-5000;
  09-AUG-2001.
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05-JUN-1996;
         07-JUN-1995;
  AAW10364;
   Sednence
   Boyan B,
   Pept.ide
  Protein
  Mus sp
   Domain
   Domain
  Domain
   RESULT 15
   AAW10364
ŝ
  0
  The present invention relates to single exon nucleic acid probes (SENP: see AAT31315-AAT37546). The present sequence is a peptide encoded by one such probe. The probes are useful for preducing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antegeral dispessis of human genetic disorders.
   Gaps
  Delin developmentally regulated enderballa) and larga 1, eacoes, discoidin 1; factor VIII-like domain; epidermal growth factor; EGF; disketic retinopathy; theumatoid arthritis, endomatriasis,
   0;
   Human genome derived single exon nucleic acid probes useful for
  Score 36, DB 22, Length 52, Pred. No. 2.2, 1; Mismatches 1; Indels
  1; Indels
       Probe; microarray; human; placenta; antenatal diagnosis; genetic disorder.
  analyzing gene expression in human placenta
   Claim 27; SEQ ID No 38484; 654pp; English.
  Penn Sd. Hanzel DK, Chen W. Rank DR;
   Human milk fat globule protein MFG-E8.
  AAW94697 standard: Protein; 221 AA
   (MOLE-) MOLECULAR DYNAMICS INC.
   2000US 0207456.
2000US-0608408.
2000US-0632366.
  83.78;
   20000S-0180312.
  96US-0659235.
   6319100-800000
  30-JAN-2001; 2001WO-US00663
   2000005-0234687
  Sounds notable
   (First entry)
   7; Conservative
   WPI: 2001-488897/53
   Query Match
Best Local Similarity
  23 vqfvqsykl 31
  1 VOFVASYKV 9
   WO200157272-A2.
                                Homo sapiens.
  30-JUN-2000;
   04-FEB-2000;
   2000;
  21-SEP-2000;
  angiogenesis
  Homo sapiens
   05-JUN-1996;
   27-SEP-2000;
04-007-2000;
  2000;
  US5877281-A.
  09-AUG-2001
  02-MAR-1999
  AAW94697;
   Sequence
   Matches
   AAW94697
qq
  Š
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The prosent sequence represents bomas will fat globale protein MFG-FB, which has bomology to the developmentally-regulated endothelial cell covers [Gerl B. The Del I protein has epidermal growth tactor (EGP) like demains and discould [Jacker VII] like domains. The Del-1 proteins have an inhibitory effect on anylogenesis (blood vessel growth), this activity may be useful elinically to present neowascularisation.
   tissues such as tumour nodules and prevention of metastasse. The anti-
anglopenic activity of Del 1 may be used to treat abnormal conditions
that result from anglopenesis, including cancer, diabetic retinopathy,
heumatoid arthrilis and endometriosis. Since Del 1 promotes
   anglogenesis it can be used to treat cardiac ischaemia, thrombotic stroke, wound healing and peripheral vascoiar disease, ixel-1 is also axeful for promoting bone tormation. Deli binds to alpha V beta 3 integrin, and is an apoptosis inducer.
   Mouse developmentally-requlated endothelial cell locus: | protein.
   "epidermal growth factor-like domain 1"
  "epidermal growth factor-like domain 2"
   Dei 1 polypeptide sequences—— aschul for treatment of vanced diabetic retinopathy, rheumatoid arthritis and endometriosis
  Score 46: UB 20: Length 321;
Fred. No. 14;
1. Mismatches 1. Lebels
  siqual transduction; cancer: tumour marker; andiogenesis; diabelle retinopathy, rhemmatoid arthritis, endometriosis; catidiac ischaemia; stroke; vascular discose; wound healing; valuerary; base formation; diagnosis; therapy.
   Del 1, derelopmentally requiated endothelial cell locus-li
   Supancie TJ:
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  Example, Column 63-64; 73pp; English.
  7. 17 je n, Zmalifiers
1...23
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   78..116
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96US-0659235.
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  03-MAY:1997 (first entry)
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  /note
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/label: EGF-3

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Murine Del-1 (AAW10364) is the polypeptide product of the murine developmentally regulated endothelial cell locus-1 (del-1) qene (AAR7388). It shows 94% amino acid homology to the human Del-1) profein (AAW10365). Structurally, members of this novel qene family contain 3 EGF-like domains and 2 discoidin L/lactor VIII-like domains. Del 1 is expressed in endothelial and certain tumour cells. Its ability to inhibit vascular formation allows its used as an anti-anglogenic agent. It can be used as a tumour marker, to identify Del-1 binding pariners, and to modulate endothelial cell qrowth and blood vessel formation. Recombinant Del-1 can be produced in transformed host cells utilising vectors incorporating del-1 nucleic acids.
  New developmentally requiated endothelial cell locus-1 (del 1) gene - used to develop prods. for the diagnosis and treatment of cancer and conditions involving abnormal anglogenesis
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/label- Discoldin-2
/note= "discoldin 1/factor VIII-like domain 2"
Znote "epidermal growth factor-like domain 3"
  Hogan B, Quertermous T, Snudgrass HR, Zupancie TJ;
  Claim 3; Fig 6; 137pp; English.
  96WO-US09456.
  95US-0480229.
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  07-JUN-1995;
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  19-DEC-1996.
   Domain
                 Domain
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Job time: 372 sec
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1 VUFVASYKV 9

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Gaps

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Query Match 83.7%; Score 36; DB 18; Length 480; Hest Local Similarity 77.8%; Pred. No. 22; Matches 7; Conservative 1; Mismatches 1; Indels

GenCore version 4.5 Cepyright (c) 1993 - 2900 Compugen Ltd.

 protein search, using sw model OM protein September 5, 2002, 15:28:53; Search time 69.78 Seconds (without alignments) 12:393 Million cell updates/see Pun on:

US-09-744-804-40 1 VOEVASYKV 9 Perfect senter Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283138 seqs, 96089334 residues Searched:

Total number of hits satisfying chosen parameters.

Maximum DB seq length: 200000000 Minimum DB seq length: 0

Listing first 45 summaries Post processing: Minimum Match 0%

pirl:\* pir2:\* pir4:\* PIF-7:.\* Patabase

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the test of exact distribution.

#### SUMMARIES

|                    | Description | milk fat globulo o | prote               | pp47 protein - pig | fat globul | ordo    | PAS 6/7 protein pr |        | probable protein k | - 13   | pol protein simi | rare lipoprotein R | ptologist ing though | hypothetical prote | integral membiane | glutamatetena ji | protoporphyrin 1X | hypethetical prote | probable xylogluca | xyleqlucan endo-1, | Yeast translation | membrane bound 17t. | ,        |        | 6 phospho beta alu | Egrethetical prote |          | DNA primase U0191 | hypelhetical proto | spindle assumbly o |
|--------------------|-------------|--------------------|---------------------|--------------------|------------|---------|--------------------|--------|--------------------|--------|------------------|--------------------|----------------------|--------------------|-------------------|------------------|-------------------|--------------------|--------------------|--------------------|-------------------|---------------------|----------|--------|--------------------|--------------------|----------|-------------------|--------------------|--------------------|
|                    | ID          | A47285             | · 4                 | ~                  | A36479     | \$65138 | 874211             | T46975 | T43420             | S15566 | S18738           | BR2250             | T40730               | B82789             | T03110            | SARSES           | HE 1479           | 7878 di            | G85040             | ्र वृष्ट्र ३ व     | AE1392            | A82588              | 377778   | JC7189 | AF0153             | 120121             | T25740   | E92884            | T2587              | 104224             |
|                    | Length DB   | 21.8               | ) (-)<br>(-)<br>(-) | 60                 |            |         |                    |        |                    |        |                  |                    |                      |                    |                   |                  |                   |                    |                    |                    |                   |                     |          |        |                    |                    |          | 641 2             |                    | 1216 2             |
| æ 0<br>0<br>0<br>0 | _           | 100.0              | 90.7                | 83.7               | $\sigma$   | 76.7    | 175                | 76.7   | 74.4               | 74.4   | ٠.               | 72 1               | 72.1                 | c i                | 72.1              | 01               | 0.1               | O.                 | o,                 | J.                 | 6. e.g            | ٠.                  | Ġ,       | ٣.     | œ.                 | ٠.                 | Ġ        | e : 69            |                    | æ e:J              |
|                    | Score       | 43                 | . E                 | 36                 | 34         | 33      | 33                 | 33     | 32                 | 32     | 32               | 31                 | 31                   | 3.1                | 3.1               | 31               | 3.1               | 30                 | 30                 | 30                 | <b>;;</b>         | O.S.                | 07       | 30     | 30                 | 30                 | <u>က</u> | 30                | C)<br>M            | S                  |
| 2000               | No.         |                    | (1)                 | 9                  | 4          | 5       | 9                  | 7      | æ                  | S      | 10               | 11                 | 12                   | 13                 | 14                | 15               | 16                | 17                 | 18                 | 5                  | C)                | <u>:</u>            | C1<br>C1 | C.I    | 74                 | G.4<br>G.5         | 9.7      | 27                | d:<br>C1           | នី                 |

| protein disulfide- | discoidin I chain | discoidin I chain | hypothetical prote | hypothetical prote | discoldin I chain | discoidin I chain | cultate/thiosultat | sulfate transport | sultate transport | sulfate transport | sulphate transport | xyloqlucan endo-1, | xyloqlucan endo-1, | Eypothetical prote | yeast translation |
|--------------------|-------------------|-------------------|--------------------|--------------------|-------------------|-------------------|--------------------|-------------------|-------------------|-------------------|--------------------|--------------------|--------------------|--------------------|-------------------|
| T17951             | DIDOID            | BO 5382           | AF 3009            | H98274             | DLDOIA            | DLDO1C            | ORFICISIT          | G91040            | AITÚ 366          | H85885            | AH9811             | A495 39            | T10523             | T26873             | AC1767            |
| .∼1                |                   | 64                | ~                  | <b>C</b> 3         |                   |                   |                    | ÷4                | : 1               | C1                | ্য                 | c i                | C1                 | <b>∵</b> ∓         | Ċ1                |
| 106                | 149               | 143               | 187                | 195                | *S2               | 253               | 17.7               | 277               | 277               | 277               | 277                | 292                | 260<br>2           | 338                | 345               |
| 67.4               | 67.4              | - 1               | 67.4               | 67.4               | 67.4              | 67.4              | 67.1               | 67.4              | 67.1              | 67.4              | 67.4               | 67.4               | 67.4               | 67.4               | 67.4              |
| 58                 | 58                | ೧                 | 58                 | 67                 | රුදු              | 53                | 62                 | 5.0               | er<br>Fu          | 53                | 67                 | 62                 | ရှိချ              | 59                 | 53                |
|                    |                   | 2                 |                    |                    |                   | <del>3</del> 6    | 3.7                | 38                | 5                 |                   |                    | <u> </u>           | ~                  |                    |                   |

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Rilarocca, D., Peterson, J.A., Orrea, R., Koniyoshi, J., Bistrain, A.M.: Ceriani, R.I. Cancer Res. 51, 4994-4998, 1991 A.Titler, A.M.: 46,000 human milk lat globale protein that in M.1855, supressed in huma A.Reference number: A47285; MOID:91371351

A;Status: preliminary

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Gaps 0: 100.0%; Score 43; DB 2; Tength 218; 100.0%; Pred. No. 0.067; 0; Indels 0; Mismatches guery Match
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b.c 9; Conservative

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144 VQFVASYKV 152 a

1 VQFVASYKV 9

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JC4915

ags protein precusor - rat NALternate names: Oracetyl Gd3 qanalioside C.Species: Pottus norvegicus (Nerway rat) C.Bale: 26-59-1996 #Seeprotein-region Of Nev-1996 #Lext\_change 20 Jun 2000 C.Accession: JG4915 E.Ggura, K.: Nara, K.: Matanabe, V.; Kohno, K.; Tai, T.; Sanai, Y B.cohne, Blochys, R.s. Cadmus, 225, 932-938, 1996 A.Title: Closisq and expression of chan for Glacetylation of GD3 qanalioside, A.Peference number: JG4915, MPTP-06274422

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A. Stoss references. LSBs. 284058, NIB. 416.20006, PIDN. BAA12210.1, FID. 416.20007

Comment. This protein is required for the O-acet, Paties of distribusiationide stall A, Experimental source: CST cell

C. Senetics:

C.Superfomily, milk fat alokule protein, discoldin Lamino terminal homology, NOF hom F.1 21/Franin, Signal property \*Status prodicted STG. F.28-CC,Sumain, EGF hamology SEG12

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A, Experimental source, milk
  Quei/ Mutch
Best Local Similarity
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R;Mather, I.H.;
  A; Pesidues:
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   RESULT
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  REBUSTIO, M.: Vogel, T.: Calvete, 1-T; Thele, H.H.: Schmidtke, J.: Matsuda, T.: Toepto
Biol. Reprod. 58, 1957-1964, 1998
AFFILL: Molecular cloning and characterization of P47, a novel boar sperm associated zo
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   Ristubbs, J.D. Lokutis, C., Sieger, K.L., Bui, A., Yezaki, D., Stinivasan, U., Purry, or
Proc. Noti. Arad. Sci. D., S. A. 87, 8417-8421, 1990.
Affilio: cinNa cloning of a meuse mammary epithelial cell surface protein reveals the exi.
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  c
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Py68-107/Remain. ESF homology >802>
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F/27: 477/Semain discoidin caming forminal homology
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   Rjaoki, N.; Kishi, M.; Taniquehi, Y.; Adachi, T.; Nakamura, R.; Matsuda, T.
Biochim. Biophys. Acta 1245, 385-391, 1995
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Ajacicule 1978: protein
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  R)Mather, I.H.: Banghart, L.R.; Lane, W.S.
Biochem. Mol. Biol. Int. 29, $45-554, 1993
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Eur. J. Riochem. 240, 628-636, 1996
  ÷
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  S74211
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  Conservative
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pol protein - simian toamy virus
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C,Species: simian foamy virus
C,Baccies: 20-Peb-1995 = acquence_revision 20-Peb-1995 = text_change [2 Apr-1995
C,Recession: S1556
E,Mergia, A., Shaw, S.E.S., Jonathan, L.E., Paul, L.A.
Sabaitted to the FMBL Data Library, March 1991
A,Description: Sequence relationships of simian framy mirus type [ with busan toamy v
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  Comperfamily, analyment Sev. The ar Tyrespecific protein bisases, protein binase bom 
C:Reywords: phosphotransferase
A.Ectronic masker, 221737
A.Accession: T37688
A.Cristor & Frontain 19788
A.Cristor & Frontain 1978
A.Millian 1978
A.Millian 1945 ADRV
A.Millian 1978
A.Milli
  ó
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CiDate: 19 Mar 1997 #sequence_revision 24-7ul-1947 #text_champe 31-ret 1997
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  R;Kupicc, J.J.; Kay, A.; Hayat, M.; Ravier, R.; Peries, J.; Gallbert, F.
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A.R. Mare and C.S. Methanococcus maripalates
A.C. Coccas references: PMPI AF000MR24: NID::92645498; PIDM:AAB87110.11; PID::92645489
C.G. Genetics:
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F19 427/Product. FAS 6/7 property #status experimental SMATA
F19 427/Product. FAS 6/7 property #status experimental SMATA
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F10 8 269 427/Fig. 1 animo terminal Some long SMIA
F10 8 269 427/Fig. 1 animo terminal Some long small status predicted
F12 8 51 49 58 46 77 77 9 49 66 205/518 115 65 bodds. #status predicted
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F13 4/Fig. 1 animo terminal F13 (covalent) #status experimental
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  Caps
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submitted to the EMBL Data Library, August 1997
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   Classion Tublio
R. Wakano, Y., Yoshida, Y., Yamashita, Y.; Koga, T.
Biochim Biophys, Arta 1442, 409-414, 1998
Alrichae ene cluster for 6-deoxy-L-talan synthesis in Actinobacillus actinomycotom Alrichae number: 214111, Mill 99023768
A. Accession: T00110
                                Riamonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq
Nature 406, 151-157, 2000
  Actinobacillus actinomycetemcomitans
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C.Speches: Actinobacillus actinomycetemecomitans
C.Fato - 22 lum 1999 #sequenci_rojsica 22:im 1999 #fext_change 21**ul-2000
   glutamate--fRNA ligase (FC 6 1 1 17) - Racillus stearothermophilus
Ablternate names: glutamay1-tRNA synthetase
C.species, Bacillus stearothermophilus
C.bate: 30-Jun-1992 #sequence_revision 30 Jun 1992 #text_charge 18-Jun-1999
  Gaps
   Gaps
  A;Title: The genome sequence of the plant pathogen Xylella fastidiosa. A;Reference number: A82515; MUID:20365717
A;Note: for a complete list of authors see reference number A59328 below
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   .;
o
  Score 31; DB 2; Length 344;
Pred. No. 51;
2, Mismatches 1; Indels
   72 1%; Score 31; PR 2; Length 308; 85,7%; Fred. No. 46;
  0; Indels
  1; Mismatches
  Query Match 72.1%;
Best Local Similarity 62.5%;
Matches 5, Conservative
  Conservative
   Local Similarity
nes 6; Conserv
  A; Molecule type: DNA A; Frsidnes, 1 308 -SIM:
  A; Contents: annotation
   202 QFIVTYKV 209
   A; Status: preliminary
  2 QEVASYKV 9
   A;Accession: B82789
  3 FVASYKV 9
  C. Accession - Record
C;Accession: B82789
  A; Gene: XF0584
   Quory Match
   RESULT 14
  RESULT 15
  Matches
   SYBSES
   Ajčross references. GB.AECO4127, GR AECO (M.C.) NIO genesavy PiFNAAF94116 1; GSPBF-CNEOT
AjExperimental source, serogroup of, strain NiGG1, biolype El for
  RiHeidelberg, J.P.; Bisen, J.A.; Nelson, W.C.; Clayton, P.A.; Cwinn, M.L., Dedson, P.J. chardson, D.; Ennolaeva, M.D.; Vanathevan, T., Bass, S., Qin, H., Dragei, T., Sellets, L., R.R.; Mckalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
  A)Residons (17217 - LYN)
A)Cross-references: EMBL ALG33388, PIDN CAAZ1890.1; GSPDR:GNGOGA7; SPDR:SPRDR87.056
A)Experimental source: strain 972h; cosmid e887
   rare lipoprotein B VC0954 [imported] - Vibrio cholerae (strain N16961 serogroup 01)
   A;Title: DNA Sequence of both chromosomes of the choleta pathogen Vibrio choietae.
A;Reference number: A82035, MUTO, 204000333
A;Accession F82250
   ó
   0
  C.Species: Vibrio cholerae
C.Date: 18-Aug-2000 #soqponco_rovision 20-Aug-2000 #foxt_change 02-Feb-2001
C.Accession ER2260
  probable rna-binding protein - fission yeast (Schizosaccharomyces pombe)
C;Species. Schizosaccharomyces pombe
C;Species. 03-bec-1999 #sequence_tevision 03-ieg-1999 #text_change na-1999
   C)Species. Xylella fastidiosa
C)Date: 18 Ang 2000 #segmrno-_projstan_PhrAng.2000 #text_phange on Ang 2000
   Gaps
   B82789
hypothetical protein XF0584 [imported] · Xylella fastidiosa (strain 9a5c)
   Rilyne, M.; Rajandream, M.A., Harrell, R.G., Lelaure, V., Galibert, F. submitted to the EMBE Data Library, November 1998
A;Reference number 221947
   0;
   0
   72.1%; Score 31; DB 2; Length 213; R5 7%; Prod No 31;
  72.1%; Score 31; DB 2, Length 217; 77.8%; Pred. No. 32;
   0; Indels
   2, Indeis
  A)Status: preliminary; franslated from GR/EMRL/PDRJ
A,Molecule type: DNA
   1, Mismatches
   6, Misautches
  C;Superfamily: rplB lipoprotein
  Ouory Match
Hest Local Similarity 77.8%
Hest Local Similarity 77.8%
   6; Conservative
   Rest Local Similarity
   A; Gene: SPDB:SPBC887.05c
  104 VDHVASYKV 112
  633 VQFIPEYKI 641
  A; Molecule type: DNA A; Residues 1 213 HFT:
  A;Status: preliminary
1 VQFVASYKV 9
   1 VQFVASYKV 9
  Db 113 FVASYRV 119
  3 FVASYKV 9
  C; Accession: T40730
   A; Accession: T40730
   A; Map position: 2
  A; Map position: 1
  A;Gene: VC0954
   Query Match
   PPSHLT 13
   Matches
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   RESULT 11
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Ribreton, R., Watson, D., Taguchi, M., Lapointe, J.

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   Ouery Match 72.1%; Score 31; DB 1; Length 489; Best Local Similarity 62.5%; Pred. No. 73; Matches 5; Conservative 2; Mismatches 1; Indels
  Search completed: September 5, 2002, 15:28:54 Job time: 359 sec
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252 IQFVSQYK 269
  1 VQFVASYK 8
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compagen Ltd

OM protein - protein search, using sw model

September 5, 2002, 15:31-42; Seconds (without alignments) 10.252 Million cell updates/sec Pun on:

US-09-744-804-40 43 1 VQFVASYKV 9 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total sumber of hits satisfying chosen parameters. 105224 seqs, 38719550 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: zounnappuna

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| bescription    | Q08431 homo sapien | an rattu | P79385 sus scrofa | P21956 mus musculu | Q95114 bos taurus | 030522 methanococc |                                              | P23074 simian foam | P22249 bacillus st | Q9ppz6 ureaplasma |               | _          | PúžBBú diotyosteli | F02887 dictrosteli |            | F41032 salmonella | _          |            |           | P11716 choristonea | -          | P28824 XCLUEUS 135 |            |            | P32537 human cuter | off (74 selenterend | Q9nhz6 raenorhabdi | P64388 dresephila | P17082 from Sapara | C66943 agaifex aen | P10301 homo sapien | 33          | PO1119 saccharomyc |
|----------------|--------------------|----------|-------------------|--------------------|-------------------|--------------------|----------------------------------------------|--------------------|--------------------|-------------------|---------------|------------|--------------------|--------------------|------------|-------------------|------------|------------|-----------|--------------------|------------|--------------------|------------|------------|--------------------|---------------------|--------------------|-------------------|--------------------|--------------------|--------------------|-------------|--------------------|
| ID             | MFGM_HUMAN         | MFGM_RAT | MFGM_PTG          | MFGM_MOUSE         | MFGM_BOVIN        | SYK_METMP          | MEK1_SCHPO                                   | POL_SFV1           | SYE_BACST          | PPIM_UPEPA        |               | HEX8_ADEF3 | LISA_FITE:         | DISC DICE:         | CYST_ECOL1 | CYST_SALTY        | FML1_MOUSE | ERF1_BLEAM | SYE_BACHD | TATE NPVOF         | TATP_NPVOP | MPP1_XFNI.A        | TTAL_H"MAN | YOR1_YEAST | Pola_HE?01         | OCRE_SCHMA          | CA2_CAEFL          | RAS2_DPOME        | PFA2_HTMAN         | HISE_AQUAE         | PPAS_HUMAN         | PFAS_MOTISE | RAS1_YEAST         |
| Length DB      | 387 1              | 427      | 409               | 463 ]              | 427 1             | 533                | L. C. S. | 1161               | 489 1              | 641 1             | <br><u>:</u>  | 223        | C 650              | 253                | 277        | 1, 1,00           | 351 1      | 436 1      | 485       | 560                |            | 928 1              | 1170       |            |                    | 130 1               |                    | 192               | 204                | 207 1              | 218 1              | 218         | 309 1              |
| Sucry<br>Match | 100 0              | 90.7     | 83 7              | 6                  | 76.7              | 76 7               | 74 4                                         |                    | 72.1               | α<br>σ<br>Ψ       | <del>-1</del> | 67.1       | 1.7                | 6.7 4              | 67.4       | 67.4              | 67.4       | 67.4       | 57.4      | 6.7 4              | 67.4       | 67.4               | 67 4       | 67.4       | 67.4               | 53                  | 65.1               | 65.1              | ري.<br>اب          |                    | 65 .               |             | 65.1               |
| Score          | 43                 | 39       | 36                | 34                 | 33                | 33                 | 32                                           | 32                 | 1د                 | 3.0               | 7,            | 62         | G.                 | 29                 | 62         | 62                | 62         | 53         | 53        | 62                 | 53         | 52                 | 53         | 23         | e ci               | 82                  | ဆင္ကာ              | ထာင္း             | 28                 | വ                  | 28                 | 58          | 8<br>6<br>7        |
| Result<br>No.  | 1                  | CI       | <b>E</b>          | 4                  | S                 | 9                  | 7                                            | œ                  | σ.                 | 10                | 11            | 12         | 13                 | 14                 | 15         | 16                | 17         | 18         | 19        | 50                 | 21         | 다                  | C4<br>C1   | ci         | ព                  | 95                  | 7.7                | 82                | 59                 | 30                 |                    | S.          | ες<br>(Ε)          |

| 29ubx8 h bcta-1,4- | new Kaditula adon | F49461 edontella s | F12783 kluyyeromye | P22250 hacillus su | Q9559a0 chlamydia p | P38111 saccharomyc | F98110 sameharom/c | Q9pr55 ureaplasma | 110327 caenorhabdi | Q9c005 homo sapien | _              |
|--------------------|-------------------|--------------------|--------------------|--------------------|---------------------|--------------------|--------------------|-------------------|--------------------|--------------------|----------------|
| B4G6_HUMAN         | HNAA_AUTAE        | SECY_CDGSI         | FLF_KIULA          | SYE_BACSU          | RPOR_CHUPW          | ESR1_YEAST         | TELL VEAST         | YORA_UPFPA        | YWR4_CAEEL         | DP30_HUMAN         | DP30_MCUSE     |
| ,_                 |                   | - 1                | - 1                | ۰,                 | ۲.                  | <del>,</del> •     | ٠.                 | ۳.                | 1 1                | -                  | <del>-</del> 1 |
| 385                | .5.<br>.5.        | L1<br>€1           | 4.17               | c)<br>c)<br>₹₹     | 1252                | 2368               | 2787               | or.               | 81                 | 66                 | 66             |
| 65.1               | ا-،<br>د<br>د     | 65.1               | 65.1               | 65.1               | 65.1                | 65.1               | 65.1               | 64.0              | 6.<br>13           | 62.8               | 62.8           |
| C1<br>ග            | x<br>i>.          | æ<br>(1            | 87                 | 87                 | 87                  | 28                 | C+                 | 5 26              | L: 1               | 27                 | 27             |
|                    |                   |                    |                    |                    |                     |                    |                    |                   |                    |                    |                |

## ALIGNMENTS

| RESULT<br>MFGM_H | RESOLD MANAMENT OF THE PROPERTY OF THE PROPERT |
|------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| C :              | MFGM_HUMAN STANDARD; PRT; 387 AA.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| A<br>C           | QUG451)<br>QUG451,<br>O1.00f (D)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
| 14               | or ott 1990 (Met. 94) treated<br>01-NOV-1997 (Roj 35, last sections undate)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
| Ξ                | le-ocr-2001 (Rel. 40, Last annotation update)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
| DE               | Lactadherin precursor (Milk fat globule-EGP factor 8) (MFG-E8) (HMFG)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
| DE               | Medin).                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
| GN               | MFGE8.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| SO               |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| ပ<br>ဝ           | Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| S                | Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
| ×<br>○           |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| Z                | [1]                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
| S.<br>Or         | SEQUENCE FROM N.A.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
| ر<br>ا           | TISSUE-Breast, and Breast Carcinoma;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
| X i              |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| ۲ i              | Couto J. P., Taylor M. P., Godwin S. G., Ceriani R. L., Peterson J. A.;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
| ¥ .              |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| 2                | BA46 reveals an RGD dell adhesion sequence presented on an epidermal                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
| FZ:              | growth lactor-like domain.";                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
| 1 2              | LINA (PIL KIOL 13.2KL-2KN(1940).                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
| 5 C              | A WOULD DOUGHT TO STANDING TO THE STANDING TO  |
| l C              | SUBJURNIE OF TO ACT FROM N.A.<br>GIGGID-Manmant Albah.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| ) A              | .:SEC MARMINI / QIMINI / QIMINI / MEDI INE-01271241 - Dobbod - 1000030 -                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
| 2 2              | ALBERTAN DESTRUCTOR TA TOTAGE PRODUCED TO RESTRAIN A M                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| . K              | 1000                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
| 5                | "A Mr 46,000 human milk for alchaic protein that is bighly expressed                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
| E-               | domains."                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
| <u> </u>         | Canter Res. 51.4994.4998(1991).                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| N                | [8]                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
| Ξ                | TARTAR SECTEMBER AND CHARACTERISTICAL                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
|                  | T1SSUE-M11k;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
| Z.               | MEDEINE 98154524, TubMed 3545276;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| ΚĀ               | Ciuffrida M.G., Cavalotto M., Giunta C., Conti A.,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
| EA               | Godovac:Simmermann J.;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| Ξ                | "Isolation and characterization of fail and truncated forms of human                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
| ΚŢ               | breast cardinoma profein BA46 from human milk fat globule membranes                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
| Ŧ                | J. Protein Chem. 17:143-148(1998).                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
| ΚN               | [4]                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
| (H<br>2E         | SEQUENCE OF 268 317, AND IDENTIFICATION OF MEDIN.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| ΣX               | MEDELNE 99342076, Pubmed 10411933;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
| ΕA               | Hacepayist B., Nacelind J., Stutten E., Westermark G.T., Masshinn C                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
| ΕΛ               | Thereberg L.C., Nordstedt C., Englithem U., Westermark F.;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
| H                | "Medin, an integral fragment of actic smooth massic cail produced                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| ΕŢ               | lactadherin forms the most common human asyloid. ";                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
| =                | PROS. Natl Acad No. II N. A. dr. Krote - Krote (1999).                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| Z                | 0                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| E.               | CHARACTERIZATION.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| Ϋ́               | MEDICINE AZERBARO, PERMANTAR DE SERV.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
| FΑ               | Taylor M.R., Conto J.R., Scallan C.D., Ceriani R.L., Peterson J.A.,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
| F                | "Lactadberia (formerly 8846), a membrane assectated glycoprotein                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
| Ξ                | expressed in human milk and breast cardinomas, promotes Arg G17 Asp                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
| ΚŢ               | (RGD) dependent cell adhesion.",                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
|                  |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |

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between the Swiss Institute of Bioinformatics and the FMBL outstation between the Swiss Institute of Bioinformatics and the FMBL outstation-the Buropan Bioinformatics institute. There are no restrictions on its use by non-profit institutions in tenneshing and this statement is not removed fiscale by and for commercial entities requires a license agreement (See http://www.isb.sib.ch/announcer.
                        Pattus norvegicus (Rat).
Eskargota, Metassa, Cherdata, Cheriata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Redentia; Sciencegnathi; Moridae, Morinae, Pattus.
   N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
EARC8631F78E6047 CRC64;
   F5.8 TYPE C 1.
F5.8 TYPE C 2.
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CELL ATTACHMENT SITE (POTENTIAL).
   High-hom Rigglys. For Compute 22-942-938(1996).
   MEDLINE-96374422; PubMed-8780713;
Ogura K., Nara K., Watanabe Y., Kobno K., Tai T., Sanai Y.;
"Cloning and expression of cDNA for 0-acetylation of GD3
  SWART, SMOOL81, EGF, 2.
SWART, SMOOL81, EGF, 2.
SWART, SMOOL81, EASHS, 2.
PROSTITE, PSOOL985, PGF_2: 2.
PROSTITE, PSOT 985, PASRC_1: 2.
PROSTITE, PSOT 985, PASRC_1: 2.
PROSTITE, PSOT 985, PASRC_2: 2.
SIGNAl, Glycoprotein, Repeat, EGF_like domain, Milk.
   Pred. No. 0.18;
  2; Mismatches
   POTENTIAL.
LACTADHERIN.
   EGF-LIKE 1.
EGF-LIKE 2.
  or send an email to licensewisb-sib.ch).
  500 1000
   Pfam, Progova, E3F, ∠,
Pfam, PP00754; P5_P8_type_C; 2,
PRINTS; PROGOTO; EGPELOOD.
   HSSP; PUU/40; 1IXA.
Interpro; TPP000561; FGF-like.
   47413 MW;
  InterPro; IPR001438; EGF_II, InterPro; IPR000421; PA58_C.
  FMBI; P84068; PAA12210.1; -
  77.88;
  20 78,
   Conservative
   427 AA;
  Query Mater
Best Local Similarity
   :|:|||||||
355 IQYVASYKV 363
   SEQUENCE FROM N.A.
   NCBI_TaxID=10116;
  1 VQFVASYKV 9
  68
73
98
  ganglioside.";
       MFGE8 OR AGS.
  TISSUE=Brain;
  DISCLFID
   PISHIPID
   DISULFID
   OLS/UE IO
  DISTIL
  DISCIPLE
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  PISHIPID
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or send an email to licensealsb-sib.ch).
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   This SWISS-PROI entry is copyright. It is produced through a collaboration
DNA CELL BIOL. 16:861-869(1997).
--I-PUNCTION: MAY BE INVOLVED IN PHOSPHOLIPID BINDING BINDS
STREETIGALLY TO FOTAVIETS AND INHIBERS (IS FELLICATION).
--I-PUNCTION: MEDIAL MAY BE MAIN CONSTITUENT OF AGPITC MEDIAL AMYLOID.
  -!- PTM: MEDIN HAS A RAGGED N-TERMINUS WITH MINOR SPECIES STARTING AT
   Gaps
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  SUBCELLULAR LOCATION: PERIPHERAL MEMBRANE PROTEIN.
TISSUE SPECIFICITY: MAMMARY EPITHELIAL CELL SURFACES AND AORTIC
MEDIA OVEREXPRESSED IN SEVERAL CARCINOMAS.
   01-NVV-1997 (Rel. 35, Last sequence update)
VoMAY-2000 (Rel. 39, Last annotation update)
Lactadherin presurson (Milk fat globule-EGF factor 8) (MFG-E8) (O-acetyl GD3 qanqlioside synthase) (AGS) (MFGM).
   0;
  CELL ATTACHMENT SITE (POTENTIAL).
  Expect, ESE-like desain; Amyleid.
   100 0%; Score 43; DB 1; Length 387; 100 0%; Pred No. 0 018;
   0; Indels
  2EE6571DEC83782D CRC64;
  LACTADHERIN.
LACTADHERIN, SHOPT FOFM.
   *! SIMILAKITY CONTAINS 1 ESE*LITRE FUMAIN *! *! SIMILAKITY: CONTAINS 2 ES/8 TYPE C' DOMAINS.
  0; Mismatches
  Pe,/8 TYPE 0 1
PS/8 TYPE 0 2
   EGF-LIKE
  SMART, SMOO181; EGF; 1.
SMART, SMOO231; FASAC; 2.
PROSITE; PSOU022; ESE_1; 1.
PROSITE; PSO1186; FGF 2: 1
PROSITE; PSO1186; FGF 2: 1
PROSITE; PSO1286; FASEC_1; 2.
PROSITE; PSO1286; FASEC_2; 2.
   Pfam; PF00754; F5_F8_type_C; 2.
   01-NOV 1997 (Rel 35, Greated)
  Interpro, Ippnünski, EGF-like.
Interpro, IPR006421, FASR_C
Pfam, PF06068, EGF, 1.
  43123 MW;
   AMINO ACID 264 AND 273.
   EMBL; U58516; AAC50549.1;
EMBL; S56151; AAB19771.1;
   9; Conservative
  STANDAPD,
   317
67
225
387
  387 AA;
  Best Local Similarity
  313 VQFVASYKV 321
  1 VOFVASYKV 9
  MIM; 602281;
  DISULFID
CAPPOHYD
  MFGM PAT
  DISULFID
   DISHIPID
  DISHIPID
  DISHIFTD
  DISULFID
  CARBOHYD
   CARBOHYD
  CARROHYD
  SECUENCE
   Query Match
  CHAIN
CHAIN
CHAIN
DOMAIN
DOMAIN
  P70490;
  SIGNAL
   Matches
   MFGM_RAT
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              Gaps
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C
PR 1; Length 427;
              O; Indels
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   Submitted (NOV-1997) to the EMPL/GenRank/DDBJ databases
--- FUNCTION: MAY BE INVOLVED IN PHOSPHOLIPID BINDING, ZONA FELLUCIDA-
BINDING PROTEIN.
  Saps
  01-NOV-1997 (Rel. 35, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
30-MAY-2000 (Pel. 39, Last annotation update)
Lactadherin (Milk fat globule-EGF factor 8) (MFG E8) (MFGM) (Sperm surface protein SP47) (PP47).
  BY SIMILARITY.
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RY SIMILARITY.
   Bakanyata, Matázsa, Chordata, Cramiata; Vertebruta, Buteleostomi.
Mammalia: Butheria: Cetarfiodactyla, Suina; Suidue, Sus.
  F5/8 TYPE C 1.
F5/8 TYPE C 2.
CELL ATTACHMENT SITE (POTENTIAL).
   -1- SURPELLULAP LOCATION: PERTPHEPAL MEMBRANE FEOTFIN
-1- TISSUB SPECIFICITY: MAMMARY EPITHELIAL CELL SURFACES AND
   83 78; Score 35, 1841, length 409,
66 78; Pred. No. 0 88;
  0; Indeis
   B0C07AF86029327A (PASA)
   -1- SIMILARITY: CONTAINS 2 BGF-LIKE DOMAINS.
-1- SIMILARITY: CONTAINS 2 F5/8 TYPE G DOMAINS
                                   409 AA.
  3; Mismatches
  EGF like domain.
                                   PRT;
  EMBL: Y11683; CAA72379.1; --
HSSP: P00740: IEDM
InterPro: IPR000561; EGF-11ke.
InterPro: IPR000421; FASB_C.
Pfam: PF00A08; EGF: 2.
Fiam: PF00A08; EGF: 2.
SMART: SM00181; EGF: 2.
SMART: SM00231; FASB_C.
PPCSITE: ES0A126; EGF: 2.
PPCSITE: ES0A126; EGF: 2.
PPCSITE: ES0A126; EGF: 2.
PPCSITE: PS0A1265; EASB_C.
PPCSITE: PS0A1265; EASB_C.
PPCSITE: FS0A1265; EASB_C.
PPCSITE: FS
   45725 MW,
  6) Conservative
                                   STANDARD;
  88
403
403
69
17
29
40
   Glycoprotein, Repeat,
DOMAIN 2 4
   Query Mater
Best Local Similarity
  129 AA.
  SEQUENCE PROM N.A.
   Sus scrofa (Pig).
   SPERMATOZOAN.
  NCB1_TaxID-9823;
   TISSUE=Testis;
   Fnsslin M.A.
                             MFGM_PIG
  CARBOHYD
  DISULFID
   DISULFID
   DISULFID
   DISULFID
   DISULFID
  CAPPOHYP
   SEQUENCE
  MFGE8
  Matches
MFGM_PIG
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335 IQYVAAYKV 343
1 VQFVASYKV 9
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   -1- FUNCTION: MAY BE INVOIVED IN PROSPHOLIPID BINDING. ZONA PELLUCIDA-BINDING PROTEIN.
             P21956, P97800; 01-Aug-1991 (Rel. 19, Created) 01-Aug-1991 (Rel. 19, Last sequence update) 15 cyr. 1991 (Pol. 19, Last unctation update) 15 cyr. 1991 (Pel. 40, Last unctation update) 15 cyr. 1991 (Pel. 40, Last unctation update) (Argument precursor (Milk fat globule-EGF factor B) (MFG-EB) (MFGM) (Sperm surface protein SP47) (MP47).
  -1- DEVELOPMENTAL STAGE: MRNA EXPRESSION IS DETECTABLE IN MAMMARY TISSUE PROM NONPERGNANT AND MALE & MAXIMAL IN THE LACTATING GLAND.
-1-SIMILARITY: CONTAINS 2 PSF-LIKE COMAINS.
-1-SIMILARITY: CONTAINS 2 PSF 3 TYPE C DOMAINS.
   "CDNA cloning of a mouse mammary epithelial cell surface protein
reveals the existence of epidensal growth factor like domains linked
to factor VIII-like sequences.";
  Mus musculus (Mouse).
Lukaryola, Motasca, Chordata, Cramiata, Vertebrata, Eureleostomi;
Mammaiia, Eulkeria, Rodentia, Sciurognathii, Muridae, Murinae, Mus
   -!- TISSUE SPECIFICITY: MAMMARY EPITHELIAL CELL SURFACES AND
  TISSUE-Mammary gland;
MEDLING-91046508; nubmod-2122462;
Stubbs J.D., Lokutis C., Singer K.L., Bui A., Yusuki D.,
Srinivasan U., Farry G.;
  Submitted (NOV 1997) to the EMRI/GenRank/UPBI databases
  -!- SITECELLULAR LOCATION: PEPIPHEPAL MEMRSANE PROTEIN.
   SWART, SWO181, ESP, 2.
SWART, SWO331, PASE, 2.
FROATT, SWO331, PASE, 2.
FROATTE, FSO131, PASE, 2.
PROSTER, PSO1285, FASE, 2.
PROSTER, PSO1285, FASE, 2.
SIJAAL, STYCKFOLDER, PASE, 2.
SIJAAL, STYCKFOLDER, PRESENT, BOLLIN, MILE.
   Proc. Natl Acad. Sci II S A 87:8417-8421 (1990).
463 AA
   F5/8 TYPE C 1.
F5/8 TYPE C 2.
   SEQUENCE FROM N.A., AND SEQUENCE OF 23 35.
   LACTAPHEPIN.
   EGF-LIKE 1.
EGF LIKE 2.
  or send an effort to tibers. Fish situah).
PRT;
  MGD, MGJ:102768; MFGR8.
Interpro; IPP000561; EGF-11ke.
Interpro; IPP0004248; EGF_II.
Interpro; IPP0004248; FASB_C.
Fram, PF00008; EGF_2.
   EMBL; M38337; AAA29534.1; ".
  SEQUENCE OF 23-463 FROM N.A.
  Y11684; CAA72380.1; -.
  PRINTS, PROUDID; EGFBLÖOD.
STANDARD;
  C1 (5)
   6.1
  FIR; A36479; A36479.
HSSP; P00740; JEDM
  NCBI_TaxID=10090;
  SPERMATOZOAN.
   IISSUE-Testis;
  Ensslin M.A.;
MFCM_MOUSE
   CHAIN
  SIGNAL
  DOMAIN
   DOMA I N
   MFGE8
                                    듐트림골문용왕왕홍교교요조순호합뇨로교교교요오는등등등등등등등등등등등등등등등등등등원음병속점점점점점점점점점점점로교교교교
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   Sales
   SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND CARROHYDRATE-LINKASE SITES.
STRAIN-HOLSTEIN, TISSUE Mammary gland;
MEDLINE-97008954; PubMed-8856064;
   16-org-2001 (Poi 40, East amoustion applator) (MPG-ER) (MPG-ER) (MPG-ER) (MPG-ER) (MRPS-ZFS) (PAS-ER) (MRPS-ZFS) (PAS-ER) (MPG-ZFS) (PAS-ER) (MPG-ER) (MPG-E
  "Melocalar clearing of glyrag teit antipag MRF7. The respicted by monoclonal antibodies raised against bovine milk fat globule
  "characterization of glycoprotein PAS-5/7 from membranes of bound milk fat globules":
   Gnkaryota, Metasou, Chordata, Graniata, Vertebrata; Euteleostomi,
Mammalia; Eutheria, Cetartiodactyla, Ruminantia; Pecora; Bovoidea;
   .) (POTENTIAL).
) (POTENTIAL)
) (POTENTIAL)
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  ) (POTENTIAL)
) (POTENTIAL)
ATTACHMENT SITE (POTENTIAL)
   AA SEQUENCE)
  Hvarregaard J., Andersen M.H., Berglund L., Pasmussen J.T.,
  79.1%; Score 34; DB 1; Length 463; 66.7%; Pred. No. 3; 66.7%; Indels
   TISSUE=Mammmary gland;
MEDLINE-96125736; PubMed 8541316;
Aoki N., Kishi M., Taniguchi Y., Adachi T., Nakamuta R.,
  -> A (IN PEP Z).
P78B6C6EFB8A724D CPC64;
   3 (IN REF. 2).
Y +> S (IN SEF. 2)
H -> T (IN PEF. 2)
L -> S (IN PEF. 2).
  -> F (IN PRF 2)
-> D (IN PRF 1)
                         BY SIMILARITY
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RY  MFGM_BOVIN STANDARD, FFT, 427 AA. 095114, 92759, P79344, 010-1NOV-1997 (Pol. 35, Created) (01-NOV-1997 (Pol. 35, Last sequence update)
   Riophys Arta 1245-385-391(1995)
   Riochem 240:628-636(1996)
  51465 MW;
   SEQUENCE OF 18-427 FROM N.A.
   SPONENCE OF 19-427 FROM N A
89
39
49
60
79
96
107
303
463
   61
266
316
30
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35
147
   Bovidae; Rovinae; Ros
  Bos taurus (Bovine).
  463 AA;
   Best Local Similarity
  391 IQYVESYKV 399
  1 VOFVASYRV 9
   NCBI_TaxID=9913;
196
309
395
   Petersen T.E.;
  Ensslin M.A.;
  Matsuda T.;
  DISULFID
DISULFID
DISULFID
DISULFID
  DISULFID
  CONFLICT
   membrane
   CONFLICT
                                 DISULFID
   Query Match
  DISULFID
   DISULFID
   CARBOHYD
  CARBOHYD
  CARBOHYD
  CARBOHYD
  SEQUENCE
  CONFLICT
   CONFILE
   CONFLICT
   Biochim
   MPGM_BOVIN
  MFGE8
   Matribos
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  Richtem, Moi, Riol Int 29-545-554(1993).
FINCTION: PROPARLY ASSOCIATES WITH PROSPHOLIPIDS ON THE SURFACE OF MAMMARY EPITHELIAL CELLS AND MITK PAT GLORULES. ZONA PELLUCIDA-
   ) (HYBETT) (IN LAST-6
   ) (BICH MANNOSE) (IN
  Mather I H., Banghart L. P., Tano W.S.;
"The major fat-globule membrane proteins, bovino components 15/16 and
guinea pig GP 55, are bomplogous to MGP-R8, a murine glycoprotein
centabiling epidermal growth factorilike and factor V/VIII like
sequences.";
   - 1. TISSUE SPECIFICITY: MILK AND SPERMATOZOAN.
- 1. FIM: THE 2 O-LINKED GLYPANS O'NSTIST OF GAL, GLCNAC AND FUC, WITH POPULAHLY FOR AS MEDUCING TERMINALS SUGAR.
- SIMILARLY: COSTAINS 2 ESF-LIFE DOMAINS.
- 1. SIMILARLY: COSTAINS 2 ESF-LIFE DOMAINS.
  11- ALTERNATIVE PRODUCTS: 2 LSOPORMS: A LONG ROFM (SHOWN HPRE) AND A SHOFT FORM; ARE PRODUCTE BY ALTERNATIVE SPLICING. THE SHORT FORM LACKS 53 AMINO ACTOS WITHIN THE F5/8 IYPE C 1 DOMAIN.
   F5/8 TYPE C 1.
F5/8 TYPE C 1.
CEL ATTACHENT SITE (POTENTIAL).
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  O-LINKED (FUC. . .) (IN PAS-6).
O-LINKED (FUC. . .) (IN PAS-7).
N I INPER (GLENAET) (HYRET)
Submitted (NOV 1997) to the EMHL/OPERHABLK/OPER databases.
  MISSING (IN SHORT ISOFORM)
A -> F (IN PEF. 1).
  4CBBEE3AlDC4EB24 CRC64;
   Pfam: PP00754; FS_F8_type_C; 2.
SMAPT: SM00181; FGF: 2.
SMAPT: SM00181; FGF: 2.
PFGF: 3.
PFGF: 3.
PFGF: 5.
PFGF
   SEQUENCE OF 140-146; 174-187; 233-246 AND 422 427
  AND PAS-7).
N TINKED (CLCNAC
  LACTADHERIN,
   EGF-LIKE 1.
EGF-LIKE 2.
  MEDLINE-932505/6; Pubmed-8485470;
  EMBL: X91895; 7AA62997.1; -.
EMBL: S80643; AAB35894.2; -.
EMRL: Y11719; CA772406.1; -.
HSSP: P00740; IEDM.
InterPro: PPR000561; EGF-like.
  47411 MW;
   427
427
427
427
427
87
47
47
47
47
   105
265
256
427
27
34
  Pfam; PF00008; EGF; 2
  Alternative splicing.
  BINDING PROTEIN.
  427 AA;
  و
م
م
  TISSUE=Milk;
   DISULFID
   CONFLICT
  DISULFID
  DISULFU
   CAPROHYD
  SEQUENCE
   DISULFID
  PISHLFID
   PISHLFIP
  DISULFID
   CARBOHYD
   CARBOHYD
   DISULFID
  APP HYD
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   entities requires a license agreement (see http://www.isb sib.ch/announce/
   Ċ,
   -!- CATALYTIC ACTIVITY: ATP + L-17sinc + tRMA(1/s) - AMP + diphosphate
   InterPro; IPRGELSON, comm.
Plan; PF07821; tRNA.synt.Lt; 1.
PPFSITE: PS0078; AA_!KNA_LLGASE_L; 1.
AT'roary! tPNA_synthetase; Frotein tills, the ass. Ligase, ATP binding.
AT'roary! tPNA_synthetase; Frotein tills ass. Ligase, ATP binding.
   Caps
  -1-1989-TENALIS).
-1-SHPCHLITIAE COATION- "YEAP!asmis (By Similarity).
-1-SIMILABITY: BELONGS TO CLASS-I AMINOACY: TRNA SYNTHETASE FAMILY.
  Gaps
   15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Bel. 36, iast sequence update)
16-OCT-2503 (Fel. 46 | iast importation update)
Lysyl tPNA synthetise (EC 6.1.1.6) (Lysine LENA ligase) (LYSES).
   MPELINE SECTORS, Planci et.CHS.
Taba M., Morgan S., Currew A. W., Pridmono D.P., Vethkogeht U.C., Gardner M., Lin M., Worsen F. F., Scott I.
"A curyarchagal lysyl LRM synthetase, recemblance to class :
   Ċ
  ..
   I -> L (IN REF. 1; AA SEQUENCE).; OATFARGRAF7AGAGE OFFG4,
   Query Match 76.7%; Score 33; DB 1; Length 533; Best Local Similarity 85.7%; Fred. No. 6; Matches 6; Conservative 1; Mismatches 0; Indels
              Score 33; 198 1; Length 427;
Pred. No. 4.7;
4; Mismutches 0, fidels
   Archaea, Euryarchaeota, Nethanococcaies, Methanococcae;
Methanococcis
  MEK1_SCHPO STANDAPD; PRT; 445 AA. 010292;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Created)
   533 AA.
   SEQUENCE FROM N.A., AND SEQUENCE OF 1-22.
  or send an email to licensewish sib.ch).
  EMBL: AF009834; AAB87416.1, ...
InterPro: IPE001412, tRNA.synt_1.
InterPro: IPE002004; tRNA.synt_1ys_1.
   PRT;
   E33 AA; F1273 MW;
              76.78;
  Séicace 278:1119-1122(1997).
  Methamococcus maripaludis.
Query Match
Best Local Similarity 55.6
1. Conservative
   STANDARD;
  353 IUYVAAYRV 361
  NCB1_Tax1D=39152;
   1 VEFVASYRV 9
  111111:
497 FVASYKI 503
  3 FVASYKV 9
   synthetases.";
   SYK METMP
  CONFLICT
  030522;
  MEK1_SCHPO
  RESULT 6
SYK_METMP
   YSS.
   RESULT
  AC DI
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   Gaps
                      Melosis specific scrim, threshine protein Vidase mekl (BS 2.7.1.37).
MEKLOR SPAC1464.03.
Schicosaccharomyres pombe (Pission yeast).
  Transferase, Serine/threenine protein kinase, ATP-binding, Meiosis.
   BOVIED K., Charcher C.M., Barrell R.G., Physharcam B.A., Wood V.,
Sufeditod (Ann-1947) to the EMEGAGOROUS/DDBJ databases.
PROFILED PROBABLE RECEIM KINARE REWITEE FOR MEIOTIC
  -!- CARAINTIC ACTIVITY: AIP + a protein - ADP + a phosphoprotein. -! SIMILARITY, RELOAGS TO THE SIBJTHE FAMILY OF FESTION KINASES. -!- SIMILARITY; CONTAINS I PHA DOMAIN
   ..
  Query Match 71.4%; Score (2); DB 1; Length 445; Best Local Similarity 75.0%; Pred. No. 8.5;
   01-NOV-1991 (Rel. 20, Created)
01-JUL-1993 (Rel. 26, Fast sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Fold polyprotein (Sontains: Eloteuse (RC 3-4.23.), Reverse Librari (Els 2-7-7-49), Endonuclease).
   1; Indels
   tync M.H., Bryant J.A., Aves S.J.,
Sibmitted (THL-1996) to the EMBL/Confank/DiRT databases.
   P (BV GMTIAPITY).
EDE2D7989AIR45B0 CRC64;
  Bakuryuta, Pungi, Asakamyada, Schindsamhur mycetes;
Schinduaddarum, Atales, Schindsamhar mycetaceae:
  ATP (BY SIMILARITY).
BY SIMILARITY.
16-oct-2001 (Rel. 40, Last annotation update)
   PRT; 1161 AA.
  PPOTEIN KINASE.
   1; Mismatches
  SMART, EMCOLDO, STRA: 1.
PROSTITE PSONIOT: PROTEIN_KINASE_ATP: 1.
PROSTITE: ESONIOT: PROTEIN_KINASE_ST: 1.
PROSTITE: PSSOOOD: PROTEIN_KINASE_DOM: 1.
PROSTITE: PSSOOOD: FHA_DOMAIN: 1.
   Interpre: IPP003719; Eth.pkinase.
Interpre: IPP002239; FUA.domain.
Interpre: IPR002290; Ser_thr_pkinase.
Ptam, FF00498; FHA: 1.
   FHA.
  ATE
   281 281 B
169 149 A
445 AA; 51151 BW;
   298596; CAB11196.1; -.
   EHBL, 271478; CAA96101.1; -.
  Pfam; PF00069; pkinase; 1.
   STANDARD;
   6; Conservative
  SMAKI, SMC0240; FHA; 1.
   116
   Settiosarcharomydes.
  HSSP; P00518; 1PHK.
  SEQUENCE FROM N.A.
   RECOMBINATION.
  SHOURNCE FROM N.A.
   :11 [1]]
75 LOFTASYK 82
  NCBI_TaxID=4896;
   1 VQEVASYK 8
   STRAIN-972;
   STRAIN-972;
  ACL_STIE
PINE WO
   POL_SFV1
   ON I HE ON
   P23074;
  NIVMOD
  NIVWOO
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   Matches
  POL_SFV1
   RESULT.
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  MEDGINE-90080148; PithMod-21=282s;
Mergia A., Shaw K.B.S., Lackner J.B., Luciw D.A.;
"Relationship of the envision and the end-one-brase damain of the pol-
quess of similar Loany virus Type 1 and human feamy virus ";
J. Virol. 64:406-410(1990).
   Op Cafes
   1 - PTM - SPECIFIC FNZYMATIC CIRAVAGES IN VIVO YIELD MATURE PROTEINS.
   Kupioc I -1 , Kay A , Hayat M , Pavior P , Porios J , Galibort P ;
"Sequence analysis of the simian foamy virus type I genome.";
Gene 101:185-194(1991).
   PRINTS, PRO0920, SPUMYIRPTASE.
Transferase, PRA directed DRA polymerase, Hydroluse, Nuclease:
   -1- SIMILARITY: THE PROTEASE RELONGS TO PEPTIDASE FAMILY A9.
   Serves 32, DR 1, Length 1161,
Prod. Rep. 21,
  2.1 Indets
  UNDUSDIDSBB4C14C CRCS4;
  "Replication and regulation of primate foamy viruses.";
              Simian foamy virus (type 1) (SPV-1).
Viruses, Fetroid viruses; Fetroviridae; Spunavirus
NCBL_TaxID*11964;
   Endonuclease, Aspartyl protease, Fetyprotein.

ACT_SITE 36 36 BY SIMILARITY.

CONFLICT 236 T -> I (IN REF. 2).

CONFLICT 910 910 S -> G (IN REF. 2).

CONFLICT 940 950 A -> T (IN PEF. 2).

SEQUENCE 1161 AA; 131717 MW; 08DO9DID65B4C14C
  489 AA
  2, Missilters
   EMBL: X54482, -; NOT_ANNOTATEL_CGS
EMBL: X58484; CAA41394 1; -
EMBL: M33561; AAA47793.1; -.
   IPR001641; Spuma_A9PTase.
   SEQUENCE FROM N.A. MEDLINE-91276270; Pubmod-1647359;
   MEDLINE-91361538; Pubmed=1653483;
  P22244;
01-AUG-1991 (Rel. 19, Created)
  SEQUENCE OF 969 1161 FROM N A
  74 48
  InterProj IPRSOjise, stasem
  Virology 184:475 482(1991).
  SHQUENCP OF 1-970 PPOM N.A.
   InterPro: IPPGood77; FVISA
  InterPro; IPR001584; Rve.
  P 00804334 [36]
   Pfam; PP00075; rnaseH; 1
  STANDARD;
  Mergia A., Luciw P.A.;
  PIR; S18738; S18738.
  PIR; A33562; A33562
  S15566; S15566
  ] MML
  Trings Sections by
New 5, Conserv
   Pfam: PF00078: rvt.
   ||||: ||:
| 633 VQFIPEYKI 641
   1 VQFVASYKV 9
  MEROPS; A09.001;
   pronakks
  HSSP; P03355;
  SYE_BACST
   InterPro;
  Query Mitch
  Matuhes
   SYE_BACST
   RESULT
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  Interpre, the prooff of the series of the prooff of the pr
  Rreton R., Watson D., Yaguchi M., Lapointe J.;
"Glutamyl-tRNA synthetases of Bacillus subtilis 168% and of Bacillus stearofher mophilus. Touling and sequencing of the gltX genes and conglation with other laminose; tFNA synthetases.";
T. Biol. Chom. 265-19248 18255(1990).
   Gaps
  ** STHEFELGRAF GARLENS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
  16-1029-2001 (Fe1. 40, Last annotation update)
Slutanyi FNA Synthetase (FC 6.1.1.77) (Slutanater-FNA liquse)
   Glass J.I., Lefkowitz E.J., Glass J.S., Heiner C.R., Chen E.Y.,
   ò
  Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
   72 1%; Score 31; DB 1; Length 489; 62 5%; Pred No 16;
   1, Indels
   Ureaplasma parvum (Ureaplasma urealyticum biotype 1)
   Bacillus stearothermophilus.
Bacteria; Firmioutes; Bacillus/Clostridium group;
Bacillus/Staphylononous group; Geobacillus.
  09PPZ6;
16 ort 2001 (Frl. 40, Created)
16 ort 200 (Frl. 40, Last Serpence apdate)
box 201 (Frl. 40, Last annotation update)
DNA primase (EC 2.7.7..).
01-AUG-1991 (Rel. 19, Last sequence update)
   2; Mismatches
   diphosphate + L-glutamyl-+PNA(Glu).
  PRT;
  STRAIN=SEROVAR 3;
MPDIINE-20500219; PubMed-11048724;
  HSSP, P27000, IGEN.
Interfree, (PROSON24, TRNA Synt_lo
InterPre), IPPO01412, tPNA-Synt_l
  MEDLINE-91909314; PubMcd-2120226;
  Mycoplasmataceae; Ureaplasma
NCBL_TaxID=134821;
  EMRL, M55072; AAA22494.1; -.
  Cuery Match
Hest Lonal Similarity 62 hm.
5: Conservative
  STANDARD;
  -!- SITRIINIT - MONOMER.
   HARMAN, SYRSES
   SEQUENCE FROM N.A.
   SPOTENCE FROM N A
  262 IQFVSQYK 269
  NCB1_TaxID-1422;
   1 VQFVASYK 8
  DNAG OR UU494.
  PRIM_UREPA
   (GluRS).
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  0
   -1- FONCTION: GALACTUSE- AND NIAPTYLGIAGACTOSAMINE-FINEDING LECTIN, MAY PRAY A POLE IN CELL-SUBSTRATUM AGHESION RATHER THAN IN CELL-CELL ADHESION, MAY BE INCRESSARY FOR THE MAINTENANCE OF NORMAL ELGINSATE MORRHOLOGY PORTING AGSPECATION.
  PIGNIC PROTEST. TOPKIN: 1.
PIGNIC PROTEST. TOPKIN: 1.
Promise PP918A7: 2F-GHC2: 1.
Proforms PA0102989. Zan_CHC2: 1.
SMART: SM00493: TOPRIM: 1.
SMART: SM00493: TOPRIM: 1.
SMART: SM00493: TOPRIM: 1.
Transferase: DNA replication; DNA-directed RNA polymerase; Primosome: Zinc inqer: Zinc; Metal Linding, Cagister Fillware 1.
SNLFING 39 63 CHC2-TYPE (BY SHMILARITY).
SRQHENCE 641 AA; 75390 MW; A69201680458E47 CRC64:
  RNA PRIMERS FOR THE OKAZAKI FRAGMENTS ON BOTH TEMPLATE STRANDS AT REPLICATION FORKS DURING CHROMOGOMAL DNA SYNTHESIS.
-!- COPACTOR: BINDS ONE ZINC ION PER MOLECULE (BY SIMILARITY).
  0; Caps
   Springer W.R., Cooper D.N.W., Barondes S.H.; "Discoidin I is implicated in cell-substratum attachment and ordered cell migration of Dictyostellum discoidenm and resembles
  Nature 407:757-762(2000).
-1- FUNCTION: DNA PPIMASE IS THE POLYMERASE THAT SYNTHESIZES SMALL.
   MEDLINE-82179475; Pubmed-6279874;
Poole S., Firtel R.A., Lamar E., Rowekamp W.;
"Suspense and expression of the discondin I gene family in
  69.8%; Score 30; DB 1; Length 641; 62.5%; Pred. No. 38;
                  "The complete sequence of the nucosal pathogen Urcaplasma
  1; Indels
   Dictyostellum discoideum (Slime mold).
Eskuryota: Myretatoa: Eletyratellida, Fielyretellida
  21-30L-1986 (Rel. 01, Created)
21-30L-1986 (Rel. 01, Last sequence update)
15-30L-1998 (Rel. 36, Last annotation update)
  149 AA.
  Pred. No. 38;
2; Mismatches
  Or send an email to license@isb-sib ch)
  -!- SUBUNIT: MONOMER (BY SIMILARITY)
   MFPLINE-85074463; PubMed=6509552;
   Discoldin 1, D chain (Fragment).
   153-273-289(1991)
  EMBL; AE002147; AAF30906.1; -.
  InterPro: IPR002694; ZnF_CHCC.
  InterPro; IPR002936; Toprim.
   Dictyostelium discoldeum.",
  Ouery Match
Best Local Similarity 62.5%
5. Conservative
  STANDARD;
   fibronectin.";
Cell 39:557-564(1984).
   CELL ATTACHMENT SITE.
  Q9X4D0: 1D0Q
   SEQUENCE FROM N.A.
   NCB1_fax1D-44689;
  70 IKIVAEYK 77
  1 VQFVASYK 8
                                      urealyticum.";
Cassell G.H.;
   Mol Riol
  DISD_DICE!
  P02888:
  RESULT 11
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  MEDINE-9633-1046; PubMed 7625129;
Reddy P.S., Nady B., Derbyshire J.B.;
"Sequence analysis of publics (VIII, E/ and Hilto regions of porcine
   Reddy F.S., Idamedanti N., Song J.T., Der J.B., Hynn B.B., Bark J.B.,
Cha S.B., Bar V.T., Theo S.K., Pakkul L.A.,
"Nucleotide sequence and transcription map of percine adenovirus type
  Gaps
  Forcine adenovirus type 3 (PAV-3).
Viruses; debWA ::ruses, no FWA stage; Adenotiridae; Mastadesovirus.
  .;
O
   62.5%; Scare 29; DR 1; Length 149; 62.5%; Pred. No. 13;
  1; Indels
   Larocque D., Malenfant F., Massie B., Dea S.;
"Porcine adenovirus scrotype 3, complete genome.";
submitted (FER 1999) to the EMEL/Genhank/DDBJ databases.
-1- SUBUNIT: TETRAMER OF FOUR DIFFERENT CHAINS (A TO D).
-1- SUBCELLULAR LOCATION: Cytoplasmic.
-1- TISSUE SPECIFICITY: STALK CELLS.
  SEQUENCE 149 AA, 16746 MW, 1B8E0F220B29E9A1 CRC64;
  Q83453; Q9YTR6;
16 CCT 2601 (Rei. 40, Created)
16-CCT-2001 (Rei. 40, last sequence update)
16-CCT-2001 (Rei. 40, Last annotation update)
Hexon-associated protein precursor (Protein VIII).
  CELL ATTACHMENT SITE.
  223 AA
  2, Mismatches
   PROSITE: PS01285; FA58C_1; 1.
PRUSITE: PS01286; FA58C_2; FALSE_NEG.
  PRI;
   MEDIINE-94054141; impMed 9837805;
  Lictjab, Dodaga; dscb.
InterPro; IPR000421; PASE_C.
Pfam: PF00754; PS_F8_1ype_C; 1.
SMART: SM00231; PASEC; 1.
  FMRI; J01285; AAA33200.1; -.
   62.58;
  Virology 251:414-426(1998).
  adenovirus type 3.";
Virus Res. 36:97-106(1995).
   Sucry Match
Best Local Similarity 62.5.
  STANDARD;
  149
  Lectin; Cell adhesion.
  PIR; AU3383; DLDOID.
   SEQUENCE FROM N.A.
   SEQUENCE FROM N.A.
   SEÇUENCE FROM N.A.
   STRAIN-6618 / IAF:
  NCBI_TaxID-35265;
   84 QWVTSYKI 91
  2 QFVASYKV 9
   STRAIN=6618;
   STRAIN=6618;
  HEX8_ADEP?
  NON_TER
  HEX8_ADEP3
   qq
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  ċ
   -!- FUNCTION GALACTOSE- AND N-ACETYLGALACTOSAMINE-BINDING LECTIN, MAY FIAY A ROLE IN CELL SUBSTRATUM ADDRESSION BATHER THAN IN CELL-CELL ADDRESSARY FOR THE MAINTENANCE OF NORMAL FLONGATE MORPHOLOGY DURING AGGREGATION.
-!- SUBUNIT: TETPAMER OF FOUR DIFFERENT CHAINS (A TO D).
Thore are no restrictions on
  Gaps
  Devine J.M., Tsang A.S., Williams J.G., "Differential expression of the members of the discoidin I multigene family during growth and development of Dictyostelium discoideum.";
   Springer W.R., Cooper D.N.W., Barondes S.H.:
"Discoidin I is implicated in cell-substratum attachment and ordered
cell migration of Dictyostelium discoideum and resembles
   Jellinghaus U., Schaetzle U., Schmid W., Bowekamp W.;
Transcription of a dictyostellum discoidin-i gene in yeast
"Transcription of a dictyostellum discoidin-i gene in yeast
alternative promoter states used in two different eukaryotic cells ",
I. Mol. Riol. 159-523-636(1992).
  Ö
  CLEAVAGE (RY ADENOVIEGS PROTEASE) 7731242P110602A1 CEC64,
  Poole S., Firtel R.A., Lamar E., Rowekamp W.; "Sequence and expression of the discoidin I gene family in Dictyostellum discoideum.";
  Score 29; DB 1; Length 223;
Prod Mo 20;
  1; Indels
   HEXON ASSOCIATED PROTEIN.
  Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
  21-JUL-1986 (Rel. 01, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-NCV-1997 (Rel. 35, Last annotation update)
  253 AA
  3; Mismatches
  BY SIMILARITY
the European Bioinformatics Institute
   Dictyostelium discoideum (Slime mold).
  PRT;
   MEDILINE-82170475; PubMed-6279874;
   REVISIONS, SEQUENCE FROM N.A. MEDLINE 83059644; Pubmed-6754951;
   MEDLINE-82233698; PubMcd-6284373;
   EMBL, AJ237815; CAB41034.1; -.
EMBL, AB026.11; AAA76972.3; .
InterPro: IPR000A45; Adenc_PVII:
Plam; PF01310; Adenc_PVIII; 1.
  MEDLINE-85074463; PubMed=6509552;
   154.274-289(1981)
  EMBL; AF083132; AAC99446.1; -.
   24281 MW:
  1.48
   - 8() Ua
  SEQUENCE OF 1-40 FROM N.A.
   Hexon-associated protein.
  4; Conservative
  STANDARD;
  39:557-564(1984).
   Cell 28:793-800(1982)
   Discoldin I, A chain.
   ATTACHMENT SITE
   223 AA:
  Query Match
Begt focal Similarity
   SEQUENCE FROM N.A.
   207 OFTANYNI 214
   NCBI_Tax1D-44689;
   112
   2 QFVASYKV 9
  tibronectin."
   J. Mol Biol
  DISA DICDI
   SECUENCE
   P02886;
  PROPER
   CHAIN
  RESULT 13
DISA_DICDI
  Matches
  SITE
  DSCA
8444&666666
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   Ċ
  CELL 39:557-564(1984).
-!- FUNCTION: GALACTOSE- AND N ACETYLGALACTOSAMINE BINDING LEXTIN. MAY
-!- FUNCTION: GALACTOSE- AND N ACETYLGALACTOSAMINE BINDING LEXTIN. MAY
PLAY A POLE IN CELL SUBSTRATION ADDRESSON MATHER THAN IN CELL-CELL
ADDRESSON. MAY BE NECESSARY FOR THE MAINTENANCE OF NORMAL BLONGATE
   Springer W.R., Cooper D.N.W., Barondes S.H., "Discoidin I is implicated in cell substratum attachment and ordered cell migration of Dictyostellum discoideum and resembles
   0; Gaps
   -!- TISSUE SPECIFICITY: STALK CELLS.
-!- TISSUE SPECIFICITY: THE SEQUENCE OF KESTODES 1-149 OF THE B CHAIN IS IDENTICAL WITH THAT OF THE C CHAIN.
   MEDLINE-82170475; PúbMcd-6279874;
Porole S., Firtel R. A., Lamar E., Bowekamp W.;
"Sequence and expression of the discoidin I gene family in
Distroctional Liscoideum.";
  67.4%; Score 29; DB 1; Length 253; 62.5%; Pred, No. 23;
  1; Indels
   MORPHOLOGY DURING AGGREGATION.
SUBUNIT: TETRAMER OF FOUR DIFFERENT CHAINS (A TO D).
  CELL ATTACHMENT SITE.
: 81263A100F1FF91E CRC64:
   Dictyostelium discoideum (Slime mold).
Eukaryota: Mycetosoa: Dictyosteliida; Dictyostelium.
   SEQUENCE FROM N.A. (C CHAIN AND B CHAIN 1-149)
   -!- SIMILARITY: CONTAINS 1 F5/8 TYPE C DOMAIN.
  -!- SIMILARITY: CONTAINS 1 F5/8 TYPE C DOMAIN.
  21-JUL-1986 (Rel. 01, Last Sequence update)
15 JUL 1998 (Rel. 36, Last annotation update)
DSCO AND DSCC. Chain and B chain.
  253 AA.
  Fred. No. 23;
2; Mismatches
  F5/8 TYPE C.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
   SUBCELLULAR LOCATION: Cytoplasmic.
   PROSITE, PSC1285, PASSC_1, 1.
PROSITE, PSC1286, PASSC_2, FALSE_NIG.
                                      TISSUE SPECIFICITY: STALK CELLS.
  PRT;
   MEDLINE-85074463; PubMed-6509552;
  Mol. Biol. 153:273-289(1981).
   Tite: PEO. IPPOCATI PASS_C.
Pfam: PEO0754; F5_F8_Lype_C; I.
SMART; SMO0231; FASSC; I.
   21-JUL-1986 (Rei. 01, Created)
   SEQUENCE 253 AA; 28239 MW;
   EMBL; J01282; AAA33197.1; -. PIR; A03381; DLDOIA.
  5; Conservative
  STANDARD;
  DictyPb; DP02000; dscA.
   Cell adhesion.
  CELL ATTACHMENT SITE
   Best Local Similarity
   NCBI_TaxID-44689;
   84 QWVTSYKI 91
  2 QFVASYKV 9
   fibronectin.";
   SUBUNIT:
   DISC_DICDI
   Query Match
  Lectin;
DOMAIN
  P02887;
  Matches
  RESULT 14
   DISC_DICUI
   ò
   qq
  A PART REPARENCE OF OUR COORDINATION OUR COORDI
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  entitles requires a liceuse agreement (See http://www.isb-sib.ch/announce) or send an email to liceuse@isb-sib.ch)
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  Caps
  Yamamoto Y., Aiba H., Baba T., Hayashi K., Inada T., Isono K., Itoh T., Kimura S., Kitagawa M., Makino K., Miki T., Mitshashi N., Misobuchi K., Mori H., Nokade S., Nakamura Y., Nashimoto H., Oshima T., Oyama S., Saito N., Sampoi G., Satoh Y., Sivasundaram S.,
  Blatther F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Piley M., Collado-Vides J., Glasner J.D., Pode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Pose D.J.,
  MEDIINE-90264337; PubMed 2198958,
Sirko A., Hryniewicz M M , Hulaninka D.M , Rowek A.;
"Sulfate and Uniosulfate transport in Escherichia coli K-12:
mucleotide sequence and expression of the cysTWAM gene cluster.";
J Barteriol 172:3357(1990).
  Bacteria, Protechasteria, gamma subdivision, Enterobacteriaceae,
  .
O
   Pacry Match 67.4%, Score 29, DB 1, Length 253, Best Local Similarity 62.5%, Pred. No. 23,
  "The complete geneme sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
   i, ludels
   CELL ATTACHMENT SITE.
  01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
01-MAR-2002 (Pel. 41, Last annotation update)
Sulfate fransport system permease protoin cyst.
  277 AA.
   2; Misautches
  PSZ8 TYPE C
  PROSITE: FS01285; FA58C_1, 1,
PPOSITE: FS01286; FAFRC_1: FALSE_NPO
  PPT;
  STRAIN=K12 / MG1655;
MEDLINE=97426617; Pubmed=9278503;
   MEDLINE=9734998U; PubMed=9205837;
   InterPro, IPR000421, FA58_C.
Pfam, PF00754, F5_P8_type_C, 1.
SMART, SM00231, FA58C, 1.
  SEQUENCE 253 AA; 28392 MW,
   EMBL; J01283; AAA33198.1; ·. PIR; A03382; DLDOIC.
   SWISS-2DFAGE; F02887, DICTY. DictyDb; DD02001; dscC.
  EMBL; J01284: AAA?2199.7;
  5, Conservation
  STANDARD;
   Lectin; Cell adhesion.
  CYSU OP CYST OP R2424
  PIP: B03382; B03382
  SEQUENCE FROM N.A.
  SEQUENCE FROM N.A.
  SEQUENCE FROM N.A.
   Mau B., Shao Y.;
  |:| |||:
84 QWVTSYKI 91
   Escherichia coli
  2 2FVASYKV 9
   NCBI_TaxID=562;
  Escherichia
   CYST_ECOLI P16701;
  DOMA!N
  CYST_ECOLI
   Matches
   셤
  5
  BARKKKKKKAPARKKKKKKOOOOONEE
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Search completed: September 5, 2002, 15:31:43

Job time: 478 sec

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  the European Bioinformatics Institute. There are no restrictions on its use b_i nor-field institutions as long as its centent is in to way modified and this statement is not removed. Usage by and for commercial entities requires a livense agreement (See http://www.istestic.oh/anneument)
   ..
Injumi B., Inkidashi B., Jakeda J., Inkemoto E., Ochaia E., Wada C., Yamaqata S., Horinoth T., Pornayata S., Horinoth T., "Construction of a contiguous 874-kb sequence of the Escherichia coli "Kiz genome corresponding to 50.0-68.8 min on the linkage map and anniysis of its sequence features.", Inna per 4.91-113(1997).

--- FUNCTION: PAPT OF THE BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEM
  Gaps
  ! SUBCELLULAR LUCATION: Integral membrane protein. Inner membrane
   SIMILARITY, WITH INTEGRAL MEMBRANE COMPONENTS OF CTHEF SINDING-
   0
  FOR SULFATE AND THIOSULFATE. PROBABLY RESPONSIBLE FOR THE TRANSLOCATION OF THE SUPETRATE ACROSS THE MPMREANE.
  PROTEIN-DEPENDENT IRANSPORT SYSTEMS, BELONGS TO THE CYSTW
  Inner membrane: Transmembrane: Sulfate transport; Transport;
   Scare 29; DB 1; Length 277; Pred. No. 26;
   1; Indels
  1392821B0DE24459 CRC64;
  67.4%; Sc...
75.0%; Pred. No. 20,
75.0%; 1; Mismatches
   Pfam; PP00528; BPD_transp; 1.
PPOSITE; PS00402; RPD_TRANSP_INN_MEMHR; 1.
   or send an email to license@isb-sib.ch).
  POTENTIAL. POTENTIAL.
   POTENTIAL. POTENTIAL.
   POTENTIAL.
   POTENTIAL
   POTENTIAL
  sistat, oysu
IPROOOSIS, BPD_transp.
  EMBL; M32101; AAA23637.1; -.
EMBL; AE000330; AAC75477.1; -.
EMBL, D50871, BAA16298.1; -.
  30.291 MW;
   EMBL, D90872, BAA16307.1, -.
  6, Conservative
  84
1119
156
205
235
263
  ЕТК, А15402, QRECST.
PIR, B35403, B35403.
   Query Match
Best Local Similarity
   Complete proteome.
TRANSMEM 17
  (Potential).
  Ecuarion, EG10197
   55 QVVAAYKV 62
   2 QFVASYKV 9
   SUBFAMILY.
  InterPro:
   FRANSMEM
   TRANSMEM
   LKANSMEM
   FRANSMEM
   TRANSMEM
   TRANSMEM
   SEQUENCE
   Matches
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2000 Compages Ltd.
GenCore version 4.5
Copyright (c) 1993 2002 Comp
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OM protein - protein search, using sw model

. Search time linible Seconds (Without alignments) 12.673 Million cell updates/sec Suprember 5, 2562, 15,31,66 Run cn.

US-09-744-804-40 Title:

BLOSUM62 Gapop 10.0 , Gapeat 0.5 1 VQFVASYKV 9 Perfect score: Scoring table: Sequence:

562222 segs, 172994929 residues Searched: 262222 Total number of hits satisfying chosen parameters.

Minimum DB seq length: 0 Maximum DP seq length: 2000000000

Maximum Mutch 1008 Listing first 45 summaries Post-fracessing: Minimum Match 98

sp\_archea:\* sp\_bacteria:\* SPIREMBL\_19:\* Database :

sp\_unclassified:\* sp\_invertebrate:\* sp\_vertebrate:\* sp\_rvitus:\*
sp\_bacteriap:\* sp\_organelle:\* sp\_phage:\* sp\_archeap:\* sp\_rodent.:\* sp\_mammal:\* sp\_mhc:\* sp\_plant:\* sp\_virus:\* sp\_fungi:\* sp\_human:\* 10:

Pred. No. is the number of results predicted by chance to have a source greater than or equal to the source of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Description                   | Q9wts3 mus musculu | Q9rlx9 mus musculu | 043854 homo sapien | 035474 mus musculu | Q960n3 drosophila | Q9vmal drosophila | Ogresi drosophila | Q919)2 culex miqr: | 09kte8 vibrio chol | 094290 schizosacch | Oopfs3 xylella fas | County them surject | Oct.5/ actinobacil | ເປັນລະພານຮະພານຮອນປະເ | C58836 methanococc | Odvkyd drosophila |
|-------------------------------|--------------------|--------------------|--------------------|--------------------|-------------------|-------------------|-------------------|--------------------|--------------------|--------------------|--------------------|---------------------|--------------------|----------------------|--------------------|-------------------|
| B 10                          | 11 Q9WTS3          | 11 Q9R1X9          | 4 043854           | 11 035474          | 5 0960N3          | 5 Q9VMA1          | 5 Q9VC31          | 12 091972          | 16 Q9KTE8          | 3 094290           | 16 Q9PFS3          | 4 Q9NW19            | 2 066257           | ११ ०्षाहर            | 17 058836          | r ogvykog         |
| %<br>Query<br>Match Length DB | 426                | 463                | 480                | 480                | 330               | 483               | 610               | 121                | 213                | 217                | 308                | 310                 | 344                | 1206                 | 1226               | 1 3 4             |
| %<br>Query<br>Match           | 90.7               | 2 06               | 83.7               | 83 7               | 74.4              | 74.4              | 74.4              | 72.1               | 72.1               | 72.1               | 72.1               | 72.1                | 72.1               | 72.1                 | C1                 | a<br>o            |
| Score                         | 39                 | 36                 | 36                 | 36                 | 32                | 32                | 35                | rd<br>m            | 3.1                | 3.1                | 31                 | 31                  | 31                 | 31                   | 31                 | 30                |
| Result<br>No.                 | 1                  | 7                  | ٣                  | 4                  | ις:               | Q.                | r.                | ဃ                  | or<br>or           | 10                 | 11                 | 12                  | 13                 | 14                   | 15                 | 16                |

SMARI; SMOOTBI; PGF; 2.

| 99mce8 bacteriopha 29424 bacteriopha 29424 bacteriopha 29424 bacteriosha 09x10 arabidopsis 25734 17copersico 07778 cquus cabal 2743 xylella fas 09x16 pyrococcus 09x16 pyrococcus 29x1777 salmonella 09x174 homo sapien 09x17 oscherichia 01874 caenorhabdi 09124 caenorhabdi 091296 caenorhabdi 091296 caenorhabdi 091296 caenorhabdi 091296 caenorhabdi 05x901 corricella | 990th paper o manda<br>998800 arabidopsis<br>999ad is cateteria r<br>99mlil paragonimus<br>99mlil paragonimus<br>98470 porcine ade<br>27779 stapkyllocov<br>996578 carnorhabdi<br>9465487 rhodobacter                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
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| 10 094R10<br>9 09MCR8<br>11 097R24<br>11 097R10<br>11 0740R40<br>11 0740R40<br>11 0740R4<br>12 177R30<br>12 097R30<br>13 098R10<br>14 090LW2<br>15 098R30<br>16 098R30<br>17 098R30<br>18 098R30<br>18 088R30<br>18 088R30<br>18 088R30<br>18 088R30<br>18 088R30<br>18 088R30<br>18 088R30                                                                                 | 10 CONNESS 10 CONNESS 10 CONTAIN |
| ######################################                                                                                                                                                                                                                                                                                                                                      |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
| သည္။<br>အေနာက္တည္တင္းတင္းတစ္တယ္ထင္းတစ္အေလး<br>အေနာက္တတ္သည္ကို တာတက္တည္အေလးအေလးအေလးအေလးအေလး                                                                                                                                                                                                                                                                                  |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
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|                                                                                                                                                                                                                                                                                                                                                                             | भ १८०० ० च च च च च<br>२१-०० ० ० ─ वा ० च ण                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |

### AL LGNMENTS

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STRAIN-HAIN, C. HISSUE-MAMMARY GLAND, MEDLING 99120991; PubMed 9920972; Dobing K., Matsuda T.: Oshima K., Aoki N., Meqi M., Kishi M., Kithi M., Kithi M., Kithi M., Kithi M., Kithi M., Kithi M., Medi M., Meqi M., Meqi M., Meqi M., Kithi M., Kithi M., Kithi M., Kithi M., Kithi M., Kithi M., Tactation-dependent expression of an mkNA splice variant with an exon for a multiply of 11yesylated domain of meuse milk rat globile glycoprotein MFG-R8.; Commun. 254.522 528(1999).
  UNIVA 1999 (TrEMBLEEL 12, Created)
01-NOV 1999 (TrEMBLEEL 12, Last sequence update)
01-DEC-2001 (TrEMBLEEL 19, Last annotation update)
MILK FAT GLORULE SLYCOPPOPERIN MF9-E8 S (SIMILAF TO MILK FAT GLOBULE-
EGF FACTOR 9 PROTEIN).
   Eukaryota, Metazoa: Chordata, Craniata, Verfebrata: Eufeleostomi;
Mammalia; Eufheria, Rodentia; Sciurognathi; Muridae; Murinae; Mus
   Submitted (FEB 2001) to the EMBL/ConBank/DNHJ databases.
-- SIMITARITY: CONTAINS 2 F5/8 TYPE C DOMAINS.
EMBL: AB025280; BAA76386.1; -
                                    426 AA.
                                    PRT;
  Pram; PP00008; EGE; 2.
Pram; PP00754; P5_F8_type_C; 2.
FRINTS; PR00010; EGFBLOOD;
   FMRI: RC024904; AAH03404.1; -.
EMBL: BC024802; AAH03892.1; -.
HESS: P00740; IEDM
INCEPPO: PPU000561; EGF-11ke.
   IPM@01438; EGF_II.
IPM@00421; FA58_C.
IPM@01092; HLB_dim.
                                    PRELIMINARY:
   Mus musculus (Mouse).
   SEQUENCE FROM N.A.
   SPOUFNOE FROM N.A.
   NCBI_TaxID=10090;
  Strausberg R.;
  InterPre:
   InterPro;
   InterPre.
   Q9WTS3;
                                    O9WTS3
RESULT
                   09WTS3
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Query Match
   Ö,
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   Gaps
  Mus musculus (Mouse).
Eukaryada, Matazada, Chardata, Zraniata, Vertebrata, Euteleastami;
Mammalia: Putheria, Rabantad, Sciuragnathi, Mutidae, Murinae, Mus
   0,
   o,
  Score 39, DB 11, Length 463, prod No 3.1;
  90 7%, Score 39, DR 11, Tength 426
77.8%; Pred. No. 2.8;
   Indels
   0; Indels
  RIMERTAL SUBLINEAR AND CONTRACTOR
   51269 MW; 071902B009086427 0P064;
  01-MAY-2000 (Tremmirel 13, tast sequence update)
01-DEC-2001 (Tremmirel 19, tast annotation update)
MILK FAT GLORDLE GLYCOPROTEIN MFG-ER LONG FORM
   ر:
   480 AA.
   463 AA
   2; Mismatches
   D, Mismatches
   Fram, PPG0754, F5_18_type_C, 2.
PRINTS; PR00010; BCFB1000
BANTS; SM00181; PGP; 2.
SMART; SM00231; PFS80; 2.
PPGSITE: PS00022; EGF_1; UNKNOWN_2.
PPGSITE: PS01186; EGF_1; 2.
PR0SITE: PS01285; PA58C_1; 2.
   01-MAY-2060 (TrEMFLIRM) 13, Treated)
  STRAIN BALB/C; TISSHE MAMMARY SLAND;
  043854; 043855;
01-.UN-1998 (TrEMBLrel 06, Created)
   PRT;
                PROSITE: PSONOTE: PSP_1; UNKNOWN_2
PROSITE: PSOILME: EGE_2; 2.
  PROJECT FOULTON DATE: 1. PROSTIE: PS01285; PA58C_1; 2. PROSTIE: PS01286, PA58C_2; 2. PROSTIE: 40% AA, 47747 MW,
   EGF-like domain; Glycoprotein
  InterProj 1PR001438; EGF_II.
InterProj 1PR000421; FASE_A
InterProj 1PR001092; HIH_dim.
Pfam: PP00008; EGF; ?
  90 7%;
77 8%;
   Conservative
   7; Conservative
  PRELIMINARY:
   PRELIMINARY;
SMART; SM00231; FA58C; 2
   Query Match
Best Local Similarity
   Local Similarity
   46 AA:
  354 IQYVASYKV 362
  391 IQYVASYKV 399
  SPOUPICP PPOM N.A.
  NCBL_Taxio-longon;
   1 VQFVASYKV 9
  1 VOFVASYKV 9
   SEQUENCE
  Query Match
  Q9R1X9
Q9R1X9;
  043854
  RESULT 3
   Matches
   Matches
  RESULT
   043854
1D 04
AC 04
DT 01
  Best
   O9R1X9
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   $\circ{\circ}{\circ}$ \text{$\circ}$  ¥4888% $
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Hidai C., Zupancic T.J., Penta K., Mikhail A., Kawana M., Opertermous E.E., Acka Y., Fukagawa M., Matsui Y., Platika D., Aberbach P., Hogan R. L. M., Smodyrass F., Guertermous T., Coloring and characterization of developmental endothelial locus-1: an embryonic endothelial cell protein that binds the alphaybeta3 integrin
  PROSITE; PS01187; EGP_CA; 1.
PROSITE; PS01286; FA58C_1: 2.
PROSITE; PS01266; A FA58C_1: 2.
PSGF-Like demain; A Hashority splicing; Signal, (wv-lopmental protein; cell adhesion; Pepeat; Vascularization
   -!- SURCELLULAR LOCATION: EXTRACELLULAR MATRIX
-!- ALTERNATIVE PRODUCTS: TWO ISOFORMS; LONG ISOFORM (SHOWN HPRE) AND
   INTERACTION WITH THE ALPHA-V BETA3 INTEGRIN RECEPTOR, INHIBITS FORMATION OF VASCULAR-LIKE STRUCTURES, MAY BE INVOLVED IN PEGILLATION OF VASCULAR MOPPHOSENESIS OF REMODELING IN PEMBRYONIC
  Chordata, Craciata, Vertebrata, Puteleostomi;
   FF/R TYPE C 1
FF/R TYPE C 1
FF/R TYPE C 2
CELL ATTACHENT SITE (POTENTIAL).
BY SIMILARITY.
BY SIM
  SEQUENCE FFOM N.A., ALTERNATIVE SPLICING, AND CHAPACTERIZATION.
TISSUE-EMBRYONIC LUNG;
  -!- FUNCTION: PROMOTES ADHESTON OF ENDOTHELIAL CELLS THROUGH
   INTEGRIN-BINDING PROTEIN DEL1.
   Eskaryota, Mctazoa, Chordata, Crisiati, Vertebrata, Putele
Kismalia, Futhesia, Prisates, Catarrhini, Heminidae, Homo.
   SHORT ISOFORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
06, Last Sequence update)
19, Last annotation update)
  1 SIMILARITY: CONTAINS 3 BSF-LIKE FOMAINS 11 SIMILARITY CONTAINS 2 F5/8 TYFE C LOMAINS.
  PROSTTE; PSOROTO; ASX_HYPPOXYT; HNKNOWN_1.
PROSTTE; PSOROT2; EGF_1; UNKNOWN_2.
PFORTTE; FSR1346; EGF_2; HNKNOWN_2.
  EGF-LIKE 2.
EGF-LIKE 3.
  INFEGRIN-BINDING PROTEIN DEL1 PRECURSOR.
   FGF-LIKE 1
   POTENTIAL
  Interpred TPROGOTES Assubydrosyl Interpred TPROGOTES BGF 11ke.
Interpred TPROGOTES BGF 2.
Interpred TPROGOTES BGF 2.
Interpred TPROGOTES BGF 2.
Interpred TPROGOTES BGF 3.
Interpred TP
   MEDLINE 98083199; PubMed 9420328;
   53765 MW;
   EMBL; 070313; AAC02649.1; -
EMBL; 070313; AAC02649.1; -.
HSSP, F12259; 103T.
  like; 2.
   SMAPT, SM00179; EGF_CA, 1. SMAFT, SM0001; EGF_11ke; SMART, SM00231; FA58C; 2.
   receptor.";
Genes Dev. 12:21-33(1998).
  01-PEC-2001 (Tremainel
  1154
474
98
37
48
59
105
  Homo sapiens (Human).
   480 AA;
   PROSITE, PS01187;
PROSITE; PS01187;
  NCBI_TaxID=9606;
  DEVELOPMENT.
   117
26
26
123
1123
161
36
26
26
37
50
78
   158
  DISTURTED
   SEQUENCE
  DISULFID
   DISCIPLE
  DISULFID
   DISULFID
  DISULFID
  DISHLFID
  DISULFID
   VARSPLIC
  VARSPLIC
  DOMAIN
DOMAIN
POMAIN
   SIGNAL
   NIVMOR
   CHAIN
   SITE
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83.7%; Score 36; DR 4; Length 480;

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0
  Hidai C., Zugancic T., Penta K., Mikhail A., Kawana M., Quertermous E.E., Aoka Y., Fukagawa M., Matsui Y., Platika D., Auerbach R., Hogan B.L.M., Shodgrass R., Quertermous T.; "Clening and characterization of developmental endothelial locus-1: an embryonic endothelial cell protein that binds the alphaybeta3 integrin receptor.";
  DEVELOPMENT,

1. SUBCELLULAR LOCATION: PXTRACELLULAR MATRIX.

1. ALTERNATIVE PRODUCTS: TWO ISOPOPHE SELLCING.

SHORT ISOFOM: PAPE PROPUCTS: BY ALTERNATIVE SELLCING.

1. TISSUE SPECIFICITY: EXPRESSED IN ANGIOBLASIS AND EACH ENDOTHELIAL CELLS. BY EMBRYONIC DAY 13.5, ALSO EXPRESSED IN A PRESTRICTED GROUP OF NON-ENDOTHELIAL CELLS. BY EMBRYONIC DAY 13.5, ALSO EXPRESSED IN A PRESTRICTED GROUP OF NON-ENDOTHELIAL CELLS.
  -1- DEVELOPMENTAL STAGE: EXPRESSED IN THE EMBRYO FROM DAY 7. AFTER DAY 15.5, EXPRESSION DECREASES AND DISAPPEARS COMPLETELY BY THE TIME
   EGF-like domain; Alternative Splicing, Signal, Developmental protein,
Cell adbesion; Repeat; Vascularization.
                     Caps
   FUNCTION: PROMOTES ADDESTON OF ENDSTHELLIAL CELLS THROUGH INTERPORT TOW WITH THE ALPHAY BEING WESELY BE INVOLVED IN BORMATION OF VASCULAR-LIKE STRUCTURES. MAY BE INVOLVED IN HESSULATION OF VASCULAR MORPHOSENESIS OF PERMORELING IN EMBRYONIC
   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  SECTENCE FROM N.A., ALTERNATIVE SFLICING, AND CHARACTERIZATION
   INTEGRIN-BINDING PROTEIN DELL
                     Indels
  01-JAN-1998 (TrEMBLrel. 05, Created)
U-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-FP7-2001 (TrEMBLrel. 19, Last annotation update)
INTEGRIM BIRGINS FFOTFIM FFL. FREQUESCS.
  77.8%; Pred. No. 15; ative 1; Mismatches
   PROSITE; PSOROIO; ASX_HYDPOXYI; TONKNOWN_1.
   POTENTIAL
   PRT;
   PEOSITE: FS03022; ESF_1; UNERDWH_3.
PROSITE: PS01186; EGF_2; 2.
PROSITE: PS01187; EGF_CA, 1.
PROSITE: PS01285; FA58C_1; 2.
PPOSITE: PS01286; PA58C_2; 2.
   InterPro, IPR000152, Asx_bydrowyl.
InterPro; IPR000561; EGF-like.
  MEDLINE=98083109; PubMed 9420328;
  Pfam; PF00008; EGF; 3.
Pfam; PF00754; F5_F8_type_C; 2.
  SMOOTIL FASBC: 7
  IPR001881; EGF_Ca.
  IPR000421; FA58_C.
  IPR000742; EGF_2.
  12:21-33(1999)
                   Conservative
  PRELIMINARY;
   MGD; MGI:1329025; Edil3.
   SMAPT: SMOO179; EGF_CA;
   480
 Best Local Similarity
Matches 7; Conserv
  402 VQFVGSYKL 410
  NCBI_TaxID: 10090;
   1 VQFVASYKV 9
   SMART; SM00001;
  035474; 035475;
   TISSUE=EMBRYO;
   OF BIRTH.
  NEURONS.
  InterPro;
  InterPro;
  InterPro;
   SIGNAL
  035474
   CHAIN
  ₹
                     Matches
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   Piciyydu, Noopicia, Endopiciyydia, Eipteia, Biachydda, Muscomorpha;
Ephydroidea: Brosophilidae, Drosophila.
  Gaps
   Stapleton M., Brokstein P., Hong L., Adbayani A., Carlson J., Change M., Charca C., Borsett V., Parfan D., Frisc E., Deurge R., Consister M., Guarin H., Liao G., Miranda A., Mundall C.J., Nurco J., Pacleb J., Paradas V., Park S., Phouanonavouri S., Wan K., Yu C., Lewis S.E., Rubin G.M., Celniker S., Phouanonavouri S., Wan K., Sheirivad (Art. 1971) - FRET, Pankark Cabb databases.

EMBL, ASSESSE: ANSWING T. PRET, Parkark Cabb databases.

ENGLISC 335 AA, 87738 MW, SUFSTREEK/THODGE CRC54;
   SITE (POTENTIAL).
  TMIQ > VIVG (IN SHORT ISOFORM).
MISSING (IN SHORT ISOFORM).
4CD91HTF9261714D GRC64;
   Eukaryeta; Metazoa; Arthropoda; Trachoafa; Hexapoda; insecta;
  83.7%; Score 36; DB 11; Length 480;
   74.4%; Score 32; DB 5; Length 330; B5.7%; Pred. No. 73;
   0; Indels
  23 Indels
  Olomor.,
01-DEC-2001 (TrEMHLEL. 19, Last sequence update)
01-DEC-2001 (TrEMHLEL. 19, Last sequence update)
01-ins-2001 (TreMHLEL. 19, Last annotation update)
  ol MAY 2000 (IEBMSLEEL 13, Created)
01-MAY-2000 (TrEMBLEEL 13, Last sequence update)
01-05C-2001 (TrEMBLEEL 19, Last annotation update)
   F5/8 TYPE C 1.
F5/8 TYPE C 2.
CELL ATTACHMENT
   BY SIMILAKITY.
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RY SIMILAKITY.
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BY SIMILAKITY.
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BY SIMILAKITY.
  PKT; 483 AA.
  330 AA.
   Pred. No. 15:
1; Mismatches
  1; Mismatches
EGF-LIKE 1.
EGF-LIKE 2.
EGF-LIKE 3.
   Fer
   Prosophila melanogastor (Fruit fly)
  53740 MW,
  77.88;
  6; Conservative
  CG11430 PROTEIN (CORTEX).
  Best Local Similarity 77.8
Matches 7, Conservative
  PRELIMINARY;
  PRETERINARY;
  CN RW SP;
  Best Local Similarity
  402 VQFVGSYKL 410
   SHOUENCE FROM N. A.
  1 VQFVASYKV 9
   Ephydroidea: Drow
NORI_TaxID=7227;
  210 GEVASYR 216
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   2 OFVASYR 8
   LD43270P.
   DISULFID
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  Query Match
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  SEQUENCE
   Query Matich
   DISULFID
   CG11330.
   0960N3;
   Q9VMA1;
  DOMAIN
DOMAIN
DOMAIN
DOMAIN
   CN0965
  Q9VMA1
  9
  Matches
   RESULT
   RESULT
  €N0960
   09VMA1
   DDDCCCONK
DDDCCCCN
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BDDCCCCCN
BDDCCCCCN
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363 OFVASYR 369

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While INF-2019/600c; Burband-1874; 42;
Addans M.D. Celuiver S.P.; Holl P.A.; Evyess P.A.; Gergyme I.E.;
Addans M.D.; Celuiver S.P.; Holl P.A.; Hoskins P.A.; Galle P.E.;
Addans M.D.; Celuiver S.P.; Holl P.A.; Ashburnar M.; Henderson S.N.;
Addans M.D.; Celuiver S.P.; Holl P.A.; Ashburnar M.; Henderson S.N.;
Addans M.D.; Carriella M.D.; Zhang O., Chen L.X.;
And J. C.; Morthan J.B.; Yandella M.D.; Zhang O., Chen L.X.;
And M. Basu M.; Basurd A., An H.J.; Holl G.; Molson C.R.; Mikles G.; G.
Addanson K. M.; Basurd A., An H.J.; Moltar Coll L.; Basasloy E.M.;
Adda Dablas M.; Basurd M.; Baruch J., Andrews-Pfennkoch C.; Raldwin D.;
And C. Busan D.A.; Barndale J.; Bayraktaroglu L.; Basasloy E.M.;
Adda Dablas M.; Basurd M.; Basurd R.; Moltar M.; Andrews Pfennkor S.; Moltar M.;
Adda Dablas M.; Cabriella M. P.; Broket Lin P.; Fortline P.;
Burtis K.C.; Busan D.A.; Runket M.; Gallou E.; Ceutert A.; Chander M.;
Adda Dablas M.; Cabriella M. P.; Broket M.; Mays A.B.; Fortline P.;
Burtis K.G.; Busan D.A.; Moltar M.; Mays A.B.; Fortline P.;
Burtis K.G.; Busan D.A.; Moltar M.; Mays A.B.; Fortline P.;
Burtis M.; Godg F.; Gorrella M.; Howel M. H.; Thegwam C.;
Alaris M. L.; Harvey E.; Howland T.J.; Wei M. H.; Thegwam C.;
And J.M.; Kalush P.; Karpen G.M.; Kee Z.; Kennison D.; Moshreif A.;
Ander B.B.; Kodlar C.D.; Kradt C.; Kradt C.; Kradt C.; Moshreif A.;
Ander B.B.; Kodlar C.D.; Kradt C.; Kradt C.; Moshreif A.;
Ander S.M.; Molthow M. A.; Hid. M.; Moltar M.; Moltar M.;
Ander S.M.; Molthow M. A.; Hid. M.; Moltar M.; Moltar M.;
And M.; Matter B.; Morthow M.; Moltar                 Drosophila melanogaster (Fruit Ily)
Eukaryota; Metazoa, Arthropoda, Tracheata, Hekapoda, Insecta;
Piteryota; Nocytera; Endopterygota; Diptera, Brachycera, Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
   "Cortex, a Drosephila gene required to complete comptensities, is a moreon of the colonylety protein \{anily,n\}
   Genesis 29-141-152(2001)
-i- SIMIIAPITY: CONTAINS 2 WE REPEATS (TRP-ASF POMAINS)
   483 AA: 55574 MW; 0070001900805735 CPC64;
   Chu T., Henrion G., Haeqeli V , Strickland S
   PROSITE; PSSOCM2; WO_PEPEATS_2; ?.
PROSITE; PSSO294; WD_PEPEATS_PEGION; 1.
   EMBL; AE303614, AAF52421 1; · · EMBL; AY033478; AAK54464 1; ·
   Science 287:2185 2145(2000)
   FlyBase: FRgn0000351; cort
   InterPro, IPPOGlaku, wran
Pfam, PFOO400; WD40; 2
   SM00320; WD40;
  SEQUENCE FROM N.A.
   Repeat; WD repeat.
   SEQUENCE FROM N A
   MEDLINE=21150807;
CG11330 OR CORT.
   SEQUENCE
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Maint MR-2018 white Primon-10731123.

Adams M.D. Callider C. S. Callider S. E. 10 PW. Heaking B. A. Canalli R. E. F. Ameratides B. Albuman and D. Callider B. Call
                                                                                                                                                                                                      Eukaryota, Motazod, Arthriqoda, Tiacheara, Hexapoda, insecta;
Protypita; Neoporta; Endoplotygota; Hiptora, Krachyoera, Moscomorpha;
Ephydroidea, Prosophilidae; Prosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BARDA MW; UENROTARRIATETTA TEC64,
                                                                              01-MAY-2000 (TrEMBLE). 13, Created)
st-MAY-2000 (TrEMBLE). 13, East sequence update)
01-Det-2001 (TrEMBLE). 19, East annotation update)
                                                                                                                                                                                           Drosophila melanogaster (Fruit fly).
                                          PRT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIYBSSC: FBQQ0039231; cg13638.
interPro; 1PR003579; Rab.
interPro; 1PPGG1806; Pas_trnsfrmng
                                                                                                                                                                                                                                                                                                                                                             MEPLINE-20194004; PubMed-10731122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PRO0449; KASTRNSFRMG.
SMART, SM00175, RAB, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE003749; AAFS6345 1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTP-binding, Lipoprotein.
SEQUEN'E Ald AA, NAMED
                                          PPFI.TMTNAPY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00071; ras; 1.
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                                                                                                                                                                                                                                                                                                                     SECTION'S FROM N.A.
                                                                                                                                                                                                                                                                              NCBI_TaxID-7227;
                                                                                                                                                CHARTH PROTEIN.
                                                                                                                                                                                                                                                                                                                                              STRAIN BEPKELEY
                                                                                                                                                                    CG1363R
                                                               Q9VC31;
                                        097031
7
RESULT
                      Q9VC31
                                                            :15:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Competition IVE
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Query Match

Matches Best

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4 FVASYKV 9
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    cholerae.";
                                                                                                                                                                                                                                                                                                                                                                                          SPBC887.050
                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X;lella.
                                                                                                                                                                                                                                                                                                              094290;
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                                                                                                                                                                                                                                                                RESULT 10
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                                                                                                                                                                                                                                                                                 0.34580
   점점등목록 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-EL TOR N16961 / SEROHPPR 01;
MEDLINE-20406833; PubMod-10952301;
MEDLINE-20406833; PubMod-10952301;
Peideon P.J., Haft Dist. Hickey E.E., Peterson J.D., Unnyum L.A.,
Gill S.P., Nelson K.E., Pead T.D., Tritrelin H., Pichardson D.,
Ermolaeva M.D., Varmathevan J., Bass S., Oin H., Fraquer C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-21488685; Pubmed-11602755;
Afonso C.L., Tolman E.R., La E., Ballinsky C.A., Muser B.A.,
Beenel J.J., Rock D.L., Kutlish G.P.;
"Genome Sequence of a Bardrottus Publicymin 'or Tulex digilpalpus.";
J. Virol 75:11157-11165(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Caps
                                 Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Protecbacteria; gamma subdivision; Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-FLORIDA1997;
Afonse C.L., Tuiman E.R., Lu S., Ballusky C.A., Meser B.A., Beenel J.J., Rock D.L., Kutish G.F.;
Submitted (JUL-2091) to the EMBL/GenBauk/TOBJ databases.
EMBL, AF403738; AAK94161.1; -.
Hypothetical protein.
SEQUENCE 121 AA; 13655 MW; 79971FD649ESB78F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72.1%; Score 31; DB 12; Length 121; 65.7%; Pred. No. 41;
Score 32, DB 5, Length 610;
Pred. No. 1.4e+02;
2; Mismatches 1; indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    l, Indels
                                                                                                                                                                                                                                                                            Culex nigripalpus baculovirus.
Viruses, dsDNA viruses, no ENA stage, Baculoviridae.
NCBL_TaxIP=130556;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             213 AA.
                                                                                                                                                                        121 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
                                                                                                                                                                                                 01-DEC-2001 (TrEMBLrel. 19, created)
                                                                                                                                                                      PRT;
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Query Match
Best Local Similarity 66.7%;
Matches 6; Conservative :
                                                                                                                                                                                                                                               CUNU83 HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 66.79
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                         SIRAIN-FLORIDA1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RARE LIPOPROTEIN B.
                                                                                        400 LDFVATYKV 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                105 VEFLALYKV 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                       SEQUENCE PROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE PROM N.A
                                                           1 VQFVASYKV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 VQFVASYKV 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fraser Ć.M.;
                                                                                                                                                                   0919J2
0919J2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09KTE8;
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                                                                                                                                                                                                                                                             CUN083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J
                                                                                                                                       RESULT 8
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O
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lyne M., Rajandream M.A., Barrell B.G., Lelaure V., Galibert F.; submirred (Nov 1998) to the EMEL/GenRank/DER1 databases.
EMBL: AL033388; CAA21890.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ·:
                                                                                                                                                                                       72.1%; Score 31; DB 16; Longth 213; 85.7%; Pred, No. 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 72.1%; Score 31; DB 3; Length 217; Best Local Similarity 77.8%; Pred. No. 76; Matches 7; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                            0; indets
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS50102; RRM; 1.
FRGSITE, PSG0630, RRM_RHP_1; 1.
SEQUENCE 217 AA; 25319 MR; 4F42BFA4ABAA0C8F CRC64;
                                                                                                            26CB5E30802C8022 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Enkarynta, Punti: Asnomycota, Schimsinchimempotes;
Schimosaccharomycotales; Schimosaccharomycotaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-00T-2000 (TrEMBLrel, 15, Created)
01-00T-2000 (TrEMBLrel, 15, Last sequence update)
01-DEC-2001 (TrEMBLrel, 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-1999 (TrEMBLrel, 10, Last sequence update)
01-DEC-2001 (TrEMBLrel, 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            308 AA
                                                                                                                                                                                                                                          1, Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schizosaccharomyees pombe (Fission yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY 1999 (IrEMBLrel, 10, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-20365717; PubMed-10910347;
Mature 406.477 483(2000).
IDMN, 78003177, AAF94116.1: -.
IIGR, VCU054: -.
Lipoprotein, Complete protrome.
                                                                                                            213 AA: 24121 MW:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PUTATIVE RNA BINDING PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYPOTHETICAL PROFEIN XF0584.
                                                                                                                                                            Ouncy Match
Hest Local Similarity 85.7*
Fos 6, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000504; RRM.
Pfam; PF00076; rrm; 1.
SMART; SM00360; RRM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Xylella fastidiosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUÇUDINCE PROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; P11940; 10VJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         104 VDHVASYKV 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 VQFVASYKV 9
                                                                                                                                                                                                                                                                                                                                                 113 FVASYRV 119
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RA Alvasonga P. Alvos I. M.C., Aroga T.F., Baia G.S., Raptista C.S., Ra Barros M.H., Bonaccorsi F.D., Pordin S., Rove J.M., Brinnes M.P.S., Burno M.R.P., Commango R.E.A., Carraro D.M., Carrare H., RA Colution M.P., Colombo C., Costa M.C., Profile M.C., Perraro J.M., Carraro D.M., Carraro D.M., Parincall A.D., Perraro J.A., Perro                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ú; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Programa (Programa Primates, Charlota, Vertebrata, Euteleostomi, Mammalia; Eutheria; Primates, Catarrhini, Hominidae; Homon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eago M.A., Zalz M., Meidanis J. Setubai J.C.; Valtore A.D., "The genome sequence of the plant pathogen Xylella fastidiosa "; Nature 406-15; 159(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tanigami A., Fujiwara T., Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y., Isogai I., Sugano S., "NEDO human cDNA sequencing project.":
Submitted (FER-2000) 14, 11,— EMBL/SPARAUP/FIRI Jatabases.
EMBL: AKOOM828: BAATITILE NO. 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chory Match 72.1%; Score 21; DB 16, Length 398, Bes' Loval Similarity 85.7%, Pred. No. 1.1e+92; Matches 6; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Store 31, FR 4, Loughh 370;
Pred. No. 1.1+02;
1; Mismatches 0, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 406:15; 159(2000)
EMBU: AE003904: AAF8394 1; -
Hypothetical protein; Complete proteome,
SEQUENCE: 308 AA; 444+4 MW; 415/1615560426-EH PPCH4;
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01-0cT-2000 (TFEMBLFA) 15, Last Sequence update)
01-0cT-2000 (TFEMBLFA) 15, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2000 (TremBLrel. 15, Last annotation up
CDNA FLT20821 FIS, CLONE ADSE00469 (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pPT;
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Best Local Similarity 85.78,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Conservative
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TISSUE-ADIPOSE TISSUE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97 FVASYRV 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "An inversion between mouse and man on chamber me 11/2p13-15 detected by high-resolution comparative mapping "; submitted (SEP 2001) to the EMEL/GenBank/FDBJ databases.
PMRE: AP424697: AA124806 1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, McLasca, Chordata, Craniata, Vertebbata; Euteleostomi;
Mammalia, Eutberia, Rodentia, Sciurognathi, Muridae, Murinae; Mus.
NCBL_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=NUTC9710;
MEDILHE GOGZTAR, Foldmed GROCOD,
NAKADO Y., YOSHIGA Y., Yamashira Y., Kega T.;
"A gene cluster for 6-decxy-1-tallo synthesis in Actinobacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ó
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C
                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72.1%; Score 31; DB 11; Length 1206; 85 78; Prod. No. 4 40012; U.V. Live 1. Mishatches 0, Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 344;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1206 AA; 136046 MW; 349A9A7C7CF0AC46 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      344 АА; 4003- МW; БЕЛЬВЬВЯВЕВВВВ СРС64;
                                                                                                                                           07, Last sequence update)
19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-5FC-2001 (TrEMBLrel. 19, Created)
01-5EC-2001 (TrEMBLrel. 19, Last sequence update)
NIAA0903-LIKE PROTEIN.
                                                                                                                                                                                                                                          Actinobacillus actinomycetemcomitans (Raemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PPT: 1206 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      artin mycetemcomitans.",
Biochim Riophys Acta 1442-409-414(1998).
EMRL; ARO10415; RAA28139 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PSUU6/8; WD_REPEATS_1; UNKNOWN_1.
                                                                                                                        01-AMG-1998 (TrEMBLrel 07, Created)
                                                                                                                                                                                                          INTEGRAL MEMBRANE ACETYLTRANSFERASE
                                                            PPT;
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Interpro; IPRuölnku; WD40.
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Best Local Similarity 62.0.
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                                                            PPFI TMTNAPY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PPELIMINAPY;
                                                                                                                                              01-AUG-1998 (TrEMBLrel.
                                                                                                                                                                                 (TrEMBLrol
                                                                                                                                                                                                                                                                         actinomycetemcomitans)
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res 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 QFVASYKV 9
                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=714;
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                                                                                                                                                                                 01-PEC-2001
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                                                                                     OK6257;
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                                                        055257
PESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
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-!- SIMILATIY: STRONG TO P.DENITRIFICANS COBN AND M.JANNASCHII
M.10907.
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Best Local Similarity 71.4%; Pred. No. Ser02;
Matches 5; Conservative 2; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Archaea, Buryarchaeota: Methanococales; Methanococcaceae;
Methanococcus,
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Plam: PF0214; cobn-Mg_cheli; I.
Bypothetical protein: Complete proteome.
SEQUENCE 1226 AA: 141327 MW: 8P7DDF4E38162AB9 CRC64;
                                                                                                                                                                                01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-05T-2001 (TrEMBLrel. 18, Last annotation update)
HYPOTHELICAL PROTEIN MJ1441.
                                                                                               PRT; 1226 AA
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STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
MEDLINE=96337999; PubMed-8688087;
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                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                Methanococcus jannaschii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=2190;
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510 QYIASYK 516
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Job time: 472 sec

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Copyright (*) 1993 - Zeus Compagna 1343.
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OM protein - protein search, using sw madel

(without alignments) 3.735 Million cell updates/sec September 5, 2002, 15 27 36 ; Search time 58.86 Seconds Pun on

US-09-744-804-41 1 FILLAALCGA 9 Title: Perfect score. Sequence

231629 seqs, 24425594 residues REGSUM62 Gapop 10 0 , Gapext 0.5 Searched.

Scoring table

231628 Total number of hits satisfying chosen parameters:

Maximum DB seg length: 2000000000 Minimum DB seq length: 0

Post-processing: Minimum Match 100% Maximum Match 100% Listing first 45 summaries

/egal2\_6/prodata/2/laay5A\_COMP\_pop.\*
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/egal2\_6/prodata/2/laay10105\_COMB.prp.\*
/egal2\_6/prodata/2/laay10105\_COMB.prp.\* Issued\_Patents\_AA:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

no Toerrintion	Bright of the second	£ Sequence 6,	Section 19	9 Sequence 9,	11 Sequence 11	Sequence 13	751-36 Sequence 36, Appl		346-1 Sequence 1, Appl.	) Sequence 1,	17	c i	5	7 Sequence 7,	4 Sequence 4,	Sequence 5,	905-11 Sequence 11, Appl	-2 Sequence 2,	3	9	3,	B-17 Sequence 17,	8	-8 Sequence 8,	44A 9 Sequence 9,	83	33-83 Serinettise H	83
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Sequence 83,	Sequence 83,	sequence 67, Appl		Sequence 37,		Sequence 37,	Sequence 37,	Sequence 6, A	Sequence 3, Appli		Sequence 195,	Sequence 105,	Sequence 46, App	Sequence 1, Appli		Sequence 38,	.~
US-08-461-361-83	US 08 485 910 83	PCT-U375 00200-07	115-04-627-376-17	45-81004-936-20-3h	US-U8-176-537-37	US UB 485 607 37	US 08 475-879-57	US U9 372:422A 6	US-08-785-065-3	US 09 676 444 47	US-08-611-757-105	PCT-US95-05980-105	US-09-372-422A-46	11 <u>S-09-838-833 1</u>	US-08-466-034-48	US:08-444-733-38	115-08-464-134-38
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# ALIGNMENTS

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APPLICANT: CERIANI, ROBERTO L.
APPLICANT: PETERSON, TERPY A.
APPLICANT: PAROCCA, DAVID J.
IIILE DE INVENTION GIORGIES (HMFS) ANIIGEN, FRAGMENIS & FUSION PROFEIN
NUMBER OF SIGUENCES. 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:

AFILIALIA NUMBER: US.05,151,401B FILLING DATE: 03-DRC-1000
                                                                                                                                                                                               ADERESSEE. Fruit, Schingdar & Poplawski
STREET: 444 South Flower St., 19th Floor
CITY: Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION NOMBER:
FILING DATE:
OLASSIFICATION: 435
PRICE APPLICATION NOMBER:
FILING DATE:
ATTORNEY ****
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 213 622-7700
TELEFAX: 213 489 4210
           ; Sequence 6, Application MS/08/52402B
; Patent No. 5972337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30,930
                                                                                                                                                                                                                                                                                                              COMPUTER: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARD
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unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vi∵iana
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MCLECULE IYPE, peptide
                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER.
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STRANDEDNESS: un}
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                                                                                                                                                                                                                                                                  USA
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COUNTRY: USE
90071
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US-08-162-402B-6
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                                                GENERAL.
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1; Mismatches
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03-DEC-1993
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TELECOMNINATORATION INFORMATION:
TELEPHONE: 213-622-7700
TELEFAX: 213-489-4210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT FILING DATE: 1997-07-09 EARLIER APPLICATION NUMBER 60,7021,685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , Sequence 11, Application US/08890719A ; Patent No. 6075125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                  IBM Compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          463 amino acids
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MEDIUM TYPE: Diskette
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                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: unknown
MOLECULE TYPE: peptide
                    NUMBER OF SEQUENCES: Z
                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
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                                                                                                                                                                                                              OPERATING SYSTEM:
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                                                                                                                                              90071
                                                                                                            S.
                                                                                                                                                                                                  COMPUTER:
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                                                                                         CITY: STATE:
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                                                                                                                                                                                                                                                                  TITLE OF INVENTION: 46 KDALTON HUMAN MILK FAT TITLE OF INVENTION: GLOBULE (HMFG) ANTIGEN, FRAGMENTS & FUSION PROTEIN
 O; Caps
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O: Indels
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APPLICANT: PETERSON, JERRY A.
THELCANT: PETERSON, JERRY A.
TITLE OF INVENTION: 46 KDALTON HUMAN MILK FAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEG for Windows Version 2.0 cUKENT APPLICATION DATA:
APPLICATION NUMBER: 18,708,142,4028
FILLING DATE: 03-DEC-1993
                                                                                                                                                                                                                                                                                                                                        E: Pretty, Schroeder & Poplawski
444 South Flower St., 19th Floor
 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0: Mismatches
                                                                                                                                                         Sequence R Application (1870R16.2402R Patent No. 5972337
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; Fatent No. 5972337
                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: CERTANT, ROBERTO I.
APPLICANT: PETERSON, JERRY A.
APPLICANT: LAROCCA, DAVID J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30,930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: P6
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IBM Compatible
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TELEFAX: 213-489-4210
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 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 2'
                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unknown
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                                                      GENERAL INFORMATION:
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                                 1 RELIAMECGA 9
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                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                            STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                            90071
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                                                                                                                                            US-08-162-402B-8
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TITLE OF INVENTION: GLORGLE (HMFG) ANTIGEN, FRAGMENTS & FUSION PROTEIN
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APPLICANT: Hunt, Henry D
APPLICANT: Fulton, Janet
TITLE OF INVENTION: Production of Antisera Specific to Major
TITLE OF INVENTION: Histocompatchility Complex Molecules in Chickens
FILE REPREMCE: DKt 0064-96 - Larry D. Haron et al.
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                                                                                                                                                                                                                                                                                                                                                                                    SYSTEM: DOS
FastSEQ for Windows Version 2.0
                                                                               ADDRESSEE: Pretty, Schroeder & Poplawski STREET: 444 South Flower St., 19th Floor CITY: Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 81.8%; Score 36; DB 3; Length 355; Best Local Similarity 87.5%; Pred. No. 20; Matches 7; Conservative 1; Mismatches 0; Indels
                           ny Indote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CRYPTOSPORIDIUM ANTIRODIES, DNA
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VECTOR AND TRANSPORMED HOST AND
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                           Selfo temat M. : I
Best Local Similarity 87.5%; Pred. No. 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DIAGNOSIS AND KIT
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FARLISE AFFLICATION NUMBER: 60/021,685
FARLIER FILLING LAIE. 1996 07-10
NUMBER OF SEC IU NOS: 39
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                                                                                                                                                                                                                                  Sequence 14, Application US/08890719A Patent No. 6075125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 36, Application US/08415751
; Patent No. 5643772
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APPLICANT: PETERSEN CAROLYN
APPLICANT: LEECH, JAMES
APPLICANT: NELSON, EICHARD, C.
APPLICANT: GUT, JIRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Wordpertect 5.1 CURRENT APPLICATION DATA:
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                        7; Conservative
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APPLICANT: Hunt, Henry D
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NUMBER OF SEQUENCES:
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                                                                                                               12 LLAAVCGA 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE:
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                                                                                                                                                                                                           US-08-890-719-13
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                      Matches
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                 resitions coded by monsense codens are identified as Xaa.
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                                                                                                                                                  480.19-2 (HHD)
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                                                                                                                                                                                                                                                                                                                                                                   Cryptosporidium parvum
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APPLICATION NUMBER (N.CO.).
APPLICATION NUMBER (1, 1993)...
APPLICATION NUMBER (1, 1993)...
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IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Fabian, Gary R. RECISTRATION NUMBER: 33,875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER | R60
TELECOMMUNICATION INFORMATION:
                                                                                                                                30,518
                                                                                                                                                 REFERENCE, TOCKET NUMBER: 48
                                                                          FILING DATE: May 29, 1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                  TELEPHONE: (415) $24-1677
TELEFAX: (415) $24-1678
INFORMATION FOR SEQ ID NO: 36:
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INFORMATION FOR SEQ ID NO: 1
                                                                                                                                                                                                                                                             361 amino acids
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                                                                                                               Hana Dolezalova
                                                                                                                                                                                                                                                                                              single
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CORRESPONDENCE ADDRESS:
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         PRIOR APPLICATION DATA:
                                                                                                                                  REGISTRATION NUMBER:
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FILING DATE: 01-FER
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                                                                                                                                                                                                                                                                           amino acid
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21P 94306-0850
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NAME/NEY:
US-08-415-751-36
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TYPE:

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GENERAL INFORMATION:
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 6 KILVALCG 13
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                                                                US-08-473-089-1
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                                                                                                                                                                                                                                                                                                                    COUNTRY:
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                                                                                                                                                       70.5%; Score 31; DB 1; Length 15; 62.5%; Fred. No. 7.5; 1; radels
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                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Mochly Rosen, Datia
APPLICANT: Ron, Dorit
LITLE OF INVENTION: Who-40 - Derived Peptides and Uses
NUMBER OF SEQUENCES: 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: MURASHIGE, KATE H. RELISTRATION NUMBER: 29,599
REPERFUNG FORTH NUMBER: 2550-0025 20
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE, Morrison & Foerster
STREET: 2000 Pennsylvania Avenue, NW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/477,346
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
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MIDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPRATING SYSTEM: PC-DOS/MS-DOS
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                                                                ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Peptide I
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; INDIVIDUAL ISOLATE: Peptide I
US-08-477-846-1
                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/08477346
Patent No. 6262023
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ATTORNEY/AGENT INFORMATION:
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Matches 5; Conservative
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            MOLECULE TYPE: peptide HYPOTHETICAL: NO
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unknown
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                           HYPOTHETICAL:
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TOPOLOGY:
                                                   ANT 1 - SENSE:
                                                                                                US-08-190-802A-1
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                                                                                                                                                         Ouery Match
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Caps

1 RLLAALCG 8

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APPLICANT: Mitchinson, Colin
APPLICANT: Wendt, Dan J.
TITLE OF INVENTION: No. 6268328el Variant EGIII-Like Cellulase Compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Caps
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                                                                                                                         Taring d Teptides and Uses
                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE. Floppy disk
COMPUTER: IRM PC Compatible
O'EMATIN: SYSTEM: PC-1m-s/Ms-1m-s
SOFTWARE. Patentin Release #1.6, Version #1.25
CURPENT APPLICATION DATA:
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CURRENT FILLNG DATE: 1098-12-18
NUMBER OF SIG ID NOS: 41
SOFTWARE: FastSeQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         მალის-სსელი
                                                                                                                                                                                                                         E: Morrison & Foerster
2000 Pennsylvania Avenue, NW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US,/08,/473,089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 17, Apriliation US/09216295
Patent No. 6268328
; Sequence 1, Application US/08473089; Patent No. 6342368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Peptide 1
                                                                      APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF HWUNTION, Mr. 45 F44
IITLE OF HWENTION, Thereof
NUMBER OF SROUGNCES: 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 29,959
PPFFPHNFFZHONKET NUMBEP: 355
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : (202) 887-1500
(202) 887-0763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-JUN-1995
N: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: MORASHIGE, KATE H.
REGISTRATION NUMBER: 29,9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       unknown
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                                                                                                                                                                                                                                                                      CITY: Washington
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                                                                                                                   Gaps
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75;0%; Pred. No. 2;30:02;
tive 0; Mismatches 2; Indels
                                                                         70.5%; Score 31; DB 4; Length 88; 100.0%; Pred. No. 43; ative 0; Mismatches 0, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8: Sterne, Kessler, Goldstein & Fox P.L.L.C.
1100 New York Ave, NW, Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Rolease #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/OB/691,814B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1383.0090001
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....лкк: US/OR/691,814В
31-JUL-1996
Nr. 435
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FILING DATE: 09-AUG-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 3, Application bs;008 cm708A
                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08691814B
Patent No. 5981218
                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION.
APPLICANT: Rio, Marie-Christine
APPLICANT: Iomasetto, cutberine
// ORGANISM: Gliocladium roseum (3)
US-09-216-298-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 13 IELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 202-371-2600
TELEFAX: 202-371-2543
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                      Jenniter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               470 amino acids
                                                        Obery Match
Best Local Similarity 100.0
Loc 6, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Basset, Paul
APPLICANT: Byrne, Jennit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , MOLECULE TYPE, protein
US-08-691-8148-2
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Bost Local Similarity
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                                                                                                                                                       3 LAALCC 8
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US-08-336-708A-9
                                                                                                                                                                                                                                                                              US-08-691-814B 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Helistr m, Ingegerd
APPLICANT: Helistr m, Karl E.
TITLE OF INVENTION. HEA HUMAN RECEPTOR TYROSINE KINASE
NUMBER OF SQUENCES: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; indels
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CURRENT APPLICATION DATA:
APPLICATION BATA:
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0; Mismatches 1:
                                                                                                     TITLE OF INVENTION: Hybrid Receptor Molecules
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          115,777,484,438
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                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DGS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Gleski, Namey
REFERENCE/DOCKET NUMBER: A-241A
INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Plowmen, Greatery D.
APPLICANT: Chlouscou, Jean-Michel
APPLICANT: Shoyab, Mchammed
APPLICANT: Slegall, Clay B.
                                                                                                                                                                                     1840 Dehayilland Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . sequence 7, Application US/08484438
; Patent No. 5811098
; Patent No. 5811098 5780031
                                         APPLICANT: Pacifiel, Robert E. APPLICANT: Thomason, Arlen R. APPLICANT: Chang, Ming-Shi
                                                                                                                                                                                                                                                                                                            3: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   644 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy of
                                                                                                                                                                      Amgen Inc.
                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
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                                                                                                                                              TORRESPONDENCE ADDRESS:
                                                                                                                                                                                                        Thousand Oaks
                                                                                                                                                                                                                                California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
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ZIP: 10036-2711
                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 LLAALCGA 9
                                                                                                                                                                                                                                                      USA
Patent No. 5521295
                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE:
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                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LINGTH.
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                                                                                                                                                                                                        CITY:
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INPORMATION FOR SEQ ID NO: 4:
                 SEQUENCE CHARACTERISTICS.
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APPLICANT: KRAUS, MATHIAS H.
APPLICANT: ARRONSON, STUBRT A.
TITLE OF INVENTICE. ESE FECEFTER SENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70.5%; Score 31; DB 2; Length 121 87.5%; Pred. No. 5.7e+02; ative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC compatible
COMPUTER: TREM PC -DOS/MS-DOS
SOFTWARE: Patentin Rejease #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S: NEEDLE & ROSENBERG, P.C.
Suite 1200, 127 Peachtree Street
                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US U//981,155
FILING DATE: 24.NOV-1992
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                             5624-230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/475,035 FILING DATE: 7 Jun 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER 1414.656
TELECOMMUNICATION INFORMATION:
                                                                                          US 08/150,704
                   CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-475-035-4; Sequence 4, Application US/08475035; Patent No. 5985553
                                                                                                                                                                                                                                                                                                               TELEPHONE: (212) 790-9090
TELEYAX: (212) 869-8864/9741
TELEX: 66141 PENNER
INFORMATION FOR SEQ. ID NO: 7.
SEQUENCE CHARACTERISTICS.
                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 562
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                          NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 33,438
                                                      APPLICATION NUMBER: 08,732 FILING DATE: 14-0CT-1994
                                                                                                          10-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                          1210 amino acids
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NAME: Perryman, David G.
 07 - HIN - 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     404/688-0770
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Rest Local Similarity 87.5%
Local 7, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                 unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein US-08-484-438-7
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
                                                                                         APPLICATION NUMBER:
FILLING DATE: 10-NOV
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                               unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
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                 CLASSIFICATION:
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No. 6268328el Variant EGIII-Like Cellulase Compositions
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                                                                                                                                          Length 1210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 68.2%; Score 30; DB 4; Length 259; Best Local Similarity 87.5%, Pred No 1.9\alpha-02; Matches 7; Conservative 0; Mismatches 1; Indels
                                                                                                                                        Query Match 70.54; Score (1): 106-2; Length 123 Best Local Similarity 97.54; Fred No. 5.76.02; Matches 7; Conservative 0; Mismatches 1; Indels Matches
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Job time: 322 sec
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CHREENT APPLICATION NUMBER-HS/704/216,295
CURRENT FILING DATE: 1998-12-18
NUMBER OF SEQ ID NOS: 41
                                                                                                                                                                                                                                                                                                                                                                           Sequence 5, Application US/09216295
Patont No. 6268328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORGANISM: Aspergillus aculeatus OS-09-216-295-5
                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Mitchinson, Colin APPLICANT: Wendt, Dan J. TITLE OF INVENTION. No. 62683
1210 amino acids
                                                         MOLECULE TYPE: protein
                      amino acid
                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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GenCore version 4.5
Copyright (c) 1993 - 2000 - compugen Ltd
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OM protein - profein search, using sw model

(without alignments) 6.310 Million ceil updates/sec Soptember 5, 2002, 15:26:32 ; Search time 158 43 Seconds Pun on.

US-09-744-804-41 1 PLLAALCGA 9 Title: Perfect score: Sednence:

Gapop 10 0 , Sapext 0 5 PLOSUM62 Scoring table.

747574 seqs, 111074796 residues Searched

Total number of hits satisfying chesen parameters.

Minimum DR seq length: 0 Maximum DR seq length: Zuumnünnün

Listing first 45 summaries Maximum Match 100% Post-promessing: Minimum Match 0%

A\_Geneseq\_0328n2.\* 1: /SIDS1/gcgdata/ Database :

| STDST/gcgdata/hoid-geneseg/genesegp-enbl/AA1994.LAT:\* | STDST/gcgdata/hoid-genesegp-msegp-enbl/AA1995.TAT:\* | STDST/gcgdata/hoid-geneseg/genesegp-enbl/AA1996.DAT:\* /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/Aal989 DAT \* /SIDSi/yegdata/hold-geneseq/geneseqp-embi/AA1990.hA1:\* /SIDSI/gogdata/hold-geneseq/geneseqp-embi/AA1991.cbl.:\* /SIDSI/gogdata/hold-geneseq/geneseqp-embl/AA1992.DAT:\* /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1998.DAT:\* /SIDS1/gcgdata/joild-geneseq/geneseqp-embl/AA1999\_DAT:\* /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AAL984.DAT:\*
/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AAL985.EAT:\*
/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AAL985.EAT:\*
/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AAL985.DAT:\*
/SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AAL988.DAT:\* /SIES1/acydata/hold-geneseq/genesegp\_embl, AA1997.DA1.\* /SIDS1/gegdata/hold-geneseq/genesegp-emb1/AA1993.DAT:\* /SIDSI/gegdata/hold-geneseg/genesegp-ombl/AA1980 [AR+\* /SIUSI/gegdata/hold-geneseg/genesegp-ombl/AA1981 (AT-\*/SIDSI/gegdata/hold-geneseg/genesegp-ombl/AA1982 DAT+\* TAT: \* /SIDSI/gcgdata/hold-genesey/yeneseyp-embl/AA2000.pAT. /SIDS1/grgdata/hold-geneseg/genesegp-ombl/AA1983  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by unalysis of the total score distribution.

SUMMARIES

/SIDS1/grgdata/hold-geneseq/geneseqp embl/AA2001.DAT

	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Description	Lactadherin (BA-46	HMFG 46 kDa antige	Human lactadherin	Mouse lactadherin	Probe F10-encoded	Chicken BFIV21 cla	Chicken BFIV12 cla	Novel human diagno	Propionibacterium	Fropionibacterium	Drosophila melanog
	ii F	TF.	AAY82846	AAR77252	AAY94453	AAY94454	AAP83149	AAY 94506	AAY94507	ABG15914	AAU40306	AAU41965	ABB70578
	r L	١.	2	9	2]	21	σ	21	21	C4 C4	77	근근	23
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	000		7	47	4	.0	36	ř	ž	3.6	3,6	7	34
	Result		7	2	m	4	S	so.	7	80	0	10	11

Eisenbach L, Carmon L, Tirosh B, Bar-haim E, Faz A, Fridkin M,

Fitzer attas C;

(YEDA ) YEDA RES & DEV CO LTD. (RIGT-) RIG-TECHNOLOGY GEN CORP.

98IL-0125508.

30-JUL-1998;

Novel human diagno	Human polypeptide	Baman secreted pro	Nevel human diagno	Mycobacterium spec	mr):	Myschacterium spec	iest	Human secreted pro		pozalam elidescril	- 02	human		upas atotota acqu	Peptide #11580 enc	Profess # # # # # # # # # # # # # # # # # #	Human brain expres	Human bone marrow	Peptide #8141 enco	Feptide #12057 enc	Propionibacterium	Propionibacterium	Human secreted pro	C. pneumoniae prot	Propionibacterium	Mycobacterium tube	Pseudomonas aerugi	Pseudomonas aerugi	Rat L'type amino a	Haman ORFX OFF1900	Homan meropane tra	Human 1. type amino	Human amise acid t
	AAC09273	AAB85537	ARC:0:09	AAY04969	AAB5.2441	AAY04970	AAS64770	AAP85557	AARBH155	ABB63196	ABG20210	ABC20216	AAG67259	AAR94PDD	ABB44074	ARRETER	AAM65095	AAX77799	AAM21707	AAM38620	AAU40067	AAC41814	AAY86223	AAY 34703	AAU41023	AAC81145	AAU36419	AAHSOO957	AAB72393	AAP4.51.55	AAY / 1::4-1	AAB72395	APB11788
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77.3	7.		S	75.0	G 2				75.0	u i	li i	75.0	u i	15, 11	70.7	~. •.	72.7	75.7	72.7	72.7	70.7	72.7	72.7	72.7	1:1	72.7	72.7	12 3			1:1	72.7	72.7
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12	53	14	15	16	~	18	e [	U.C.	17	C1	C1	<	25	45	27	3. 14	<u>କ</u> ଥ	3.0	31	ci Ci	33	3.4	35	36	3.7	38	68	40	41	7.7	<b>.</b>	44	u 😝

### ALIGNMENTS

Lactadherin (BA 46) pertide itagment (tumour associated antigen). prostate specific autigen, prostate specific membrane antigen; prostate acid prosphatase, mucin, lactadherin; teratocarcinoma derived growth factor; PSA; PSMA; PAP; CRIPTO-1. treatment, prevention; core, anti-tument vaccine; metastases; broad, badder; prostate, parateas, ovary, hyroid, colon, stomach, carcinoma; MHC Class I; HLA-A2; human; Major Histocompetibility Complex; uroplakin; Pureur associated antigen peptide; TAA; cancer; carcinoma; AAY82840 standard; peptide; 9 AA. 99WO-11 00417. (first ontry) Woloupu6723-Al. Homo sapiens. 29 - JUL- 1999, 19-JUN-2000 10-PER-2000 AAY82846; AA182846 PRSULT 

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46 kD apparent molecular weight human milk fat globule antigen
                                                                                                                                                                                                                                                                                                                                                      AAY94453
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                                                                                                                                                                                                                                                      Those tunnour associated antiques described in records AAY82896-Y82824 and AAY82855 YY82865 are derived from Oropiakin, such as Oropiakin II. Groplakin II. Those described in records AAY82825-Y82829 are derived from prostate specific antique (PSA). Those described in records AAY82835 are derived from
                                                                                                                                                                                   molecules and are generally between 8 to 10 amino acids in length. The amino acids located at positions 2 and 9 of the tumour associated antiques are the another residues which participate in the binding to MHG class 1 molecules, more specifically HIA A2. More tumour associated associated associated associated associated associated associated artiques are described in GENESEQ records AAPP2806-Y828R2.
                                   Tumor associated antiques peptidas, especially decised from uroplakin, useful as varmines to propert or the various including breast, bladder, prostate, panereas, ovary, thyroid, colon and stomach -
                                                                                                                                                                                                                                                                                                                                                               from Lactadherin (BA:46). These described in records AAY82847.Y82854 are derived from Marin and those described in records AAY82871-Y82882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HMFG; human milk fat globule; antiqen; immunogen; vaccine; virucide; epithelium; tumor; breast cancer monocional aptibody; MAb
                                                                                                                                                                                                                                                                                                                       prostate specific membrane antigen (PSMA). Those described in records YY82836-AAY82839 are derived from prostate acid phosphotase (PAP). Those described in records AAY82840-Y82846 are derived
                                                                                                                                   treatment, prevention and cure of cancer or cancer metastases. The cancer may be breast bladder, prevate, paperray every, thyroid, colou, stomach, head or neck cancer or a carcinoma. The tumour associated antigens are presentable to the immune system by HLA-A2
                                                                                                                                                                                                                                                                                                                                                                                          are derived from Teratocarcinoma derived growth factor (CRIPTO-1).
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                                                                                                                     Tumour associated antiqen peptides (TAA) may be used for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 44; DB 21; Length 9; 100.0%; Pred. No. 6.4e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ceriani M., Larocca D.J., Peterson JA;
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                                                                                         Claim 17; Page 100; 113pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HMFG 46 kDa antigen.
           WPI: 2000-205463/18
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Lactadherin protein was found in exosomes produced by dendritic cells. The protein is invelved in the phanorytosis of particulate antideous by dendritic cells. Exosomes produced by dendritic cells exposed to tumour antiques induce potent immune responses. Lactadherin or variants of it may be used in the mediation of an immune response. Variants of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chimeric isolated (human) lactadherin polypeptide that functions as an adaptor of cross-priming to eliminate pathogenic antigens, e.g. in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                   A complete cDNA sequence for the 46 kDa HMFC antiqen, a major component of the apical surface of the normal breast epithelial real, was obtained by PCR and RACE methods. cDNA clones can be used to prepare MAPs for ise in immunotherapy, immunohistopatheleay, proquosis, diagnosis, imaging and therapy. Recombinant antiqen can be expressed in prokarpetic or (4), cosylated) in cakarpetic cells.
used in assays to determine the presence of a cancerous tumour of epithelial origin, and in a vaccine against neoplastic tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 44; DB 16; Length 387; 100.0%; Pred. No. 6.7; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; lactadherin; MGF-E8; anti-tumour; immune response;
exosome; dendritic cell.
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/label= Integrin_binding_site
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/label= Secretion_signal
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/label= Lactadherin
                                                                                           Cluim 6, Euge 46 47, 68pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY94453;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide
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δλ qq

also be used to monitor an immune response, more specifically a CTL (gittscore T-Lymphocyte) response and also to produce CTLs specific for a selected antiqen. The present sequence is the mouse lactadherin protein.

Seduence

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lactadherin may be used for inhibition and/or stimulation of the cross-priming of antigens and stimulation of the phagocytosis of antigens by denditier rells. Compositions derived from lactadherin can also be used to monitor an inhume response, more specifically a Cit Cytotoxic T. Tymphocyte) response and also be preduced from selected antigen. The present sequence is the human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chimeric isolated (human) lactadherin polypeptide that functions as an adaptor of cross-priming to eliminate pathogenic antigens, e.g. in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lactadherin protein was found in exosumes produced by dendritic cells.
                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                          .
                                                                                                                                                                                                                                                                                                        Score 44, DB 21, Length 387,
Pred. No. 6.7;
Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; lactadherin; MGF E8, anti-tumour; immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= Integrin_binding_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (INRM ) INSERM INST NAT SANTE & RECH MEDICALE
                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /labcl= Secretion_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note- "encoded by GI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= Lactadherin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY94454 standard, Protein, 426 AA.
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                                                                                                                                                                                                                                                                                                              100.0%
                                                                                                                                                                                                                                                                                                                                         100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse lactadherin protein.
                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          exosome; dendritic cell.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80
                                                                                                                                                                    lactadherin protein.
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                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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                                                                                                                                                                                                                       387 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                            1 RLLAALCGA 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-NOV-1998;
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                                                                                                                                                                                                                          Sequence
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AAY94454
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                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Product F10 is mard in PETF analysis of chicken erythmosph, builted DNA, it corresponds to a MFC chass I anthern and was obtained from the Lotal mENA at different tissues of chicken.
See also AANNORSE and AANNORSE
                                                                                                                                                                                                                         chicken erythrosyte: histocompatibility complex class Lantique, restriction fragment length polymorphism (RFLP); probe F10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ion chickens, asing crythiosyte LNA tragments and hybidisation probe derived from histocompatibility complex antigen.
                                   0
           Length 426;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Restriction fragment length polymorphism genotyping test -
                                  0; Indels
                                                                                                                                                                                                      Probe F10 encoded protein of MHC class I of chicken.
                                                                                                                                                                                                                                                                                                                  "cleaved from mature protein"
           Score 37; DB 21;
Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Auffray C, Behar G, Billault A, Chausse AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                /labelrcytoplasmic extremity
                                  1; Mismatches
                                                                                                                                                                                                                                                                                                        /label=signal peptide
                                                                                                                                                                                                                                                                                                                                                                                                         /label=transmembrane
                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                   AAP83149 standard; protein; 345 AA.
                                                                                                                                                                                                                                                                                                                                                                                   /label=alpha 3
                                                                                                                                                                                                                                                                                                                                         /label-alpha 1
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           84.18;
87.5%;
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Ouery Match
Best Local Similarity 87.55
Free 7, Conservative
                                                                                                                                                                               27-NOV-1990 (first entry)
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N-PSDB; AAN80603.
                                                                             5 rvlaalcg 12
                                                        1 RLLAALCG 8
                                                                                                                                                                                                                                                            Gallus gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27 MAY-1988,
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                                                                                                                                                          AAP83149;
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with class I and class IV MHC proteins. The present sequence is {\rm BFIV21}\ {\rm class}\ {\rm I}\ {\rm MHC}\ {\rm protein}\ .
                                                             Sequence 355 AA;
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|2 ||aavcqa ||9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                 2 LLAALCGA 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gallus gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Producing antisera specific to major histocompatibility complex (MHC) proteins in chickens involves administering transfected cells expressing heterologous chicken MHC class I protein capable of
                                                                                                    Gaps
                                                                                                  .,
                                                           Length 345;
                                       Score 36; DB 9; Length 340, Pred. No. 1.46+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label- transmembrane_and_cyptoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                               Chicken; MHC; major histocompatibility complex; BFIV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'label * N-glycosylation_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= N-glycosylation_site
                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label- signal_peptide
22..109
/label= alphal_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= alphā2_domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                           AAY94506 standard; Protein; 355 AA.
                                                                                                                                                                                                                                                                                                                                                                                            Chicken BFIV21 class I MHC protein.
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                                                         81.8%;
87.5%;
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291
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                                                                                                  7; Conservative
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                                                                            Local Similarity
  345 AA;
                                                                                                                                                            ||||:|||
|2 ||aavcqa ||9
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                                                                                                                                     2 ::LAA::3GA 9
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    sodnence Sednence
                                                             Query Match
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Matches
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Producing antisera specific to major histocompatibility complex (MHC) proteins in chickens involves administering transfected cells expressing beterologous chicken MHC class I protein capable of
                                                                             Gaps
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                                                                        .,
                        Score 36; DB 21; Longth 355;
Prod. Bo. 1.5e<sup>4</sup>02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= transmembrane_and_cyptoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chicken; MHC; major histocompatibility complex; BFIV;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= signal_peptide
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201..291
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                                                                                                                                                                                                                                                                                         AAY94507 standard; Protein; 355 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacon LD, Fulton JE;
                        81 8%;
87.5%;
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Query Match
Best Local Similarity 87.50,
These 7; Conservative
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N-PSDR; AAA48670
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sequence may be generated. The Lateralogous BFTV protein produced by these cells may be used as an immanagen to produce edition mid-lass specific antisors. This subtisors may then be used to determine the BF haplotype of any thicken RFTV specific antisors may be used to determine the RFTV specific antisors may be used to determine the RFTV specific antisors may be used to determine the RFTV produced with reduced cross reaction with class I and alass IV MHC proteins. The present sequence is BFTVIZ class I MHC proteins. The present sequence is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saps
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diagnostics, forensics, gene mapping, identification of motations
responsible for genetic disorders or other traits and to assess
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food supplement; medical imaging; diagnostic; genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                              Length 355;
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Prod. No. 1 Gain2.
Transtohes 0, Indels
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23-AUG-2000; 200008-0649167
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Best Local Similarity
Trakes 7; Conservat
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                                                                                                                                                                                                                                                                                                  Sequence 355 AA;
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polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and displacis of medical conditions caused by the treatment, prevention and displacis of medical conditions caused by the disorders include SAFHO syndichne (syndovitis, and properties), prestricts, hyperrosis and osteomyelitis), uvertis and endophthalmitis. Pracess is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the central lesions associated with ache vulgaris. A method for detecting the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
and to produce other types of data and products dependent on PNA and amine acid seperates. ABCDDS10-MBCDD377 represent novel human diagrams is amine acid sequences of the invention of the human between the sequences. Between the product of the printed specification, but was obtained in clottonic format directly from WIPD at ILp.wipo.int/pub/pub/ished_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SAPHC syndrome; synoritis; acne; pustulosis; hypertosis; esteemyelitis; or orbits; endophilainitis, bone, joint, settrai nervoue system; BLISA; intlammatory lessen; acne vidgatis, entope linked immunosorbont assay; dermatological, osteopathic; neuroprotectant.
                                                                                                                                                                                                                                                                                   Saps
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                                                                                                                                                                                                                                  79.5%; Score 35; DB 22; Length 365;
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Conservative 9. Missatches 0. Indels
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L'maisonneuve J, Zhang Y, Jen S, Carter D;
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02-JUN-2000; 2000US-208941P
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Matches 7, Conserv
                                                                                                                                                               365 AA;
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downrequister expression and activity of Larines polymetribes and therefore treat Plannes inferious. The antibudies may also be used as diagnostic agents for determining a cornes presence, for example, by ensyme linked immunosorbent assay (BLISA).

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formal directly from WIFO at 11p wipo.int/pub/published_pol_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endopih hainitis; bone; joint, central nervous system; ELISA; inflammatory lesion; acte vulgaris; enzyme linked immunostrbust assay; dermatological; osteopathic; neuroprotectant.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Propionibacterium acnes polypeptides and nucleic acids useful for
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has | l; Indels
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L'maisonneuve J. Zhang Y. Jen S. Carter D;
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                                                                                                                                                                                                                                            Score 34; DB 22;
Pred No. 1 5ex 02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU41965 standard; Protein; 197 AA.
                                                                                                                                                                                                                                            Query Match 77,3%;
Best Local Similarity 66.7%;
Matches 6; Conservative
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2000US-216747P
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                                                                                                                                                                             Sequence 160 AA;
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The invention is
                                                                           enzyme linked immunosorbent assay (ELISA).
Note: The sequence data for this patent did not form part of the printed
specification, but was obtained in electronic format directly from WIPO
eposition for f. actors proteins. These actibulies can be used to downcopiate expression and activity of P. across polypetides and therefore treat P. across identifiers. The antibulies may also be used as diagnostic agents for determining P. across presence, for example, by
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated nucleic acid detection readent expable of detecting 1600 or more genes from the expaint the invention useful in developmental biology and in elucidating cell signalling and explicitly interactions in higher cobargodes for the development of insecticides, therapeuties alpha harmaceutical drugs. The invention discusses genomic bNA sequences (ARLIGITE ARLAGIT), expressed DNA sequences (ARLIGITE) and the encoded proteins
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                                                                                                                                                                                                                                  Score 24, DP 22, Length 197;
Prof. No. 1 90:02,
2; Mismatches 0: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster polypeptide SEG ID NO 38526.
                                                                                                                                    at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                         2; Mismatches
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                                                                                                                                                                                                                                                                         6; Conservative
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Best Leval Similarity
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                                                                                                                     Caps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chromosome mapping, gene therapy, foreupping, propingly, forensic, upplement; medical imaging diagnostic, genetic diagnostic,
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                                         Score 34, DB 22, Length 466,
Prod No. 4 26+62,
1; Mismatches 1; Indels
                                                                                                                     1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel human diagnostic protein #18809.
                                                                                                                                                                                                                                                                                                                                                                                                                                           ABG18818 standard; Protein; 1754 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drmanac RT, Liu C, Tanq YT;
                                         77.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAR-2001; 2001WO-US08631.
Query Match
Best Local Similarity 75.v.,
6. Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-MAR-2000; 2009US:0540217.
23-AUG:2000; 2000US 0649167.
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N-PSDB; AAS83005.
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                                                                                                                                                                                         1 RLLAALGG 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABG18818;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                              Gaps
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77.8%; Pred. No. 1.56-03;
Eive O: Mismatches 2; Indels C
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77.8%, Fred. No. 1.50+03;
ive 0, Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                AA009273 standard; Protein; 1759 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human polypeptide SEQ ID NO 23165.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-FEB-2001; 2001WO-US04927.
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18-MAY-2000; 2000US-0577409.
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    Bust Local Similarity 77.8
Matches 7, Conservative
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Best Local Similarity
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                                                                                                                                     1 RLLANICGA 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 disorders
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1754 AA;

Sequence

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Gaps

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Indels

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1; Mismatches

6; Conservative

Matches

Human; chromosome mapping, gene mapping; gene therapy; toreusic; food supplement; medical imaging; diagnostic, genetic disorder.

Novel human diagnostic protein #20200.

18-FEB-2002 (first entry)

ABG20209;

ARG20209 standard; Protein; 106 AA.

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RESULT 15
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Inked immunosothent assays (ELISA) Disorders which are diagnosed or treated inclined autonium diseases e.g. the underthanked and arthritis.

Inked immunosothent assays (ELISA) Disorders which are diagnosed or cardiovascular disorders e.g. to crebral isorders e.g. notice to a caused by bacteria, viruses and fungional coular disorders e.g. vortueal infertion. The polypertides can also be used to add wound healthy and epithelial cell proliferation, to prevent supporting cell culture of primary tissues, to regenerate tissues and in preservative to increase or decrease storage capabilities. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                encoding them. The secreted proteins can be expressed by standard recombinant methodology, the secreted proteins and polynucleotides are used to prevent, treat or amelionate a medical condition in e.g. humans,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention provides novel human secreted proteins and polymucleotides
                                                                                                                                                                                                                                                                                                                                                                                                      secreted protein, immunosuppressive, antiarthitic) antitheumatic, an iprollferntise, \gamma tostatis, cardian, vasatnefic, cerebroprotective, nootropic, neuroprotective, antibacterial, virucide, fungicide, human,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Birse CE, Suppet DR, Olsen HS,
Shi Y, Choi GH, Fiscella M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note≃ "Xaa can be any amino acid"
                                                                                                                                                                                                                                                                                                                     Human secreted protein (clone 1d HCHPU32).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ROSER CA, Komatsouiis GA, Baker KP,
Moore PA, Wei P, Ebner R, Duan DR,
Ni J, Puben SM, Barash SC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/qualifiers
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                                                      AAR85537 standard; protein; 80 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      opthalmalogical; gene therapy
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12-SEP-2000; 20000S-0231968.
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                                                                                                                                                                                                                                   25-SEP-2001 (first entry)
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N-PSDB; AAH46947.
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AAB85537
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Drmanac RT, Liu C, Tang YT:

(HYSE-) HYSEQ INC.

WPT; 2001-639362/73

N-PSDR; AAS84396

40-MAP-2001; 2001W0-HS08631.

WO200175067-A2.

11-OCT-2001.

Homo sapiens

2000075-0649167

2 4 - Affek Bromes

31-MAP-2000; 200048 0540217

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The invention relates to isolated polynucleotide (1) and polynetase chain reaction (FCR) primers, objanes, and for chromosome and general interaction (FCR) primers, objanes, and for chromosome polynucleotides are also used in disquestics as expressed sequence tags for identifying expressed genes (1) is useful for identifying expressed genes (1) is useful for extore normal activity of (11) or to treat discose states involving to restore normal activity of (11) or to treat discose states involving qualitating a polynedial in tissue, as molecular weight markers and as a tood supplement. (11) and its binding partners are useful in medical imaging of sites expressing (11). (1) and (11) are useful for treating the contraction of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The polypoptide and polynocievide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess blodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pet_sequences.
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diagnostics, forensics, gene mapping, identification of mutations
responsible for genetic disorders or other traits and to assess
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Rost Loral Similarity
6, Conserve
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Score 23, DB 22, Longth 80, Pred. No. 1.2e+92;

Query Match Best Local Similarity

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Search completed: September 5, 2002, 15:26:33 Job time: 373 sec

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Copyright (c) 1993 2000 domp
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OM protein - protein search, using sw model

September 5, 2002, 15:28:54; Scarch time 65:78 Seconds (Without alignments) 12:393 Million cell updates/see Run on:

1 RLLAALCGA 9 Title: Perfect score: Sequence:

US-09-744.804 41

Gapop 10.0 , Gapext 0.5 BLOSUM62 Scoring table:

283138 seqs, 96089334 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Listing first 45 summaries Post-processing: Minimum Match 09 Maximum Match 104

PIR\_71:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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C1 C5	C.														

ags protein precursor - rat.

NiAlternate names: O-acetyl-dd3 qanglioside CiSpecies: Eatins noivequeus (Norway rat) CiSact 26 Sept-1966 "sequence\_revision: Ni-Nov-1998 #foxt\_change 20-Jun-2000 CiSactession: Jo5995 Riogura, K.: Nara, K.; Watanabe, Y.; Kohno, K.; Tai, T.; Sanai, Y. Biochem. Biochys. Res. Commun. 225, 992-938, 1996 Affille: Cloning and expression of cDNA for o-acetylation of GD3 qanglioside. A. Reference number: JC4915; MUJD:96974422

Asstatus: preliminary A; Molecule type: mRNA

A,Residues. 1 427 <6500: A,Cross reterences. DEBJ.D84068, MID.41620906, PIER.BAAJ2219.1; PIP.41629997 A,Experimental source: CST cell

C; Comment: This protein is required for the O acetylation of distaloganglioside siali C; Geneties:

C, Superlaminy, milk fat globule protein, discoldin L amino terminal homology: BGF hom E, L 2,70xmulin, signal sequence estatus predicted (SIO) P128-60,70xmulin: BQF homology (SEG) P128-60,70xmulin: BQF homology (SEG) P128-10,70xmulin: BQF homology (SEQ) P119-P27,70xmulin: BGF homology (SEQ) P119-P27,70xmulin: Birrholdin: Lamino terminal homology (SM) P127,70xmulin: Birrholdin: Lamino terminal homology (SM) A;Gene: ags

or Gaps 94 19: Secret 37: DB 2; Longth 427; 97.59; Pred, No. 29; 0; Indels 1; Mismatches 7, Conservative Bost Local Similarity Matches 7, Conserv Granty Matob Bost Local

## 1 RELAMENG 8

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milk tat globule membrane protein - mouse A36479

C;Species: Mus musculus (house mouse)

Cyaccession: A36479 #Sequence\_revision 19 Sep 1099 #text\_change 10-Sep-1999 Cyaccession: A36479 #Sequence\_revision 19 Sep 1099 #text\_change 10-Sep-1999 Cyaccession: A36479 #Sequence\_revision 19 Sep 10 Sep

A,Accession: A36479 A,Status: preliminary A,Molecule type: mRMA A,Residues: 1-463 <SIU>

A.Creas reference: GB:M38337; NID:q199142; PIDN:AAA39534.1; PID:q199143

<u>2</u>

5

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A;Cross-references: GB:M31012
R:Guillemot, F.; Billault, A.; Pourquie, O.: Behar, G.; Chausse, A.M.; Zoorob, R.; Kr
EMBO 3. 7, 2775-2785, 1988
A;Title: A molecular map of the chicken major histocompatibility complex: the class I
A;Fitle: A molecular map of the chicken major histocompatibility complex: the class I
A;Feference number: S91172: MUID:89030642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A:Map position: 16
O:Superfamily, class 1 histocompatibility antique; immunoqlobulin homology
C:Reywords: glycoprotein: heterodimer; transmembrane protein
E:1 22/Dommain: signal sequence #status predicted ~SiGs
E:23-45/Fn-Airy rolass I histocompathalily antique B:F IV alpha chain #status predi
E:23-102/Dommain: extracellular #status predicted <EXT>
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Eur. J. Immunol. 25, 2009-20076, 1995
A.Title. Functional analysis of acian class ! (BPIV) alycoproteins by epitope tanding A.Reference number. 151309, MUID.95347411
A.Recession: 151309
A.Stone, profile from translated from GE/EMRG/DDBJ
                                                                                                                                                                                                                                                                         MHC class I histocompatibility antiqen B-F IV alpha chain precursor - chicken C;Species: Gallus agalus (chicken) C;Species: 36 Jun 1992 #sequence_revision 30 Jun 1992 #text_charge 22-Jun-1999 C;Accession: A45846; S01172
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C;Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 21-Jan-2000
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A;Residues: 1-345 <CUI>
A;Gross-references: EMBL:X12780; NID:q63089; PIPN:CAA31272.1; PID:q63090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F.111-201/Domain: alpha-2 <EXT2>
F.214-279/Domain: alpha-2 <EXT2>
F.214-279/Domain: immunoqlobulin homology <1MM>
F.302-324/Domain: transmembrane #status predicted <1MM>
F.325-3245/Domain: intracellular #status predicted <1MT>
F.525-107/Eniding site: carbohydrate (Asn) (covalent) #status predicted
F.121-183,221 277/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                            RjKroemer, G.; Zoorob, R.; Auffray, C.
Immunogenetics 31, 405-409, 1990
A/Tille, Structure and expression of a chicken MHC class I gene.
A;Reference number: A45846; MUID:90316612
A;Accession: A45846
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P:213-278/Domain: immusoglobulin homology <1MM>
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A; Residues: 1-345 < KRO>
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A; Residues: 1-355 <FUL>
                                                                                                          242 VLAALCGA 249
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                                          2 LIAMICGA 9
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P:Fulton, J.E., Thac
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C.Supertomilly milk fat globule protein; discoldin Lamino-terminal homology; PGP homold C.Knywords membrane protein P.28-60/termin: ECF homology SEG1. P.28-60/termin: ECF homology SEG2. P.56-60/termin: ECF homology SEG3. P.56-60/termin: ECF homology SEG3. P.56-60/termin: ECF homology SEG3. P.56-60/termin: ECF homology SEG3. P.56-60/termin: Act of main discoldin Lamino: terminal homology. ENC:
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R.Stover: C.K.: Pham. X.C.: Erwin, A.I.: Mizoquchi, S.D.; Warreber, P.; Hickey, M.Y.; Radman, Y.: Brody, I. I.: Coulter, S.N.: Polger, K.P.; Kas. A.; Larbig, K.; Lim., J. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
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Atketerence number AR2950; MTIP-20437337
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AbExperimental source: strain PA01
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adman, S.; Yuan, Y.; Bredy, I.I.; Coulter, S.N.; Polger, K.P.; Ras, A.; Larbig, K.; Uim,
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A:Experimental source: strain PAOI
C:Geneties:
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AJROTETORO number: AR2950; MUID:20437337
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C.Dare: 15-Sept2000 #sequence_revision 15-Sept2000 #text_change 31.bec.2000
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C;Date: 15-sep-2000 #sequence_revision 15-sep-2000 #text_change 31-Dec-2000
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Pred, No. 18;
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Pred No 32;
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Nature 406, 959-964, 2000
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A;Residues: 1-287 <STO>
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Caulchacter crescentus

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C.Species: Caulobacter crescentus
C.bate. 23-Apr.2501 #sequence_revision 20 Apr 2501 #text_change 20 Apr 2001
C.Accession: D87446
                                                  hypothetical protein GG1999 (imported)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best tocal Similarity 87.5%
Matches 7, Conservative
                                                                                                                                                                                                                                                                                                                         A.Status, preliminary
A.Molecule type: DNA
A.Residues: 1-230 <STO>
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Astoleculo type: DNA
A Besidues: 1 171 :310
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                              D87446
                                                                                                                                                                                                                                                               MHC class i histocomputibility untigen ErF ulpha chain describen
CiSpecies: Gallus gallus (chicken)
CiDate: 15-Oct-1999 *sequence_revision if Cot:1999 *text_change Do Jun 2000
C;Accession: T28149
Rimino, S.: Kaufman, J.: Beck. S.
Submitted to the EMBL Data Library, May 1998
A:Description: LNA sequencing and analysis it the chicken major histocompatibility compl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Albescription: DNA sequencing and analysis of the chicken major histocompatibility comp
Alkeforence number: 220475
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C:Species: Gallus gallus (chicken)
C:Pate: 15:3rt 1999 #Sequence_registen 15:3rt 1999 #1.xt_charge 20:Jun 2006
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A.Introns: 22.7 110,7 1717 1717 128,7 224, 22,1
C.Superlamily: class I histocompatibility antigen, immunoglobulin homology
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                                                       337.8
  Score 36; DB 2; Length 355; Pred. No. 38; Pred. No. 38; 1; Mismatches 9; Indels
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A.Status: preliminary: translated from GB/EMBL/DDRJ
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A)Molecule type: DNA
A)Residoes: 1-385 -XML>
A)Cross-references: EMBL:AL023516; PIDN:GAN18972.1
A)Experiencial source: clone CB12
C)Genetics:
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A)Experimental source: clone cB12
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R.Milne, S.; Kaufman, J.; Beck, S.
submitted to the EMBL Data Library, May 1998
81.8%;
87.5%;
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Best Local Similarity 87.2...
7; Conservative
                         Best Local Similarity 87.59
Matches 7; Conservative
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A,Map position: 16
     Query Match
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Existerman, W.C., Feldblyum, T.V., Pautsen, L.T., Nelson, K.E., Elsen, J., Heidelberd, B., Laub, M.T., DeBoy, R.T., bodsen, P.J., Purkin, A.S., Gwinn, M.L., Haft, D.H., Kon, J., Ermolaeva, M.J., White, O., Salzberg, S.L., Shapiro, L., Venter, J.C.: Fraser, C. Proc. Natl. Acad. Sci. U.S.A. 98, 4146-4141, 2001
A.Tille. Complete Genome Sequence of Caulobacter croscentus.
A.Keterence number, A87249, MCJLL173698, FMLL.HILSJ&47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R.Mierman, W.C., Feldblyum, T.V., Faulben, L.T., Nelsen, K.E.; Eisen, J.; Heidelberg, B.; Laub, M.T.; DeBoy, R.T.; Dvdson, R.J.; Durkin, A.S.; Awinn, M.T.; Heatt, H.H.; Koln, J.; Ermolaeva, M.; White, C.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C. Proc. Natl. Acad. Sci. U.S.A. 98, 4186-4141, 2001
A.Title: Complete Genome Sequence of Caulobacter crescentus.
A.Feterence namees: A@7244; MTTP:21173649; PMID:111269447
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Closentius:
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C.Bate. 03 Dec 1999 #sequence_register 53 Dec 1999 #text_change 17 Nar 2000
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C.Accession: C87418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79.5%; Score 35; DB 2; Longth 240; 87.5%; Pred. No. 41;
Lize 0; Mismatches 1; Indels
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1ive 0; Mismatches 1; Indels
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Best Lasal Elmilarity 87.00.
7: Conservative
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A;Cross-references: GB:M14823
A;Accession: B29177
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A;Residues: 1448-1474 <PE2:
                             1 22 (BEL)
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     A;Molecule type: DNA
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                             A; Residues:
                                                                                                           Ajūross-references: CB.AE001914, CB.AE066513, NID grāf8253, Film AAF16140 1, FID grāf829
AjExperimental source: strain R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probable PTS system permease (imperfed) - Saimenelia enterica subsp. enterica servar Ly
C.Species: Salmonella enterica subsp. enterica serovar Typhi
A.Note: this species has also been called Saimonelia Lyphi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 413, 848-857, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford. K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enteries serow
A:Pererone- number: ARGGGG; IMIL:11677508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cidate 09.Nov-2001 #Sequence_revision 09.Nov-2001 #Lext_change 09.Nov-2001 C.Ancerssion. Alf0958
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomsen, N.R.; Pickard, D.; Wain, J.; Churcher, th. T.; Connecton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Monte, S.; ofganz, P.
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A:Reference number: 156095; MUID:91108639
A:Aeression: 156095
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NiContains: classical complement pathway C3/75 concertuse (E7 3 4 21 43) C4E sabunit.
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C.Date: 25 Feb 1985 #sequencc_revision 23 Aug 1996 #fext_change 08 Dec 2006
C.Accession: 154045; A29177; B29177; A90815; A19311, A92337, S12846, A17245, A22335
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Actille: Polymorphism of human complement component C4
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                                                                                                                                                                                                                                                                                                                  DB 2; Length 376;
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75.0%; Pred. No. 1.1e:02;
tive 2; Mismatches 0; Indels
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A;Molecule type: DNA
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A,Accession: A29177
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                                                                                                                                                                                                                                                                                                                  77.38;
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                                               A:Molecule type: DNA
A:Mosidues: 1-376 <WHI>
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                             A;Status: preliminary
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A; Accession, F75503
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                                                                                                                                                                                              A;Gene: DR0560
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A.Residues: 757,47,759-771,980-990 <HES>
R.Campbell, R.D.: Gapton, J.: Porter, R.R.
Brochem, J.: Hwy. 199-370, 1981
A.Pitle: Anino acid sequence around the thiol and reactive acyl groups of human compl.
A.Peference number: A17268; MPID: 82182029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AsTitle: Importance of the alpha(3)-fragment of complement C4 for the binding with C4 Askederence number. Sibbb, MUID:91032049
AsAccession: $12866
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A,Residues: 957 1612, 12, 1014-1044 «CAM»
A,Residues: 957 1612, 10. Campbell, R.D.: Porter, R.R.
Mol. Immand:1, 24, 1187-1197, 1987
A;Title: The chemical structure of the G4d fragment of the human complement component
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A.Pesidos: 957-1012 'E'.1014-1104,'T'.1110-1175,'S'.1177-1270,'V'.1272-1346, CHA.
A.Note: 1073-61y, 1129-Lou, 1121-Ser, 1124-116, 1125-His, 1297 Als, 1210-Arg were als
R.Chakravarti, D.N.; Campbell, R.D.; Gaquon, J.
FEBS Lett. 154, 387-390, 1983
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A.Fasidues: 1199 1276, VV.1272 1299, VV.1281 1394 7882
R.Waitdues: 1199 1276, VV.1272 1299, VV.1281 1394 7882
R.Whitehead, A. S.; Goldberger, G.; Woods, D.E.; Markham, A.F.; Colten, H.K.
Proc. Natl. Acad. Sci. U.S.A. 80, 489-5491, 1983
A.Tille: Öse of a cDNA clone for the fourth component of human complement (C4) for an A.Reference number: 158991; MUID:83299979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PjSargent, C.A.; Anderson, M.J.; Hsich, S.L.; Kendall, F.; Gemez-Fscobar, N.; Campbel
Hum. Mol. Genet. 3, 481-488, 1994
A.Title: Characterisation of the newel gene Gll lying adjacent to the complement C4A.
                                                                                                                                                                                                                                                                                                                                                                                                                A/Posidues: 29-346,/S7,348-417,/A7,419-725,/P7,727-1200,/S7,1202-1205,/S7,1207-1418,1
A/Cross-references: GB:K02403
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                                                                                                                                                                                                                         A;Title: The structural basis of the multiple forms of human complement component c4.
A;Reference number: A90845, MUID.84156544
A;Accession. A90845
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A.Residues: 1195-1285, S./1287-1294 <CAR>
A.Stasidues: 1195-1285, S./1287-1294 <CAR>
A.Stasidues: 1195-1285, S./1287-1294 
B.Moon, K.E., Gorski, J.P., Hadi, T.E.
J. Biol. Chem. 256, 8685-8692, 1981
A.Title: Omplete primary stracture of human C4a anaphylatoxin.
A.Reference number: A92337; MUID:81264286
A.Reference number: A92337; MUID:81264286
A.Melecale type, DNA
A)Residues: 1056-1225 (BE3)
A)Cross-references: GB:M14824; NID:q179675; PIDM:AAA52292.1; PID:q553210
B;Relt, K T : Carroll, M C.; Porter, R.R.
Cell 36, 907-914, 1984
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A.Molecule type: protein
A.Rosidues: 680-725, 'rN', 728-756 -MCOS-
R.Hessing, M.; Van't Veel, C., Hackeng, T.M., Bouma, B.N.; Iwanaqa, S.
PEBS Lett 271, 131-136, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RiCarroll, M.C.; Porter, R.R.
Proc. Natl. Acad. Sci. U. 3.A. 80, 264-267, 1983
A;Title: Cloning of a human complement component C4
A;Reference number: A19311; MUID:83117835
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A,Accession: 137399
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A:Residues: 757, Y',759-771,980-990 <HES>
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completed, September 5, 2002, 15,28:55
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A. Press reterences.
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                                                                                                                                                                                                                                                                                ay CS convertase. Convertase, is a pasoactive peptide and a mediator of inflammation. C)Comment: The anaphylatoxic is a pasoactive peptide and a mediator of inflammation. C)Comment. The artisty of C4E is regulated by protectly its cleavage involving C4D-bindin C)Comment: Persidues 1444 or 1449 may be the carboxyl end of the alpha chain. C)Comment: There are at least two genes coding for C1, C4A and C4B. Each gene has many a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Superioranity; adults phases complement classical pathway; glycoprotein; hydrolase; inflamma C.Keywords, acute phases complement classical pathway; glycoprotein; hydrolase; inflamma Fil-19/Twwain-signal sequence #status predicted SIGS
E10-657/Product complement C4 bits attack predicted C4FE.
E20-675,757 1446,1454-1744/Product. C4b #status predicted c4FE.
E20-675,757 1446,1454-1744/Product. C4b #status predicted cAEP.
E20-675,757 1446,1454-1744/Product. C4 aigha chain #status predicted cAEP.
E20-675,757 1446,1454-1744/Product. C4a mana chain #status predicted cAMP.
E20-675,754-1446,1454-1744/Product. C4d fragment estatus are significant C1s) #status experimental
E100-1013/Cross-link: thiolester (Cys-Gn) #status experimental
E1128/Prinding site. carbokydrate (AsL) (concloct) #status experimental
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Altitle: Only and a sequence of Yorshia pestis, the causative agent of plague.
A.Reference number: AB0001; MUID:21470413; PMID:11566360
A.Reference number: AB0001; MUID:21470413; PMID:11566360
A.Reference number: AB0001; MUID:21470413; PMID:11566360
A.Reference number: AB0001; AMD:21470413; PMID:11566360
A.Reference number: AB0001; MUID:21470413; PMID:11566360
A.Reference number: AB0001; MUID:21470413; PMID:11566360
A.Reference number: AB0001; MUID:21470413; PMID:11566360
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                                                                                                     AJCross-references: EMBL:X77491; NID:9453410; PIDM-CAA54627.1, PID:9453411
CJComment: This protein is synthesized as a single-chain precarsor and, prior to seared:
                                                                                                                                                                                                              C.Comment: The activation of complement of by complement subcomponent Cls releases the Coff complement factor 2 to form the classical complement pathway CS convertuse. The CAR,
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C.Dato: 02-Nov-2001 #sequence_revision 02 Nov-2001 #text_change 09 Nov 2001
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C;Supertamily: signal transduction protein DJ-1
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A;Cross-references: GFR:119732; CMIM:120816
A; Status: translated from GB/EMBL/DDBJ
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Matches 7, Conservative
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A; Residues: 1-21 <RE3>
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A,Authors, Squites, E., Saloton, J.L., Earlor, E., Whitehead, E., Bartell, E.S.
A,Title. Deciphering the biology of Mycobacterium tuberculosis from the complete geno
A,Reference number: A70500, MUID:98295987
                                                                                                                                                                 F.Cole, S.T., Brasch, P., Parkhill, J., Garnier, T., Chareber, C., Harris, D., Gordon, Gommon, R., Baviers, R., Devlin, K., Ecitawell, T., Genties, S., Rantin, N., Holloyd, Esjandreau, M.A., Ecerts, J., Eatter, S., Seeger, K., Skelton, S., Squares, S.
Nature 333, 537-544, 1998
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                 C.Species. My obacterium Tuberculosis
C.Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 29-Jul-2900
C.Aacasion, F70524
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h_{\rm QF} otherical protein {
m Er0209} = {
m M_{
m C}} when terium tuberculosis (strain {
m H37RV})
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Rest Local Similarity 77.48%, Pred, No. 90).
Warthuse Community 77.48%, Pred, No. 90).
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# Gendore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

September 5, 2002, 15,31,43 , Scarch time 33,39 Seconds (Without alignments) 10,252 Million cell updates/sec Run ch:

US-09-744-804-41 44 1 RLLAALCGA 9 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

105224 seqs, 38719550 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived  $k_f$  and pais of the total scare distribution.

## SUMMARIES

		Description	S.	F70490 rattus norv	-	P29370 psecudomenas		000462 homo sapien		005594 salmonella	P57931 pasteurella	Q52679 rhodobacter	Q04557 agrobacteri	Q09102 agrobacteri	P25016 agrobacteri	P03868 agrobacteri	-	Q10518 mycobacteri	Q9zjl2 salmenella	Q9sZri streptomyce		1,000 my color				008654 rattus norv	Q02166 arabidəpsis	F75521 myceplasda	P47359 mycoplasma	29.4889 East Carl		_	Q10977 mycobacteri	F78820 schillasanah	Q46948 escherichia
SOLETAN LES		ID	MFGM_HUMAN	MFGM_RAT	MFGM_MOUSE	dVdSd_Sd.15	HA1F_CHICK	MANB_HUMAN	CO4_HUMAN	CBIM_SALTY	THIM_PASMU	COBT_RHOCA	HYI1_AGRV1	HYIN_AGREH	HYI2_AGRVI	HYIN_AGRT4	RSEC_ECOLI	CORP_MYCTU	SYK3_SALTY	CORT_STRCO	MRS1_SACDO	THILLMYOTT	THIL MYCLE	U183_HUMAN	U183_MOTSE	U183_EAT	TRFD_ARATH	SYN_MYCEN	SYN_MYCGE	LAT2_MOUSE	LAT2_PAT	LAT2_HUMAN	PPSA_MYCTU	- 1	THIJ_ECOLI
		DB	-	e- 1	_		_	_	-	_	_	-	_	r1	-	_	<del>-</del> 4	<u>, , , , , , , , , , , , , , , , , , , </u>	٠.		П	_		-	7	-	۲-,	۲,	_	r 1	e-4	-	П	٦	_
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æ	Query	Match	100.0	 &	84.1	81.8	81.8	77. 3	77.3	75.0	S.	(C)	LC:	75.0	un.	n.	ci.	ς.	ci.	c i	ζ.	ci	ć.		72.7	ci.	ci.	á	72.7	ci.	ci.	C-	. ⊲	ci.	70.5
		Score	44	37	3.7	36	36	34	34	33	33	33	333	33	33	33	32	32	32	32	32	35	32	<u></u>	ei ei	25	₹ *	c.	32	32	25 E	32	32	CI m	31
	Result	NO.	7	2	æ	v	5	9	ŕ	ဆ	<u></u>	10	11	12	13	14	15	16	17	18	19	< > C1	21	C1	C.I	24	K)	d,	27	င္း သ	50	30	31	C1	33

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## ALIGNMENTS

QUENTITY OF CREENS AND OTHER STATE OF CREENS	(Rel. 34, Greated) (Rel. 35, Last sequence update) (Rel. 36, Last sequence update) precursor (Milk fat globule-EGF helial autigen HA46) (MFGM) (Co (Human). letazoa; Chordata; Craniata; Ver ttheria; Primates; Catarrhini; He 606; M. N.A. 1, and Bteast Carcinoma; 3908; PubMed-8639264; 17 aylor M. R., Godvin S. G., Ceria 18 equence analysis of human bre 18 equence analysis of human bre 18 et min cell adhesion sequence 19 relice domain."	uence update) otation update) t globule-EGF factor 8) (MFG-E8) (HMFG 6) (MFGM) [Contains: Medin]. Craniata: Vertebrata: Euteleostomi; Catarrhini; Hominidae: Homo. inoma; 64; n S.G., Ceriani R.L., Peterson J.A.; of human breast epithelial antiqen ion sequence presented on an epidermal) ) 32;
	ast sequence ast annotation milk fat glob gen HA46) (MFG andets; Catarriantes; Catarri	update) n update) ule-EGF factor 8) (MF4 GM) [Contains: Medin] ta, Vertebrata; Eutelt hini; Hominidae: Homo, man breast epithelial quence presented on ar
	dast annotation Milk fat glob gen HA46) (MK gen HA46) (MK gen HA46) (MK indtes; Catarri mates; Catarri material	n update) ule-EGF factor 8) (MFC GM) [Contains: Medin] ta; Vertebrata; Entelt hinl; Hominidae: Homo, man breast epithelial quence presented on at
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	ordata; Crania' mates; Catarri ud-8639264, Godwin S.G., Godwin S.G., inalysis of hur ladheston ser inalia';	ta: Vertebrata: Butele hini: Hominidae: Homo , Ceriani R.L., Peters man breast epithelial quence presented on ar Kuniyoshi J., Bistra
	mates; Catarri mates; Catarri ust Carcinoma; d-869264, Godwin S.G. malysis of hur i adhesion se ini.;	ta, Vertebrata, Butele hini, Hominidae: Homo, Ceriani R.L., Peters man breast epithelial quence presented on ar Kuniyoshi J., Bistra
	ordata; Grania mates; Catarri st carcinoma; de869284; Godunalysis of hu i adhesion se in adhesion se in adhesion se	ta; Vertebrata; Entert hini; Hominidae: Homo , Ceriani R.L., Peters man breast epithelial quence presented on an Kuniyoshi J., Bistra
	mates; catarrist carcinoma; ed-8639264; carcinoma; radysis of the radhesion serial radhesio	Ceriani R.L., Peters man breast epithelial quence presented on an Kubiyoshi J., Bistra
	st carcinoma; 4d-8639264; Godwin S.G. malysis of hur l'adhesion ser l'adhesion ser RAK(199K)	, Ceriani R.L., Peters man breast epitholial quence presented on ar Kubiyoshi J., Bistra
	ist carcinoma; id-86:9254. dodwin S.G. malysis of hur ladhesion ser ladh.";	, Ceriani R.L., Peters man breast epithelial quence presented on an Kuniyoshi J., Bistra
	ist carcinoma; ed-8639264; Godwin S.G. malysis of hur ladysisn's in.'; RR(1996)	Geriani R.L., Peters man breast epithelial quence presented on an Kuniyoshi J., Bistra
	d-8639264; Codwin S.G. malysis of hur adhesion sertin; RK(1994)	, Ceriani R.L., Peters man breast epithelial quence presented on an Kuniyoshi J., Bistra
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	!86(1996) ** Y. A	Kuniyoshi J., Bistra
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	M M.A.	Kumiyoshi J., Bistra
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	d 1909932;	Kuniyoshi J., Bistra
	A., Urrea R.,	
RA Ceriani R.L.;		
. "A Mr 46,000 houman milk fat globule protein that is highly expressed	. 1at 4lobule	protein that is highly
	contains fact	or VIII-like domains."
_	8(1991).	
	HARACTERIZATIO	ON.
	d 9535276;	
	to M., Giunta	C., Conti A.,
RA Godovac Zimmermant 3.,		
	erization of fo	ull and truncated form
	a BA46 from h	sman milk tat globule
	١-148(1998).	
	R. CHENTER CALL	LIN IF WEDIN.
	d=10411933;	
RA Handappist B , Nackland I , Sletter R , Westernark G T , Morchiano	11/11/6	K , Westermark G T , Myorhiang G.,
	edt C., Engstro	oem U., Westermark P.,
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	0.0.A. M.0.0	
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RX MEDIUNE 97405885, FLEM	3 9200929;	
	, Scallan C.D	., Ceriani R.L., Peter
"Lactadherin (formerly BA46), a membrane-associated alycoprotein	BA46), a memb	rane-associated glycop
	and broast o	ardinomas, promotes Ar
	lhesion.";	

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                                                                                                                                                                                                                                            the European Bioinformalies Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license alterneut (see http://www.isb:sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Micinformatics and the EMRL entstation \gamma
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                                                                                                       MEDIA, OVEKEXPRESSED IN SEVERAL CARCINOMAS.
-!- PTM: MEDIN HAS A RAGGED N-TERMINUS WITH MINOR SPECIES STARTING AT AMINO ACID 264 AND 273.
                               Gaps
                                                                   -i- SUBCELLULAR LOCATION: PERIPHERAL MEMBRANE PROTEIN.
-i- TISSUE SPECIFICITY: MAMMARY EPITHELIAL CELL SURFACES AND AORTIC
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BY SIMILARITY.
N. LINKED (GLUNAC). (PUTENTIAL).
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COMAY-2000 (Pel. 39, Last annotation update)
Lactadherin precursor (Milk fat globule-EGF factor 8) (MFG-E8) (O-acetyl GD3 ganglioside synthase) (AGS) (MFGM).
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             FUNCTION: MAY BE INVOLVED IN PHOSPHOLIPID BINDING. BINDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 44; DB 1; Length 387; 100.0%; Pred No 0.57;
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LATIACHERIN, SHOKT FORM
                                                                                                                                                          -!- SIMILAPITY: CONTAINS 1 EGF-LIKE FOMAIN.
-!- SIMILARITY: CONTAINS 2 F5/8 TYPE C DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EGF-LIKE.
F5/8 TYPE C 1
F5/8 TYPE C 2
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InterPro; IPROGO421; FA58_C.
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67
225
387
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232
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268
268
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327
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O
                    Fukaryola, Metazoa; Chondala, Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia, Sciulognathi; Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                   Firefirem. Ringligs Res Commun. 225-442-448(1946).
-i- FUNCTION: MAY RE INVOLVED IN PHOSPHOLIPID BINDING. SEEMS TO PARTICIPATE IN THE O-ACETYLATION OF GD3 GANGLIGSIDE STALIC ACID.
-i- SUBCELLULAR LOCATION: PERIFHERAL MEMBRANE PROTEIN.
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F5/8 TYPE C 1.
F5/8 TYPE C 2.
HY SIMILAPITY
BY SIMILAPITY.
CELL ATTACHENT SITE (POTENTIAL).
N-IINKED (GLUNAC. . ) (POTENTIAL).
N-IINKED (GLUNAC. . ) (POTENTIAL).
N-IINKED (GLUNAC. . ) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                       -i TISSUE SPECIFICITY SPIER, DING, HEART, BRAIN AND MUSCLE.
- SIMILAKITY, CONTAINS 2 EGF-LIKE DOMAINS.
-i SIMILAKITY, CONTAINS 2 FF/8 TYPE C TOMAINS.
                                                                                                                                                                      equta K., Nata K., Watanaha Y., Kohno K., Tai T., Sanai Y., "Cloning and expression of cDNA for G acetylation of GD3 ganglioside.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84.1%, Score 37; DB 1; Length 427; 87.5%; Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
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EGF-LIKE 1.
EGF-LIKF 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to livense@ish sib ch).
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InterPro; 1PR000561; EGF-like.
InterPro; 1PP001438; EGF_II.
Pfam; PF00008; EGF, 2
Pfam; PF00008; EGF, 2
Pfam; PF000754; F5_F8_Lype_C; 2.
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PROSITE; PSG1186; EGP_2; 2.
PPOSITE; PSG1285; FASRG-1: 2.
FROSITE; PSG1286; FASRG-2; 2.
Signal; G1ycoprotein; Peproat; PY SIGNAL
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SMART, SMOOTRI, BOR, 2.
SMAPT, SMOOZRI, PASRO, 2.
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Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                          SECUENCE FROM N.A.
                                                                 NCBI_TaxID=10116;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation for Extractionaries in the European Boinformatics has finite. There are no restrictions on its use by non-profit institutions as bung as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- FUNCTION: MAY BE INVOLVED IN PHOSPHOLIPID BINDING. ZONA PELLUCTDA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE FROM NUMPREGNANT ANIMALS & MAXIMAL IN FHE LACTATING GLAND. -!- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS. -!- SIMILARITY: CONTAINS 2 FE/8 TYFF G DOMAINS.
                                                                                                                                                         01-ANG-1941 (Pol. 19, Last sequence update)
16-007-2001 (Pol. 40, Last, anochatkon update)
Lactadherin precursor (Milk Lat. qubbule-EGF Lactor 8) (MFG-E8) (MFGM)
(Sperm surface protein SP47) (MP47).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 reveals the existence of epidermal growth factor-like domains linked to factor VIII-like sequences.";
Proc. Natl. Acad. Sri TFS A R7-8421(1990)
                                                                                                                                                                                                                                                                                                                                                 Fokaryota, Motaroa, Chordata, Craniata, Vertebrata, Euteleostomi.
Mammalia, Estheria, Rodentia, Sciurognathi, Muridae, Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- DEVELOPMENTAL STAGE: MRNA EXPRESSION IS DETECTABLE IN MAMMARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stubbs J.D., Lekutis C., Singer K.L., Bul A., Yuzuki D., Skiniyasan D., Parry G.; "cDNA cloning of a mouse mammary opithelial cell surface protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- TISSUE SPECIFICITY: MAMMAKY EPITHELIAL CELL SURFACES AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (NOV-1997) to the PMHL/GenBank/PERT databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SUBÇELLULAR LOCATION: PERIPHERAL MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE: PS00023, BGF_11 2, PROSITE: PS0186: EGF_21 2, PROSITE: PS01285: FASFG_11 2, PROSITE: PS01285: FASFG_2 2, EGF_11ke domain, Milk. Signal; Glycoprotein, Pepcat, EGF_11ke domain, Milk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PS/8 TYPE C 1.
FS/8 TYPE C 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND SEQUENCE OF 23:35.
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EGF-LIKE 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to licensewish-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Mammary qland;
MEDLINE=91046008; PubMed=2122462;
                                                                                          P21956; P97800;
01-AUG-1991 (Pol. 19, Created)
01-AUG-1991 (Pol. 19, Iast sequ
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PRINTS; PR00030; E3PRLOOD.
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InterPro, 1PR001438; BGF_11.
InterPro, 1PR000421; PA58_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M38337; AAA39534 1; --
EMBL; Y11684; CAA72380.1; --
PIR; A36479; A36479.
HSSP; P00740; 1EPM,
MGD; MGI:102768; Mf988.
InterFig. 1PR0000761; EGF-138c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEÇHPNOP OF 23 46? FROM N.A.
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SMART; SM00231; FA58C; 2.
                                                                  STANDARD;
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463
                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 177 FROM N.A. MEDLINE 92041562; FERMED-1978865; Schwed-1978866; Schwed-1978866; Schwed-1978866; Schwed-2der H.P.; Schwed-1978866; Schwed-2der H.P.; The aging steer of proceedings of algorithm and environments of putative activator for algorithm factorism in Pseudomonas acroatinosa."; J. Bacteriol, 173:6798-6806(1991).

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N-LINKED (GICNAC. ...) (POTENTIAL).
S > F (IN REF. 2).
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CELL ATTACHMENT SITE (POTENTIAL).
                                                                                                                                                                                                                          AA SEQUENCE)
                                                                                                                                                                                                                                                                                                                                                                        Query Match

Rest Local Similarity 87.5%; Pred. No. 12;
Matches 7, Conservative 1; Mismatches 9; Indels
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Y -> S (IN RBF. 2).
H -> T (IN RBF. 2).
L -> S (IN RRF. 2).
E -> A (IN RRF. 2).
F -> A (IN RRF. 2).
A: (IN RRF. 2).
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D (IN REF. 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GLPS_PSEAE STANDARD: PRT: 287 AA. P29370; 91 DE0. 24, Created) 11 Control (Rel. 24, Created) 16-0CT-2001 (Rel. 40, Last annotation update) 16-0CT-2001 (Rel. 40, Last annotation update) Sensor protein 91PS (BC 2.7.3.-).
                 HY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-20437337; PubMed=10984043;
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395
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266
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                                                                        This SWISS-PROT outry is copyright It is produced through a collaboration between the Swiss Institute of Bicinformatics and the EMBL outstation the European Bicinformatics institute. There are no restrictions on its use by non profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial cutifies requires a linears agreement (See http://www.ish-sib.ah/Announce.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Enkuryota: Metazoa, Chordata; Craniata; Vertebrata: Euteleostomi;
Archosauria; Aves; Neoqnathae: Galliformes; Phasianidae; Phasianinae;
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Class I histocompatibility antigen, F10 alpha chain precursor (B F
histocompatibility F10 antigen) (B-F-beta-IV) (B12).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Structure and expression of a chicken MHC class I gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 81.8%; Score 36; DB 1; Length 287; Bost Local Similarity 87.5%; Pred. No. 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    287 AA; 29693 MW; 19A611183716766 0F074;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  345 AA
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                                                                                                                                                                                                                                                                                                                                                           or send an email to licensealsb-sib.ch).
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EMBL; M31012; AAA48947.1; -.
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EMBO J. 7:2775-2785(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000620; DUF6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEGUENCE FROM N.A.
STRAIN-R12; TISSUE LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL: M60805; AAA25828.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gallus qallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00892; DUF6; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              THE IMMUNE SYSTEM.
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242 VLAALCCA 249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HA1F_CHICK
P15979;
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"Human beta mannosidase CDNA characterization and first identification of a mutation associated with human beta-mannosidesis.";
Hum. Mol. Genet. 7:75-83(1998)
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Friderici K.H.,
                                                                                                                                                                                                                   CLASS I HISTOCOMPATIBILITY ANTIGEN, F10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. Chang H.-M., Tsai S.-F.; Chang H.-M., Tsai S.-F.; "Genome sequencing of the chromosome 4q region implicated in human "Genome sequencing of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Momo sapiens (Human).
Foblanda Matazaa, Chardata, Crandata, Verrebrata, Enteleostomi;
Foblanda Matazaa, Momo,
                                                                                                                                                                                                                                                                                                                                                                                   N-LINKED (GLCNAC, ...) (POTENTIAL).
N-LINKED (GLCNAC, ...) (POTENTIAL).
P > PDEEGGSSSSST (IN REF. 2).
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- i- FUNCTION: PROGRAMOSE THE SINGLE HPTA-TINKED
MANNOSE RESIDIE FROM THE NON-BEDICING END OF ALL N-LINKED
GLYCOPROTEIN OLIGOSACCHARIDES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     000462; Q9NYX9; Q96BC3;
15-JUL-1998 (Rel. 36, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2022 (Rel. 41, Last annotation update)
Beta-mannosidase precursor (EC 3.2.1.25) (Mannanase).
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©
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81.8%; Score 36; DB 1; Length 345; 87.5%; Pred. No. 15;
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Mammalia, Eutheria, Primates, Catarrhin; Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                      430DCCF8091B69A4 CRC64;
                                                                                                                                                                                                                                                 EXTRACELLULAR ALPHA-1.
FYTEATEL HIAP ALPHA-2.
EXTRACELLULAR ALPHA-3.
                                                                                                                                                                                                                                                                                                      CONNECTING PEPTIDE.
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BY SIMILARITY.
                                                                                                                                                                                   Clycoprotein; Signal.
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                                                                                                                                                                                                                                      ALPHA CHAIN.
                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        38246 MW;
                                             InterPro; IPR003006; 19_MHC.
InterPro; IPR003597; 19_c1.
                                                                                                                                                                   PROSITE; PSO0290; IG_MHC; 1.
                                                                               IPRO01039; MHC_I.
                                                                                               Pfam; PF00047; iq; i, Pfam; PF00129; MHC_1; 1, ProDom; PD000050; MHC_1; 1.
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301
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345
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               PIR; A45846; A45846.
HSSP; P03989; IHSA.
                                                                                                                                                   SM00407: 1Gc1
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S01172; HLCHB4.
                                                                                                                                                                                                                                                                                                                                                                                                                                    345 AA;
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                                                                                    InterPro;
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This EWISS-FROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBE outstation for Employed Bioinformatics in There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial cutilies requires a lineause agreement (See http://www.isb-sib.oh/angounce/
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                              mannose residues in beta D'mannosides.
PATEWAY: PENULTIMATE STEP IN N LINKED OLIGOSACCHAFIDE CATAROLISM
CATALYTIC ACTIVITY: Hydrolysis of terminal, non reducing beta-D-
                                                                              SUBCELLULAR LOCATION: LYSOSOMAL.
DISEASE: DEFECTS IN MANBA ARE THE CAUSE OF A MILD DISORDER THAT
AFFECTS PERIPHERAL AND CENTRAL NERVOUS SYSTEM MYELLN.
SIMILABITY: RELONGS TO FAMILY 2 OF GLYGOSYL HYDROGASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROTON DEADE (BY SIMILARITY).

N-LINKED (GLONG. ) (POTENTIAL).

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Belt K.T., Carroll M.C., Porter R.R.; "The structural basis of the multiple forms of human complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ç,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77.3%; Score 34; DB 1; Length 879; 87.5%; Pred. No. 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukarycta, Metamoa, Chordata, Craniata, vercebiata, mannal
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001649; Glyco_bydro_2.
Plam: FF02836; Glyco_bydro_2.c, I.
Hydrolase; Glycocidase; Glycoprotein: Lysosome; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CO4_HUMAN STANDARD; PRT; 1744 AA. P01028: QUIPF: QNNKS; QUIRGE; QUARTS; QUARTS; C1-JUL-1986 (Pel 01, Greated) C1 MAR-2002 (Pel 41, last sequence update) 01-MAR-2002 (Pel 41, last annotation update) Complement C4 precursor [Contains: C4A anaphylatoxin].
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
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Belt K.I., Carroll M.C., Porter E
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SEQHENCE PROM N.A. (C4A)
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SPETTITITIES SPETTING                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Š
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Sargent C.A., Anderson M.J., Hisleh S.L., Kendall E., Communication M.J. Campbell K.D.;

Communication of the novel arms CHI lying adjacent to the Characteristation of the homen major histocompatibility complex.";

Hum. Mol. Genet. 3:481-488(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRUCTURAL BASIS OF POLYMORPHISM.
MEDLINE-87680272; PubMed-2431962;
Yu C.Y., Belt K.T., Giles C.M., Campbell R.D., Porter R.R.;
Structural basis of the polymorphism of human complement components
C4A and C4E: gene size, reactivity and antigenicity.";
                                                                                                                                                                                                                                                                     Rowen L., Dankers C., Baskin D., Faust J., Loretz C., Ahearn M.E.,
Banta A., Swartzell S., Smith T.M., Spies T., Hood L.,
"Gequence determination of 300 kilobases of the human class III MHC
lorus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hortin G., Sims H., Strauss A.W.; "Identification of the site of sulfation of the site of sulfation of the fourth component of
"The complete exon-intron structure of a human complement component
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIME 82182029; PubMed-6978711;
Campbell R.D., Gagnon J., Porter R.R.;
"Amina acid sequence around the third and reactive acyl groups of
buman complement component C4.";
Biochem. J. 199:359-370([981]).
                                                                                                                                                                                 Complete sequence of the complement O4 gene from the HLA-Al. RB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-82150875; PubMed-6950384;
Harrison R.A., Thomas M.L., Fack B.F.;
"Sequence determination of the thiolester site of the fourth
                                                                                                                               Object D. Townerd D.C., Chilabiansen F.T., Baskins R.L.,
Abraham L.J.;
                   C4A qene. DNA sequences, polymorphism, and linkage to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDITHE 81264286. FubMed 6167582;
Moon K.E., Gorski J.P., Budil T.E.;
"Somplete primary strandure of human G4a anaphylatoxin.";
J. Broi. Chem. 256.8688 8692(1981).
                                                                                                                                                                                                                                                                                                                                                  Substitted (OCT-1999) to the PMPL, Weekink, TYPBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (APR-2000) to the EMBH, Sentuck, TEBE databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SECURNCE OF 1.22 ARE 1855 FROM N.A. MEDLINE 8515569; PubMed-3838531; HOLL K.L. Yu G.Y. Carroll M.C., Porter R.R.; "POLYMORPHISM Of busine complement component (4."; managenetics 11.17s-180(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            component of human complement.";
Proc. Natl. Acad. Sci. U.S.A. 78:7488-7392(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1405-1431, AND SULFATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biol. Chem. 261.1786 1793(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-21 FROM N.A.
MEDLINE-94282044; PubMed-8012361;
                                                                                                                           MEDLINE«96163032; PubMed-8575831;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIINE 86111851; Pubmed-3944109;
                                                                                                                                                                                                 C4AQO, C4B1, OR3 haplotype.";
Immunogenetics 43:250-252(1996).
                                    -hydroxylase gene.";
Immunol. 146:1057-1066(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBO J. 5:2873-2881(1986).
                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (C4A).
                                                                                        SEQUENCE FROM N.A. (C4B)
                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (C4B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 957-1044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SHOUENCE OF 990-1037.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 680-756.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human complement.
                                                                                                            SSUE-Blood;
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                                                                                                                                                                                                                                                                                                                                                                                    OF NONIDENTICAL CHAINS (ALPHA, BETA, AND GAMMA).
POLYMORPHISM: HUMAN COMPLEMENT COMPONENT C4 IS POLYMORPHIC WITH ALLEAST TWO FOCT. C4A AND C4R. 13 ALLETES OF C4A AND 22 ALLELES OF
                                                                                                                                                                                                                                                                                                                                                SUBUNIT. THIS PROTEIN IS SYNTHESIZED AS A SINGLE-CHAIN PRECURSOR AND, PRIOR TO SECRETION, IS ENZYMATICALLY CLEAVED TO FORM A TRIMER
               MEDLINE-92242995; PubMed-1573268; Anderson M.J., Milner C.M., Cotton C.H., Compbell R.D.; Anderson M.J., Milner C.M., Cotton C.H., Compbell R.D.; "The coding sequence of the hemolytically inaction (AAA alloays of human complement component of reveals that a single arginine to tryptophan substitution at beta-chain residue 458 is the likely cause
                                                                                                                                                                                                                                        FUNCTION: DEFIVED FROM PROTECTIVE DEGRADATION OF COMPLEMENT C4, C4A ANAPHYLATOXIN IS A MEDIATOR OF LOCAL INFLAMMATORY PROCESS. IT INJUGES THE CONTRACTION OF SMOOTH MUSCIE, INGREASES VASCULAR FERMERBILITY AND CAUSES HISTAMINE FELFASE FROM MAST CELLS AND HASOPHILIC LEUKOCYTES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POLYMORPHISM: THE CAA ALTELES CAPRY THE RICON SPOND POPCEPS WHILE THE CAB ALLELES CARRY THE RICON CHINO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MISCELLANEOUS: C4 1S A MAJOR HISTOCOMPATIBLEITY COMPLEX CLASS-III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MISCELLANKOUS: C4A ALLOTYPES REACT MORE RAPIDLY WITH THE AMINO GROUP OF PEPTIDE ANTIGENS WHILE C4R ALLOTYPES PEACT MOPE RAPIDLY
                                                                                                                                     Immunol. 148:2795-2802(1992).
PUNCTION: G4 PLAYS A CENTRAL ROLF IN THE ACTIVATION OF THE PUNCSICAL PATHWAY OF THE CAMPLEMENT SYSTEM IT IS PROGRESSIO BY ACTIVATED CI WHICH PEMOVE FROM THE ALPHA CHAIN THE C4A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISEASE: THE C4A6 ALLOTYPE IS TOTALLY DEFICIENT IN HEMOLYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAB HAVE BEEN DETECTED THE ALLELP SHOWN HEPE IS C4A4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: CONTAINS 1 ANAPHYLATOXIN-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WITH THE HYDROXYL GROUP OF CARBOHYDRATE ANTIGENS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: TO C3, C5 AND ALPHA-2-MACROGLOBULIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; K02404; AAA59651.1; -. EMBL; M59815; AAA51855.1; -. EMBL; M54816; AAA51845.1; -. EMBL; U5478; AAA9717.1; -. EMBL; AE019413; AAB57980.1; -. EMBL; AL049547; CAB89302.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, M14823; AAA35217.1; -. EMBL, M14824; AAA52292.1; -. EMBL, X77491; CAA54627.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL: K02403; AAB59537.1; -.
VARIANT C4A6 ALLOTYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; A01262; C4BU.
PIR; A17265; A17265.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR: B20807; B20807.
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                                                                                                                                                                                                                           ANAPHYI,ATUXIN.
                                                                                                                        of the defect.";
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InterPro; IPR001599; Alpha\_2\_macroqlobin. InterPro; IPR090020; Anaphylatoxin. InterPro: IPPOOL840; Anaphylatoxn

InterPro; IPR002890; A2M\_N.

120820; 120790; MIM: 120810;

HSSP; P01031; 1KJS. SWISS-2DPAGE; P01028; HUMAN.

InterPro; IPRG01134; Netrin\_C Ptam; PF00207; A2M; 1.

Probom; PD003264: Anaphylatoxin

PRINTS; PRÜÜÜÖ4; ANAPHYLATOXN

Ptam; PE01835; A2M.N; 1. Ptam; PE01821; ANATO: 1. Ptam; PE01759; NTP; 1.

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McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Perwellik S., Ali J., Dante M., Du F., Hou S., Layman D., Loobard S., Hanges C., Scott K., Holmes A., Grewal N., Mulvaney E., Leyan F., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Characterization of the cobalamin (vitamin B12) blosynthetic genes
                                                                                                                                                                                                                                                     ...) (PSTEMTIAL)...) (PSTEMTIAL)...) (PSTEMTIAL)...) (PSTEMTIAL)...)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria, Proteobacteria, gamma subdivision, Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                 -> G (IN C4A1, C4B1 AND C4B3).
                                              Complement pathway; Plasma; Glycoprotein; Sultation; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lawrence J.G., Rubentield M., Kieffer-Hiqqins S.,
                                                                                                                                                                                                                                                                                                                                                                      Score 34; DB 1; Length 1744;
                                                                                                                                                                                                                                                                                                                                                                                 Fred. No. 1.3e+02;
0; Mismatches 2, Indels
                                                                                                                                       COMPLEMENT C4, GAMMA CHAIN.
                                                                                                                  COMPLEMENT C4, ALPHA CHAIN
                                                                                           COMPLEMENT C4, BETA CHAIN.
                                                      Inflammatory response, Polymorphism; Disease mutation; Blood group antigen.
                                                                                                                                                                                                                                                    N LINKED (GLCNAC).
N-LINKED (GLCNAC).
N-LINKED (GLCNAC).
N-LINKED (GLCNAC).
R -> W (IN C4A6).
                                                                                                                                                             ANAPHYLATOXIN-LIKE.
                                                                                                                                                 C4A ANAPHYLATOXIN.
                                                                                                                                                                                                                                                                                                              /FTId=VAR_001987.
P -> L (IN C4A3).
/FTId=VAR_001988.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91-79N 1994 (Rel. 29, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
SMART: SM00104; ANATO: 1.
PROSITH; ISSO477; ALPHA_2_MACROGIABULIN; 1.
PROSITE: PS01177; ANAPHYLATOXIN_1; 1.
PROSITE: PS01178; ANAPHYLATOXIN_2; 1.
                                                                                                                                                                                  BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                        SIMILARITY.
                                                                                                                                                                                                                    SULFATION.
SULFATION.
SULFATION.
N LINKED (
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MEDLINE 21534948; PubMed=11677609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of Salmonella typhimurium.";
J. Bacteriol. 175:3303-3316(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE 93273696; PubMed=8501034;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-1994 (Rel. 29, Created)
                                                                                                                                                                                                                                                                                                                                                                      77.3%;
                                                                                                                                                                                                                                                                                                                                                                                  77.88;
                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                     1073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Salmonella typhimurium
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                                                                                                                          1447
1454
680
702
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702
703
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1422
226
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CBIM OR STM2023.
                                                                                                                                                                                                                                                                                                                                                1073
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Church G.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CBIM_SALIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-LT2;
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                                                                                                                                                                                                                                                                           CARBOHYD
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MOD_RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      O, Jups
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    May B.J., Zhang C. Li L.L., Paustian M.L., Whittam T.S., Kapur V., Propplete genomic sequence of Pasteurials multopida Pm70."; Prom Natl Acad Sci US A 08-3466-3466,2001)

--- CATARYTH ACAD SCI US 4 --- Thillian Control of the Acad Sci US A 4-methyl 5-(2-hydroxyethyl)-thillianole --- ADP + 4-methyl 5-(2-hosphoethyl) thillianole.
--- COGACIOE: MASURSIUM (48 SUMILBALLY).
--- COGACIOE: MASURSIUM (48 SUMILBALLY).
--- PATHAMY: FIRAMINE HOSYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thiamine biosynthesis, Itansferase, Kinase, Air binding, Magnestam, Complete protection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Manteria, Proteobacteria, qumma subdivision, Pusteurellaceae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-oCT-2001 (Rel. 40, Last sequence update)
16-oCT-2001 (Rel. 40, Last annotation update)
18-oCT-2001 (Rel. 40, Last annotation update)
18-fockelly Lidabole Kinase, (EC 2.7.1.56) (4 methyl 5 kela
hydroxypelly Lidabole Kinase) (TEZ Kinase) (TH Kinase).
THIM OR PM1262.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            75,0%, Smore 33, DR 1, Longth 245
66,7%: Pred, No. 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      l, indels
                                                                                                                                                                                                                                                                                                                                                      Probom; Ph005331; CbiM; 1.
Cobalumin blosynthesis, Complete protecte:
SPGMPYPF 245 AA; 2620v MW; C183CGPC31E21E22 GP054;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      267 AM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2, Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL: AEOONINS; AAKORRASI,
Literes, 195000417, Bycthgr_kluase.
Pfam: PF02110: HK: 1.
                                      -!- FUNCTION: NOT KNOWN.
-!- PATHWAY: COBALAMIN BIOSYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE 21145866; PubMed 11248100;
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                                                                                                                                                                                                                                                         EMBL; 1,12006; AAA27264.1; -.
                                                                                                                                                                                                                                                                              EMBL: AE008789; AAL20927.1;
                                                                                                                                                                                                                                                                                           InterPro; PR00275; cbiM.
Prim: PF01891; CbiM.
Pronce.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6, Conservative
                   Nature 413:852 856(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pasteurella multocida.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
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72 KVLLALCGA 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 RILLAALCGA 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pasteurella
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P57931;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHRI_PHOCA STANDARD; PRT; 334 AA.
052679.068087; Created)
16-071-2001 (Rel. 40, Created)
16-071-2001 (Rel. 40, Last Sequence update)
16-071-2001 (Rel. 40, Last annotation update)
16-071-2011 (Rel. 40, Last annotation update)
17-071-2011 (Rel. 40, Last annotation update)
18-071-2011 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pollich M., Klug G.; "Identification and sequence analysis of grows in charles in late steps in cetalactic ("traming FL2) synthesis in Physicacter capsulatus."; I. Sacteriol, 177:4481-4487(1995).
                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J. Racteriol. 177:4481-4487(1995).
-i- FUNCTION: CATALYZES THE SYNTHESIS OF ALPHA-RIBAZOLE-5'-PHOSPHATE FROM NICOTINATE MONONUCLEGIIDE (NAMN) AND 5,6-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vicek C., Faces V., Maltsey M., Faces J., Haselkorn R., Paustein M.; "Sequence of a 1895kb sequent of the chrow-some of Rhedblacter programatus SB1003.", It S.A. 94:9484-9488(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nicofinate · NI-(5-phosphe-alpha-D-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bhodobacter Lipsalitus (Rhodopsendomonas capaliata).
Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
                                                                                                                                                                                                                                        ë
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF02277; DBL_PRT; 1. Cabalamin biosynthesis; Transferase:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DIMETHYLBENZIMIDAZOLE (DMB).
                                                                                                                                                                      Guery Match 75.0%; Score 33; DB 1; Length 267; Best Local Similarity 75.0%; Pred. No. 41; Matches 6; Congervative 2; Mismatches 0; Indels
MAGNESIUM (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
                                                        BASE (BY SIMILARITY).
C710H90C6BB5E971 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   356A74BDEA623637 CRC64;
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A \rightarrow F (IN REF, 2).
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ribosyl) -5.6-dimothylbenzimidarole.
t parHWAY, comatanth Rickynthesis.
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SUPATH ADOT 33302 (* 810)
POSTINE (6762627) FORMOG-7635831)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-97404404; PubMed 9256491;
91 91 MAC
123 123 MAC
194 194 BAX
267 AA; 28215 MW; (
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Interpro: IPR003200: DBI_PRT.
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STRAIN-SB1003 / ST LOUIS:
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ACT_SITE 303 30
CONFLICT 49 1
CONFLICT 66 0
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                                                                                                                                                                                                                                                                                                                                                         195 LLSAVCGA 202
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                                                                              Gaps
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01-MAR-2002 (Rel. 41, Last annotation update)
Indoleacetamide hydrolase (EC 3.5 1 -) (TAB) (Indole-3-acetamide
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01-NNV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Indoleacetumide hydrojase (ET 3.5.1.1) (TAH) (Indoles are lamide
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PROSITE, PSGGT71, AMIDASES, 1
Hydrolaso: Auxic blosynthosis, Crown gail tumor, T-DNA, Flasmid
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"Organization and functional analysis of threm T.DNAs from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MAL GAN GANAL 2345-292-303(1992)
-!- CATALYTIC ACTIVITY: INDOLE-3-ACETAMIDE (IAM) = INDOLE-3-
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75.0%; Score 33, DR 1; Length 334; 66.7%; Prod No. 49;
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                                                                          1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                       462 AA.
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                                                                      2; Mismatches
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Plasmid pris4.
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Matches 7, Conserv
                                     Local Similarity
                                                                                                                                                                                                                227 REIAAMCGA 235
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                                                                                                                                             1 RLLAALCGA 9
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Q04557;
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                                                                                                                                                                                                                          Agrobacterium Thiogenes agrocine type plasmid #FiA4, nucleotide sequence analysis and introduction into tobacco plants."; Mol. Plant Microbe Interact. 4:15% 162(1991).
-i. CATALYTIC ACTIVITY: INDOLE-3-ACETAMIDE (IAM) - INDOLE-3-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P25016;
01-MAR-1962 (Fe). 21. Created)
01-MAR-1902 (Fe). 21. Last sequence update)
01-MAR-2002 (Fe). 41. Last annotation update)
Indolescetamide hydrolase (EC 3.5.1.) (IAH) (Indole-3-arctamide
                                                                 Basteria, Frotesbacteria, aipha subdivision, Ehiscbiaecae group;
Rhizobiaceae; Rhizobium.
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Rhizobiaceae; Rhizobium.
                                                                                                                                                                                       Camilleri C., Jouanin L.;
"The TR-DNA region carrying the auxin synthesis genes of the
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PATHWAY: SECOND STEP IN THE BIOSYNTHESIS OF AUXINS FFOM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam: PF01425; Amidase; 1.
PPCSTIE, PS0671, AMIDASE; 1.
HYDROLASE, Awxin biosytulesis, T.DNA, Plasmid.
SEQUENCE 466 AA; 49533 MW; 7375A5994R903995 CHC64;
                                                                                                                                                                                                                                                                                                                                                    -! - SIMILARITY: BELONGS TO THE AMIDASE FAMILY.
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MEDLINE:91329707; FubMcd-1868204;
                                                                                                                                                                         MEDIJINE=92044088; PubMed=1932811;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TPRODO120, Amidase.
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                                  Agredanterium rhizogenes
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                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                     NCBI_TaxID=359;
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                                                    Plasmid pFiA4.
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 hydrolase).
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SEQUENCE FROM N.A.
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      RAMAMANTANA MARAMANA MA
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-:- SIMILARITY- PELONGS TO THE AMIDASE FAMILY.
-:- CAUTION: THE PLASMID PITTMA CAPPIES TWO T-PECIONS, THE TA AND TERRESON, BOTH OF WHICH HAVE AN IAMH GENE, WITH LOW HOMOLOGY BETWEEN THEM. ONLY THE TB-IAMH GENE SERMS TO RE FINALLOWAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21.JUL 1986 (Fel 01, 7:-41.4)
21.JUL-1988 (Pel 01, 13.5 Sequence update)
01.MAR-2002 (Pel 01, 13.5 Innotation update)
Indoleacetamide hydrolase (EC 3.5.1..) (IAH) (Indole-3-acetamide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plasmid Flacts, Plasmid Flackno, and Plasmid Flisgss.
Patteria, Protecharteria, aigha sabdivision, Misobiacoae group;
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SEQUENCE 467 AA, 49441 MW, HARCHADRSHAITON OPC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Barker R.F., Idler K.R., Thompson D V., Kemp. I.D.; "Nucleotide sequence of the T-DNA region from the Agrobanterium tumefaciens octopine Ti plasmid Pril5955."; plant Mol. Biol. 2-335-350(1983)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75.0%; Score 33, DB 1, Length 467, 87.5%; Pred No 66; Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Agrobacterium tumefaciens (strain Ach5), and
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                                                                                                                                                                                                                                                                                 EMBL; X56185; CAA39649 1; ALT_SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PLASMID=pTiA6NC;
MEDLINE=84144041; PubMed=6366736;
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                                                                                                                                                                                                                                                                                                                                                              Pfam; PF01425; Amidase; 1.
PROSITE; PS00571; AMIDASES; 1.
                                                                                                                                                                                                                                                                                            . $5525; HJAGT.
$15961, $15001
rPro, TPRO00120, Amidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sciaky D., Thomashow M.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Agrobacterium tumefaciens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 87.5%
7; Conseivative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rhisobiaceae; Rhisobium.
NCBI_TaxID=176298, 358;
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                                                                                         Klov H., Montoya A., Horodyski F., Livitenstein C., Garfinkel D., Fulker S., Ekores C., Peschos J., Rester E., Sordon M.; Nucleotide sequence of the tims genes of the pilabow octopine Ti Frashid. Two gene plane Livited in plant tunoligenesis.", Proc. Narl Acad Sci. H S.A. RI 1728-1730(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSTEP, PS00571; AMIDASES; 1.
Hydrolase; Auxin biosynthesis; Crown gall tumor; T-DNA; Plasmid.
SEQUENCE 4+7 AA; 45405 MW; JEOTES (P. 2011) (PC64);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Recteria; Profesharteria, gamma subdivision, Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                   , Shu J., Sqer F.M., Schrammeljer B., Hoerkaas P.J.,
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O
                                                                                                                                                                                                                                                                                                                                                                                                        "Octopias type Ti plasmid sequence.",
Sminitted (MAF-2800) to the EMMS/SenkusP/FiRJ dutubases.
-!- CAIALYPIC ACTIVITY: INDOLE-3-ACETAMIDE (IAM) = INDOLE-3-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACETIC ACID (IAA).
-i- PATHWAY: SECOND STEP IN THE BIOSYNTHESIS OF AUXINS PROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75.00, Spore 33, DB 1, hength 467, 87,00, incd. No. 200 at a tive 0, Mismatches 1, Indels
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Submitted (SEP-1995) to the EMML/OceBank/ODBS databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILAKITY: BELÖNGS TÖ THE AMIDASE FAMILY.
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01-NCV-1995 (Pel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last amolation update)
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                                 PLASMID*pTiA6NC;
MEDLINE=84170374; PubMed=6594906;
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Pest Codal Similarity (97-89)50
Transmissaryotive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIP; Krowen; Rray66.
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                                                                                                                                                                                                                                                                                   SHUTHEN'E PROM N.A.
CENCE PROM N.A.
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                                                                                                                                                                                                                                                                                                                     PLASMID=pTiAch5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRYPTOPHAN.
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P46187;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN*IZ / MG1655,
MEDLINE-97426617; PubMed-9278503;
Blattuer F.R. , Punkett G III, Block C A , Perna N T , Rurland V ,
Riley M., Collado-Vides J., Glasner J D., Rode C.K., Maybew G.F.,
Gregor J., Davis N W , Rirkpatrick H.A , Goeden M.A., Pose D.J.,
Mau B., Shao Y.;
"The complete genome sequence of Escherichia coli K-12.";
                                                                                                                                                                                                                                                                                                                                              -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
                                                                                                                                                                                                                                                                                                        Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 72.7%; Score 32; DB 1; Length 159; Best Local Similarity 85.7%; Pred. No. 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                          Nashimoto H., Saito N.;
Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.
                                    Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80 100 POTENTIAL.
101 121 POTENTIAL.
159 AA; 15039 MW; BCFD8970DF6277CU CRC64;
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Transmembrane; Inner membrane; Complete proteome.
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                   Connolly L., de Las Penas A., Gross C.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, U37455; AAC45320.1, -.
EMBL, D64044; BAA10917.1, -.
EMBL, AE000343; AAC75623.1, -.
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                                                                    SECUENCE FROM N.A.
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STRAIN-K12;
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Search completed. September 5, 2002, 15 31 44 Job time: 479 sec

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Page 1

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Copyright (c) 1903 - 2000 Compugen 15d.
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OM protein - protein search, using sw model

Run on: September F, 2002, 15:91:97 : Search time 122.86 Seconds (Without alignments) 12:673 Million cell updates/Sec

Title: US-09-744-804-41 Perfect score: 44 Sequence: 1 PLLAAL™A 9 Scoting table: BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched: 56222 sels, 172954929 ics.lucs

Total number of hits satisfying chosen parameters.

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Minimum DB Seq Tength: V Maximum DB Seq Length: Zöögeggegg Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

sp\_unclassified:\* sp\_invertebrate:\* sp\_vertebrate:\* sp\_bacteriap:\* sp\_archea:\* sp\_bacteria:\* sp\_fungi:\* sp\_human:\* sp\_organelle:\* sp\_rvirus:\* sp\_archeap:\* sp\_rodent:\* sp\_mamma]:\* sp\_plant.\* sp\_virus:\* SPTREMBL\_19:\* sp\_phage:\* sp\_mhc:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is defined by analysis of the test is seen distributed.

## SUMMARIES

	Description	Q9bt19 homo sapien	O9wts3 mus musculu	Q9rlx9 mus musculu	Oshx34 pseudomenas	065601 4411118 4411	O31400 dallus dall	046788 gallus gall	046789 qallus qall	046790 gallus gall	O46791 qallus qall	073901 qallus qall	073904 qallus qall	O9nxy3 homo sapien	OgažyO canlobactor	0910kl streptomyce	Q93h51 streptomyce
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16 C9A8J1 2 C9L0Z3 116 Q9RWVS 5 C9VCP2 2 C9VCP2	4 Q9NXX9 4 Q96BC3 4 Q1 0160 4 Q901PS 1 J9NEKS	4 013905 11 09WTS1 11 09ULR6 16 0072236	00 00	2 Q9RHQ5 2 O9WWB5 2 Q9R695 2 Q9R712 2 O9WWE0	2 194205 2 CHYRAR 3 059907 2 0931.17
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### ALIGNMENTS

Query Match 100.0%; Score 44; DB 4; Length 335; Post Loval Similarity 100.0%; Pred No. 1.6; Malches 9; Conservative 0; Mismatches 0; Indels 0; Caps

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NCBI_Tax ID-10090;
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Q9HX34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Supp
                                                                                           01-NoV-1999 (TreMatrel, 12, Created)
01-NoV-1999 (TreMatrel 12, Test sequence update)
01-DEC-2001 (TreMatrel, 19, Last amnotation update)
MILK FAT GLOHUE GLYCOPROTEIN MEG-ER S (SIMITAR TO MILK FAT GLORUEP-
                                                                                                                                                         Eukaryota, Melazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Enkaryota Merazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sriurognathi, Muridae, Murinae, Mus.
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87,5%; Pred, No. 40;
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                                                                                                                                                                                                                                                                                                                       Submitted (FEB-2001) to the FMRI/GenBank/DDRI databases
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PROSTE; PS01286; PA58C_2; 2.
PCF-Tike dendin: Glycoperation
SEQUENCE 426 AA: 47147 MW. RIB2E4A20629881A CRC64;
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01-DEC-2001 (TrEMBLE). 19, Last annotation update)
MILK FAT GLOBULE GLYCOPROTEIN MEG-E8 LONG FORM.
                                                                                                                                                                                                                                                                           Biochem. Biophys. Res. Commun. 254:522-528(1999).
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FKT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00231; FA58C; 2.
PPOSITE; PS00022; EGF_1; UNRHUMH_2.
PROSITE; PS01186; EGF_2; 2
                                                                                                                                                                                                               STRAIN-HALH/C; TISSHE=MAMMAPY GLA
MEDLINE-99120894; PubMed=9920372;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00754; F5_F8_type_C; 2.
PKINTS: PK00010; EGFBLOOD.
                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000561; EGF-like.
InterPro; IPR001438; EGF_11.
InterPro; IPR000421; FA58_C.
                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPROUI092; HLH_dim.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7; Conservative
                                                                         PPET IMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINAPY;
                                                                                                                                     EGF FACTOR 8 PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                              Ptam; PF00008; EGF; 2.
                                                                                                                                                  Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART: SMOOTBL: PGF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Hest Local Similarity
                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                   5 RLLAALCGA 13
                                                                                                                                                                                                     SECUENCE FROM N.A.
                                                                                                                                                                                NCB1_Tax1D*10090;
1 RULAALOGA 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 RVLAALCG 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 RELAMENCE R
           Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                           HSSP; P00740;
                                                                                    Q9WTS 3;
                                                                         O'SWES 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09R1X9;
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                                                               COWTES
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STRAIN-BALLKC, TISSUE-MAMMARY GLAND, MEDLINE-99120894; PubMed 9920772; Oshima K. Acki N. Negi M. Kishi Matsuda T.; ILactation-dependent expression of an mRNA splice variant with an exon for a multiply O-glycosylated domain of mouse milk fat qlobule glycoprotein MEG-E8.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stover C.K., Pham X.-Q.T. Erwin A.L., Mizoquchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnaqle W.D., Kowalik D. Lagrou M., Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Endy L.L., Coulter S.N., Folger K.R., Kas B., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen L.T., Heizer J., Saier M.H., Hancock R.E.W., lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PAOI, an opportunistic pathogen."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      daps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hacteria: Protecbacteria, gamma subdivision, Pseudomonadaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84.1%; Score 37; DB 11; Length 463; 87 5%; Pred. No. 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      o, indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P719P2BE090P6427 CPC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-WAR-2001 (TrEMBLiel. 16, Last sequence update)
C1-OCF-2001 (TrEMBLiel. 18, Last annotation update)
                                                                                                                                                                                                           Biochem, Biophys, Pcc. Commun. 254:522-528(1999).
- SIMILAPITY: CONTAINS 2 PS/R TYPF C DOMAINS.
- BMBL, AB021130: BAA35180.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <u>.</u>.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1, Mismatches
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EXPOTHELICAL protein, Complete proteome. 
SEQUENCE: 143 AA; 15937 MW; 884580660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART: SMOOIBL: EGF: 2.
SMART: SMOOIBL: EGF: 2.
SMART: SMOOIBL: FASRC: 2.
PROSITE: PSOIDSE: FGF: 2.
PROSITE: PSOIDSE: FASRC: 1: 2.
FROSITE: PSOIDSE: FASRC: 1: 2.
EGF: Hike domain: Glycoprotein.
SEQUENCE: 463 AA: 51269 MW; F719F2
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STRAIN-AICC 15692 / PAO1;
MEDLINE-20437337; Pubmed 10984043;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00754; F5_F8_type_C; 2. PRINTS; PR00010; EGFR100D.
                                                                                                                                                                                                                                                                                                         HSSP; P00740; IEDM.
InterPro; IPR000561; FGF-Uike.
                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001438; EGF_T1.
InterPro; IPP000421; FA58_C.
InterPro; IPP001092; HLH_dim.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pseudomonas aeruginosa.
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SEQUENCE FROM N.A.
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046788;
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-i- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICPOSIOPHILIN) (PY SIMILARITY).
EMBL: S78682: AA834945.1, -...
                                                                                                                                                                                                                            MEDLINF-94347411; PupMod-7621880;
Fulton T.E., Thackor P.L., Racca I.B., Bant H.D.,
"Functional analysis of axian class I (BFIV) alymoproteins by epitope
tagging and mutagenesis in vitro.";
Eur. J. Immuno! 25:22669-2078(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathan, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                   Galius gallus (Chicken).
Bukaryota: Metassa; Chordata, Craniata, Vertebrata, Euteleostumi;
Archosauria: Aves; Neognathae: Gallitormes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                firEE 1997 (TriMRLES). 02, Created)
01-EEB-1997 (TrEMBLES). 02, Last sequence update)
01-DEC-2001 (TrEMBLES) 19, Last annotation update)
MAJOR_HISTOCCMPATIBILITY COMPLEX CLASS 1 GLYCOPROTEIN HAPLOTYPE B21
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O
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                                                                                                                                                                                                                                                                                                                          Submitted (JAN-1998) to the FMR!/ManBank/PPR' databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glycoprofein; MHC; Transmembrane.
SEQUENCE 355 AA; 38960 MW; A751A09946D94EE9 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MATOR CLASS I GLYCOPROTEIN PRECURSOR.
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                                                                              FFT,
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InterPro: IPR003506; Ig_MHC.
InterPro: IPR001039; MHC_I.
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Pfam; PF00129; MHC_I; 1.
ProDom; PU000050; MHC_I: 1
SMARI; SM00407; IGcl; 1.
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                                                                              PERTURARY
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                SEQUENCE FROM N.A.
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      1 RLLAALCGA 9
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                                                                                                                                            HFIV21 OR B-FIV
                                                                                                                                                                                                                                                                                                                 Hunt H.D.;
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Gallus gallus (Chicken).
Eukaryota, Metazoa, Chordata, Craniata, Vertekrata, Euteleostomi;
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae;
             STRAIN-CB: TISSUE-BURSA;
Wallay H., Avita D., Riegert F., Salomonsen J., Vilbois F., Wiles M.,
Kaufman J.;
                                                                                                              sample, and resistance to intentious
                                                                                  "Peptide motils for the dominantly expressed class implecule of the chilibra Major bistochampalibility complex and resistance to intectious pathogens."
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STRAIN 1555 BS CONCONIC:
BIRLING 9821119; Pubmed 9553152;
Hunt H.D., Fullon J.B.;
"Analysis of polymorphisms in the major expressed class I lovus (B-FIV) of the chicken."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81.8%; Score 36; DB 7; Lenath 355;
87.5%; Pred. No. 52;
ative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clyoprofess, Signal, Transmembrane.
Signal 1 21 POTENTIAL.
CHAIN 22 355 MAJOR CLASS I GLYCOPROTEIN.
SPORTEN SET AS 1870 MM, DSP987452F18467A DRUG4.
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19, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSTTE: PSO0290; IG_MHC; UNENGWN_1
                                                                                                                                                                                                                                                                                                       InterPro; IPR003597; 19_c1.
InterPro; IPR003006; 19_MHC.
                                                                                                                                                                                                                                                                                                                                              InterPro; iPR001039; MHC_I.
Pram; PF00047; iq: 1.
Priam; pF00129; MHC_I; 1.
Probom: PP000050; MHC_I; 1.
SMART; SM00407; IGG1; 1.
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InterPro: IPR003006; IQ_MHC.
InterPro; IPR001039; MHC_l.
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Pfam, PF00129; MHC_1; 1.
ProDom; PD000050; MHC_1: 1.
SMARI; SM00407; IGC1; 1.
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MHC CLASS I GLYCOPROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Hest Local Similarity
SEQUENCE FROM N.A.
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SMART; SM00407;
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Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Analysis of polymorphisms in the major expressed class I locus (B-FIV) of the chicken.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazea; Chordata; Craniata, Vertebrata; Euteleostomi,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IMMUNE SYSTEM (BY SIMILARITY).
-1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN) (BY SIMILARITY).
                                                                                             81.8%; Score 36; DB 7; Longth 355; 87.5%; Pred. No. 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81.8%; Score 36; DB 7; Length 355; 87.5%; Pred. No. 52;
                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                  355 AA; 38953 MW; F7BCF9BB8F6158ZE CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel. 06, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
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(TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                  355 AA
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1; Mismatches
                                                                                                                                       1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                     01-JUN-1998 (TrEMBLrel, 06, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-1998 (TrEMBLrel, 06, Created)
                                                                                                                                                                                                                                                                                                                                  PRT;
PROSITE; PS00290; IG_MHC; UNKNOWN_1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-1515 R2 CONDENIC:
MEDLINE-98221119; PubMed-9553152;
Hunt H.D., Fulton J.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunogenetics 47:456-467(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF013492; AACÎ7589.1;
InterPro; IPR003597; Iq_c1.
InterPro; IPR003006; Iq_MHC.
InterPro; IPR001039; MHC_I.
                 Glycoprotein; Transmembrane,
SEQUENCE 355 AA; 38953 MW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ProDom; PD000050; MHC_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glycoprotein; Transmembrane.
                                                                                                                                           7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                      MHC CLASS I GLYCOPROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7; Conservative
                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MHC CLASS I GLYCOPROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ptam; PF00047; ig; 1.
Ptam; PF00129; MHC_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B-FIV.
Gallus qallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00407; IGr1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                     Hest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SECUENCE FROM N.A.
                                                                                                                                                                                                          NCB1_Tax1D-9031;
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                                                                                                                                                                                  2 LLAALCGA 9
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01-DEC-2001
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                                                                                                    Ouerry Match
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-i- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM (BY SIMILARITY).
-i- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunogenetics 47:456-467(1998).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM (BY SIMILARITY).
Archosauria, Aves, Neoquathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Archosauria, Aves, Neognathae, Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                       "Analysis of polymorphisms in the major expressed class I locus (B-FIV) of the chicken.";
Immunogenetics 47:456-467(1998).
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Hunt H.D., Fulton J.E.;
"Analysis of polymorphisms in the major expressed class i locus (B-FIV) of the chicken.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata: Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 - SURUNIT - PIMER OF ALPHA CHAIN AND A HETA CHAIN (BETA-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81.8%; Score 36; DB 7; Length 455; 87.5%; Pred. No. 52;
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                           MICROGLOBULIN) (BY SIMILARITY).
EMBL; AF013494; AAC17591.1; -.
InterPro; 1PP003597; 19_c1.
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EMBL; AF013495; AAC17592.1; -.
HSSP; P13599; 3FRU.
                                                                                                                                                                 MEDEINE-98221119; PubMcd-9553152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; 1PR003006; 1g_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00129; MHC_I; 1,
ProDom; PD000050; MHC_I; 1.
SMART; SMO407; IGC1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glycoprotein; Transmembrane.
SEQUENCE 355 AA; 39398 MV
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InterPro; IPR003006; Ig_MHC.
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Pfam; PF00129; MHC_I; 1.
ProDom; PD000050; MHC_I; 1.
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                                                                                                                                         CONCENIC;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gallus gallus (Chicken).
                                                                                                                                                                                               Hunt H.D., Fulton J.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00047; ig; 1.
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Matches 7; Conserv
                                                                                                           SEQUENCE FROM N.A.
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                                                  NCBI_TaxID-9031;
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Guillemot E., Rillaut A., Pourquie O., Behar G., Chausse A.M.,
Foorob R., Kreibich G., Aufliay G.;
"A molecular map of the chicken major histocompatibility complex: the
class II beta genes are closely linked to the class I genes and the
                                                                                                                                                                                                                                                                                                                                                                                                                             Gabs
                                                                   Caps
                                                                                                                                                                                                                                                                                                                                                                                   FEQUENCE FROM N A Milne S., Kaufman J., Reck S ; Milne S., Kaufman J., Beck S ; "DNA sequencing and analysis of the chicken major histocompatibility
                                                                                                                                                                                                                                           Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosautia, Ares, Neudrathae, Inlificines, Fhazianidae, Thasianidae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81.8%; Score 36; DB 13; Length 355;
87.5%; Pred. No. 52;
                                            81.8%; Score 36; DB 7; Length 355;
87.5%; Pred. No. 52;
                                                                 0; Indels
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              SKRZB7709AKANFH CPC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38695 MW; 648D24F592FD98AB CRC64;
                                                                                                                                                                                         07, Last sequence update)
19, Last annotation update)
                                                                                                                                                           PRT; 355 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
                                                      Pred. No. 52;
; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FPT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MICROGLOBULIN) (BY SIMILARITY)
Glycoprotein; Transmembrane, scoursers 355 AA; 34170 MW:
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HSSP; Q30201; 1A62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003597; [q_c1.]
InterPro; IPR003006; [q_MHC.]
InterPro; IPR001039; MHC_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transmembrane.
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                                                                                                                                                                                                                                                                                                                                                         nuclear organižer.";
EMBO J. 7:2775-2785(1988).
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                                                                  Conservative
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Pfam; PF00129; MHC_I; 1.
                                                                                                                                                          PRELIMINARY;
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                                                                                                                                                                                                              B LOCUS F ALPHA CHAIN 2.
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                                                                                                                                                                                                                                 Gallus gallus (Chicken)
                                                                                                                                                                              01-AUG-1998 (TEFMRIFAL
01-AUG-1998 (TERMRIFE).
                                                                                                                                                                                                   01-DEC-2001 (TrEMPLIFE)
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                                Onory Match
Best Local Similarity
7; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            355 AA;
                                                                                                                                                                                                                                                                                             SEUVENCE FROM N.A.
                                                                                                        12 L.I.AAVCGA 19
                                                                                                                                                                                                                                                                          NCBI_TaxID=9031;
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073904
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MEDINE-89030642; PubMed-3141149;
Guillemot F., Billaut A., Pourquie O., Behar G., Chausse A.M.,
Zoorob R., Kreibich G., Aufray C.;
"A molecular map of the whirken major historompatibility complex; the
class II beta genes are closely linked to the class I genes and the
                                                                                                                                                                                        Eukaryota; Motazoa; Chordata; Graniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Gallitormes; Phasianidae; Phasianinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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"DMA sequencing and analysis of the chicken major histocompatibility
concless"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ohara O., Kikuno B., Nagase T., Okumura K.;
"The nucleotide sequence of a loug conA clone isolated from human
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Mammalia: Butheria: Primates, Catarrhini, Hominidae: Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
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Conscrutive 1; Mismatches 0: 104010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IMMUNE SYSTEM (BY SIMILARITY).
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BELA CHAIN (BETA-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schmitted (LEB 1630) to the LMKG becausank/DOBJ databases.
EMBL: AK000002: BAA92227.1: -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39200 MW; D8D987452F18467A CRC64;
                              of-APY-1999 (TrEMBLEOL 19, 1981 surperce update)
01-DEC-2001 (TrEMBLEOL 19, Last annotation update)
B LOCUS F ALPHA CHAIN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01 OCT 2000 (TrEMBLrel, 15, Last sequence update)
01-DEC-2001 (TrEMBLrel, 19, Last annotation update)
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01-AUG-1998 (TrEMBLrel, 07, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE: PS00290; IG_MHC; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MICKOGLOBULIN) (BY SIMIFARITY).
EMBL: AL023516; CAA18972.1; '.
HSSP; P13599; 3FRU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glycoprotein; Transmembrane,
SRQUENCE 355 AA; 39200 MW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FLJ00002 PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Print, Pr00129; MHC_I; 1.
Protom; PD000050; MHC_I; 1.
SMAKT; SM00407; IGC1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      catestro; srk003006; iq_MHC
interPro; 1PR001039; MHC_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBO J. 7:2775-2785(1988).
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                                                                                                                                                             Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ptam; PF00047; ig; l.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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Streptomyces coelicolor.

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WEDLINE-21173698; PubMed 11259447;

Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,

Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,

Potocka I., Nelson W.C., Nowton A., Stephons C., Phadke N.D., Ely B.,

DeBoy W.T., Doodson R.J., Durkin A.S., Gwinn M.J., Haff D.H.,

Kolonay I.F., Smill T. Crawen M.B., Rhouri H., Shetty J., Berry K.,

Illterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,

Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;

"Complete genome sequence of Caulobacter crescentus.";

Proc. Natl. Acad. Sci. U.S. A. 98:4136-4141(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                     81.8%; Score 36; DB 4; Length 1513; 77.6%; Pred. No. 2e+02; Live 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79.5%; Score 35; DB 16; Length 230;
87.5%; Pred. No. 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                   SEQÜENCE 1513 AA; 163831 MW; FBAA7AABDE68AE3C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein; Complete proteome.
SEQUENCE 230 AA; 24454 MW; DEB4CD3F28E54BD1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-07T-2000 (TrEMBLrel, 15, Created)
01-07T-2000 (TrEMBLrel, 15, Last sequence update)
01-0FC-2001 (TrEMBLrel, 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2001 (TrEMBLrel, 17, Created)
01 JUN-2001 (TrEMBLrel, 17, Last sequence update)
01-DEC-2001 (TrEMBLrel, 19, Last annotation update)
                                                                                                                 SMART, SM00382, AAĀ, 2.
PROSITE: PSO0211: ARC_TPANSPORTER; DNKNOWN_?
AIP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                              230 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
            InterPro; IPR001593; AAA.
InterPro; IPR001140; ABC_transporter_them.
                                                 InterPro; IPR003439; ABC_transportr.
InterPro; IPR001687; ATP_GTP_A.
                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                              Piam; PF00664; ABC_mombrano; 2
Pfam; PF00005; ABC_tran; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYPOTHETICAL PROTEIN CC1589.
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Rest Local Similarity 77.05
Fest Local Similarity 77.05
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                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caulobacter crescentus.
HSSP; P13569; INBD.
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                                                                                                                                                                                                                                                                                                                                            24 RLLAQLCGS 32
                                                                                                                                                                                                                                                                                                           1 RELABLCGA 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID 69394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 LLAALCGA 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Caulobacter.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          O9L0K1
O9L0K1;
                                                                                                                                                                     NON TER
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"A set of ordered cosmids and a detailed genetic and physical map for
the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
EMBL: AL161691; CARRH855.11: -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
Bactéria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomysetales, Streptomycineae, Streptomycetaceae; Streptomyces.
NCBI_Tax1D=1902;
                                                                                                                                                                                                                                                                                    Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J.,
Kinashi H., Hopwood D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                            79.5%; Score 35; DR 2; Length 611; 87.5%; Pred. No. 1.30.02;
                                                                                                                                                                      STRAIN=A3(2);
Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
Sobmitted (MAR-2000) to the FMRI/GenBank/AnnHl databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                        Seeger K.J., Harris D.,
Submitting (MAR-2009) to the EMBE, Genfamb_DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                 61744 MW; 8F959720773AEDF9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: September 5, 2002, 15:31:08
                                                                                                                                                                                                                                                      STRAIN=A3(2);
MEDLINE=97000351; Pubmcd-8843436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 87.59
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                              Ptum: PF02687; DUF214;
SEQUENCE 611 AA; 61
                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                            SHORINGE FROM N. A.
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                                                                                         STRA1N=A3(2);
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